

PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
 XX disorder, or ataxia.
 PS Claim 4; SEQ ID NO 6620; 417pp; English.
 XX
 CC The present invention relates to an antisense compound targeted to a
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The
 CC compound and composition are useful for treating a disease or condition
 CC associated with Nav1.3, e.g. pain including but not limited to
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate
 CC headache; seizure disorder such as childhood seizure disorder, including
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
 CC sequence represents a chimeric phosphorothioate oligonucleotide with
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
 CC human Nav1.3 expression, the oligonucleotides are designed to target
 XX different regions of the human Nav1.3 RNA.
 SQ Sequence 20 BP; 12 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3260 GATATTTTATTTGCTT 3275
 Db |||||
 16 GATATTTTATTTGCTT 1
 RESULT 2081
 ID ADN48306
 ID ADN48306 standard; DNA; 20 BP.
 XX
 AC ADN48306;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human Jun N-terminal kinase 1 (JNK1) oligonucleotide #17.
 XX
 KW Human; Jun N-terminal kinase; JNK; Jun N-terminal kinase 1; JNK1;
 KW hyperproliferative disease; cell cycle progression;
 KW protein phosphorylation; tumour growth; cancer; apoptosis;
 KW prostate cancer; inflammation; fibrosis; fibrotic disease; scarring;
 KW peritoneal adhesion; lung fibrosis; conjunctival scarring; cytostatic;
 KW antiinflammatory; vulnery; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2004029823-A1.
 XX
 PD 12-FEB-2004.
 XX
 PF 15-JAN-2003; 2003US-00345444.
 XX
 PR 13-AUG-1997; 97US-00910629.
 PR 07-AUG-1998; 98US-00130616.
 PR 07-APR-1999; 99US-00287796.
 PR 15-SEP-1999; 99US-00396902.
 PR 31-JAN-2001; 2001US-00774809.
 XX
 PA (MCKA/) MCKAY R.
 PA (DEAN/) DEAN N M.
 PA (MONI/) MONIA B P.
 PA (NERO/) NERO P S.
 PA (GAAR/) GAARDE W A.
 XX
 PI Mckay R., Dean NM, Monia BP, Nero PS, Gaarde WA;
 XX WPI; 2004-168941/16.
 DR
 XX New oligonucleotides, which specifically hybridizes with Jun N-terminal

PT kinase protein, useful in diagnosing or treating inflammation, fibrosis
 XX or a fibrotic or hyperproliferative disease or condition.
 PS Example 3; SEQ ID NO 17; 71pp; English.
 XX
 CC The invention relates to an oligonucleotide comprising 8-30 nucleotides
 CC connected by covalent linkages, where the oligonucleotide has a sequence
 CC specifically hybridizable with a nucleic acid encoding a Jun N-terminal
 CC kinase (JNK) protein and modulates the expression of the JNK protein. The
 CC invention also relates to a pharmaceutical composition comprising the
 CC oligonucleotide(s) or its bioequivalent and a pharmaceutical carrier, a
 CC method of treating an animal having, suspected of having or prone to
 CC having a hyperproliferative disease, a method of modulating the
 CC expression of a JNK protein in cells or tissues, a method of modulating a
 CC cell cycle progression, phosphorylation of a protein phosphorylated by a
 CC JNK protein and expression of a cellular protein that promotes one or
 CC more metastatic events in cultured cells or the cells of an animal, a
 CC method of inhibiting the growth of a tumour in an animal, a method of
 CC inducing apoptosis in a cell, a method of treating a human having a
 CC disease or condition characterised by a reduction in apoptosis and a
 CC method of treating an animal having a disease or condition associated
 CC with a JNK protein. The oligonucleotide and composition are useful in
 CC diagnosing or treating a disease or condition characterised by a
 CC reduction in apoptosis (e.g. prostate cancer), a disease or condition
 CC associated with a JNK protein (e.g. inflammation, fibrosis), a fibrotic
 CC disease or condition (e.g. scarring, peritoneal adhesions, lung fibrosis,
 CC conjunctival scarring) or a hyperproliferative disease or condition (e.g.
 CC cancer), or in inhibiting the growth of a tumour. This sequence
 CC represents a human JNK1 oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1060 GCGTCATCAGCTCCA 1075
 Db |||||
 5 GCATCCATGAGCTCCA 20
 RESULT 2082
 ID ADN89289
 ID ADN89289 standard; DNA; 20 BP.
 XX
 AC ADN89289;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE P16DF PCR primer #1.
 XX
 KW P16DF; primer; ss; nucleic acid label; hybridization assay;
 KW primer extension; terminal transferase addition; ligation; end labelling;
 KW PCR; nick translation labelling; reverse transcription;
 KW Southern blotting; Northern blotting; enzyme linked immunosorbant assay;
 KW ELISA; arrays; SKYS; cloning; transcription; abortive transcription;
 KW sequencing.
 XX
 OS Synthetic.
 XX
 PN US2004054162-A1.
 XX
 PD 18-MAR-2004.
 XX
 PF 29-APR-2003; 2003US-00425037.
 XX
 PR 30-OCT-2001; 2001US-00984664.
 PR 29-OCT-2002; 2002WO-US034419.
 XX
 PA (HANN/) HANNA M M.
 XX
 PI Hanna MM;
 XX

DR WPI; 2004-281628/26.
 XX Labeling nucleic acid which is used in hybridization assays, primer
 PT extension, terminal transferase additions, involves incorporating 8-S-
 PT substituted purine or 5-S-substituted pyrimidine analog into nucleic
 PT acid.
 XX
 PS Disclosure; SEQ ID NO 1; 104pp; English.
 XX
 CC The invention relates to a method of labelling a nucleic acid which
 CC involves incorporating at least one nucleotide analogue into a nucleic
 CC acid, where the analogue comprises an 8-S-substituted purine or 5-S-
 CC substituted pyrimidine analogue. The method is useful for labelling a
 CC nucleic acid. The method is useful for detecting a second nucleic acid of
 CC interest. The method is useful for labelling a nucleic acid which is used
 CC in hybridization assays, primer extension, terminal transferase
 CC additions, ligation, end labelling, PCR, nick translation labelling,
 CC reverse transcription, Southern blotting, Northern blotting, enzyme
 CC linked immunosorbent assay (ELISA), arrays, SKVE, cloning, therapeutic
 CC abortive transcription, sequencing, diagnostic techniques, therapeutic
 CC applications, and treatment and prevention of diseases and conditions.
 CC The labelled nucleic acids are useful in assessing methylation state of
 CC specific genes, detecting presence of known genetic mutations, detecting
 CC mRNA expression levels, detecting presence of pathogenic organisms, and
 CC detecting and amplifying proteins. The present sequence represents a
 CC PL6DF PCR primer.
 XX
 SQ Sequence 20 BP; 1 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1209 TGGGAGGGCTGCTTC 1224
 DB 5 TGGCGAGGGCTGCTTC 20
 RESULT 2083
 ADM14899/c
 ID ADM14899 standard; DNA; 20 BP.
 XX
 AC ADM14899;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1086.
 XX
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
 KW microsomal prostaglandin E2 synthase inhibitor; cytotostatic; antidiabetic;
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
 KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
 KW reperfusion injury; ophthalmic disorder; immunological disorder;
 KW cardiovascular disorder; neurological disorder; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 FT modified_base 16..20
 FT /*tag= c

FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 XX
 PN W02004028458-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 25-SEP-2003; 2003WO-US030374.
 XX
 PR 25-SEP-2002; 2002US-0413549P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Gierse JK;
 XX
 DR WPI; 2004-305094/28.
 XX
 CC New antisense compound, having a sequence targeted to a nucleic acid
 CC encoding mPGES-1, useful for preparing a composition for treating e.g.,
 CC inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
 CC ischemia.
 XX
 PS Claim 4; SEQ ID NO 1086; 132pp; English.
 XX
 CC The present sequence represents a chimeric antisense oligonucleotide
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
 CC human mPGES-1 gene is located on chromosome 9, more specifically to
 CC 9q34.3. The present invention also describes: (1) antisense compounds,
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
 CC mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
 CC inhibits its expression; (2) a method of inhibiting the expression of
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
 CC antisense oligonucleotides and antisense compounds have cytostatic,
 CC antidiabetic, immunomodulator, cardiant, neuroprotective,
 CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
 CC ophthalmological, immunomodulatory, and cardiovascular activities, and can
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
 CC can be used for preparing a composition for treating a disease or
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
 CC ophthalmic, immunological, cardiovascular or neurological disorder.
 XX
 SQ Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2316 TCTGTGTGTGTGTGTG 2331
 DB 16 TCCGTGTGTGTGTGTG 1
 RESULT 2084
 ADM72001/c
 ID ADM72001 standard; DNA; 20 BP.
 XX
 AC ADM72001;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human glucose transporter-4 antisense oligonucleotide #42.
 XX
 KW ss; human; antisense therapy; glucose transporter-4;
 KW hyperproliferative disorder; probe.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= Other


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FT      /note= "Phosphorothioate backbone. All cytidines are 5-
FT      methylcytidines"
FT      modified_base 1. .5
FT      /tag= a
FT      /mod_base= Other
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT      modified_base 16. .20
FT      /tag= c
FT      /mod_base= Other
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX      US2004101848-A1.
XX      27-MAY-2004.
XX
XX      23-NOV-2002; 2002US-00303266.
XX
XX      23-NOV-2002; 2002US-00303266.
XX      (ISIS-) ISIS PHARM INC.
XX      Ward DT, Borchers AH, Dobie KW;
XX      WPI; 2004-399677/37.
XX
XX      New antisense oligonucleotides for modulating Glucose transporter-4
XX      expression, useful for diagnosing, preventing or treating conditions
XX      associated with the transporter's expression e.g. hyperproliferative
XX      disorders.
XX
XX      Example 15; SEQ ID NO 54; 54pp; English.
XX
XX      The invention relates to antisense oligonucleotides targeted to a nucleic
XX      acid molecule encoding Glucose transporter-4. The oligonucleotides
XX      specifically hybridise with the nucleic acid molecule encoding Glucose
XX      transporter-4 and inhibit the expression of Glucose transporter-4. The
XX      antisense oligonucleotide is useful for inhibiting the expression of
XX      Glucose transporter-4 in cells or tissues to prevent or treat diseases
XX      associated with their expression, such as a hyperproliferative disorder.
XX      In addition, the compound is used for diagnostics, prophylaxis, or as
XX      research reagents or kits. The present sequence represents a human
XX      glucose transporter-4 antisense oligonucleotide of the invention.
XX
XX      Sequence 20 BP; 5 A; 5 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX      Query Match 0.4%; Score 14.4; DB 1; Length 20;
XX      Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX      Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      QY 2107 CCCAGCTCCAGCTCCT 2122
XX      Db ||| ||||| |||||
XX      18 CCTGCTCCAGCTCCT 3
XX
XX      RESULT 2085
XX      ADN72077
XX      ID ADN72077 standard; DNA; 20 BP.
XX
XX      AC ADN72077;
XX
XX      DT 12-AUG-2004 (first entry)
XX
XX      DE Human glucose transporter-4 antisense oligonucleotide #118.
XX
XX      ss; human; antisense therapy; glucose transporter-4;
XX      hyperproliferative disorder; probe.
XX
XX      OS Homo sapiens.
XX
XX      PN US2004101848-A1.
XX
XX      PD 27-MAY-2004.
XX
XX
XX      Query Match 0.4%; Score 14.4; DB 1; Length 20;
XX      Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX      Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      QY 2107 CCCAGCTCCAGCTCCT 2122
XX      Db ||| ||||| |||||
XX      18 CCTGCTCCAGCTCCT 3
XX
XX      RESULT 2086
XX      ADP82143/C
XX      ID ADP82143 standard; DNA; 20 BP.
XX
XX      AC ADP82143;
XX
XX      DT 26-AUG-2004 (first entry)
XX
XX      DE Human DR1-associated protein 1 antisense oligonucleotide ISIS #171291.
XX
XX      KW DR1-associated protein 1; DRAP1; negative cofactor 2 alpha; NC2-alpha;
XX      developmental disorder; therapy; human; antisense;
XX      phosphorothioate backbone; ss.
XX
XX      OS Homo sapiens.
XX
XX      OS Synthetic.
XX
XX      Key Location/Qualifiers
XX      modified_base 1. .20
XX      /tag= b
XX      /mod_base= OTHER
XX      /note= "Phosphorothioate backbone where all cytidines are
XX      5-methyl cytidines"
XX      modified_base 1. .5
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "2'-methoxyethyl nucleotides"
XX      modified_base 16. .20
XX      /tag= c
XX      /mod_base= OTHER
XX      /note= "2'-methoxyethyl nucleotides"
XX
XX      US2004110703-A1.

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PD 10-JUN-2004.
XX
PF 10-DEC-2002; 2002US-00317279.
XX
XX 10-DEC-2002; 2002US-00317279.
PR 10-DEC-2002; 2002US-00317279.
XX
XX (ISIS-) ISIS PHARM INC.
PA Chiang M, Dobie KW;
XX
XX WPI; 2004-440383/41.
DR
XX New compounds, particularly oligonucleotides targeted to a nucleic acid
PT encoding DRI-associated protein 1, useful for treating diseases
PT associated with DRI-associated protein 1, e.g. developmental disorders.
XX
XX Example 15; SEQ ID NO 22; 33pp; English.
PS
XX The present sequence is directed to antisense oligonucleotides targeted
CC to DRI-associated protein 1 [also known as DRAP1 and negative cofactor 2
CC alpha (NC2-alpha)] and which modulates to the expression of DRI-
CC associated protein 1. The invention is useful for treating a disease or
CC condition associated with DRI-associated protein 1 such as a
CC developmental disorder. The present sequence is human DRI-associated
CC protein 1 antisense oligonucleotide. This sequence is used in the
CC exemplification of the invention.
XX
XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1545 CTTCAAGGACCTGGTG 1560
DB 16 CTTGAAGGACCTGGTG 1
RESULT 2087
ADP82172
ID ADP82172 standard; DNA; 20 BP.
XX
XX ADP82172;
XX
XX 26-AUG-2004 (first entry)
DT
XX Human DRI-associated protein 1 target oligonucleotide #4.
DE
XX DRI-associated protein 1; DRAP1; negative cofactor 2 alpha; NC2-alpha;
XX developmental disorder; therapy; human; ss.
XX
XX Homo sapiens.
XX
XX US2004110703-A1.
PN
XX 10-JUN-2004.
XX
XX 10-DEC-2002; 2002US-00317279.
PF
XX 10-DEC-2002; 2002US-00317279.
PR
XX (ISIS-) ISIS PHARM INC.
XX
XX Chiang M, Dobie KW;
XX
XX WPI; 2004-440383/41.
DR
XX New compounds, particularly oligonucleotides targeted to a nucleic acid
PT encoding DRI-associated protein 1, useful for treating diseases
PT associated with DRI-associated protein 1, e.g. developmental disorders.
XX
XX Example 15; SEQ ID NO 51; 33pp; English.
XX

CC The present sequence is directed to antisense oligonucleotides targeted
CC to DRI-associated protein 1 [also known as DRAP1 and negative cofactor 2
CC alpha (NC2-alpha)] and which modulates to the expression of DRI-
CC associated protein 1. The invention is useful for treating a disease or
CC condition associated with DRI-associated protein 1 such as a
CC developmental disorder. The present sequence is human DRI-associated
CC protein 1 target oligonucleotide. This sequence is used in the
CC exemplification of the invention.
XX
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1545 CTTCAAGGACCTGGTG 1560
DB 5 CTTGAAGGACCTGGTG 20
RESULT 2088
ADO39459
ID ADO39459 standard; DNA; 20 BP.
XX
XX ADO39459;
AC
XX 26-AUG-2004 (first entry)
DT
XX Novel human CD25 antibody-related PCR primer SeqID42.
DE
XX monoclonal antibody; CD25; IL-2 binding; immunosuppressive;
XX antiinflammatory; cytostatic; gene therapy; transplant rejection;
KW graft-versus-host disease; autoimmune; inflammatory disease;
KW inflammatory skin disorder; hyperproliferative skin disorder;
KW lymphoid neoplasm; PCR; primer; ss; human.
XX
XX Homo sapiens.
OS
XX WO2004045512-A2.
PN
XX 03-JUN-2004.
PD
XX 14-NOV-2003; 2003WO-US036126.
PF
XX 15-NOV-2002; 2002US-0426690P.
PR
XX (GENM-) GENMAB AS.
PA
XX Schuurman J, Havenith CEG, Parren P, Van De Winkel JGJ;
PI Williams DL, Petersen J, Baadsgaard ODMS;
PI
XX WPI; 2004-420514/39.
DR
XX New human monoclonal antibody that binds to human CD25 and inhibits IL-2
PT binding to CD25, useful in treating or preventing e.g., autoimmune or
PT inflammatory disease or hyperproliferative skin disorder or lymphoid
PT neoplasm.
XX
XX Example 2; SEQ ID NO 42; 114pp; English.
PS
XX This invention relates to a novel isolated human monoclonal antibody
XX which binds to human CD25 and inhibits IL-2 binding to CD25. The
CC invention may be useful for the development of compounds with an
CC immunosuppressive, antiinflammatory or cytostatic activity whilst the
CC disclosed sequences may be useful for gene therapy. The monoclonal
CC antibody is useful in treating or preventing a disorder involving cells
CC expressing CD25, for example transplant rejection, graft-versus-host
CC disease, autoimmune or inflammatory disease, inflammatory or
CC hyperproliferative skin disorder or lymphoid neoplasm. The present
CC sequence is that of a PCR primer which was used for amplification of a
CC region of sequence encoding part of a novel human CD25 antibody and which
CC was used in the exemplification of the invention.
XX

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SQ Sequence 20 BP; 3 A; 3 C; 8 G; 4 T; 0 U; 2 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGTGAGGC 872
:|||||:|||||:
Db 1 SAGGTGCAGCTGKTGGAGTC 20

RESULT 2089
ADP49595
ID ADP49595 standard; DNA; 20 BP.
XX
AC ADP49595;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human BAF53 antisense oligonucleotide ISIS280388.
XX
KW Human; ss; antisense; chromatin; BAF complex; BRG1/brm-associated factor;
KW BAF53; BRG1-associated factor 53kDa; cancer; tumour;
KW actin-related protein; hyperproliferative disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
XX
PN US2004110147-A1.
XX
PD 10-JUN-2004.
XX
PF 09-DEC-2002; 2002US-00316243.
XX
PR 09-DEC-2002; 2002US-00316243.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW, Jain R;
XX
WPI; 2004-440336/41.
XX
New oligonucleotide compound that inhibits expression of BAF53, useful
for preparing a composition for treating hyperproliferative disorder,
e.g. cancer.
XX
Example 15; SEQ ID NO 82; 72pp; English.
XX
The invention relates to a compound, having a sequence comprising 8-80 bp
targeted to a nucleic acid encoding BAF53 (a member of the BAF complex
(BRG1/brm-associated factor), BRG1-associated factor 53kDa which is an
actin-related protein), specifically hybridises with the nucleic acid
encoding BAF53 comprising 28001-bp sequence (derived from human
chromosome 3) and inhibits expression of BAF53, i.e. an antisense
oligonucleotide. Also included are inhibiting the expression of BAF53 in
cells or tissues, screening for a modulator of BAF53, a diagnostic method
for identifying a disease state, a kit or assay device comprising the
compound and treating an animal having a disease or condition associated
with BAF53. The oligonucleotide compound is useful for preparing a

SQ Sequence 20 BP; 7 A; 8 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3069 CCACACCCCAACACTT 3084
|||||:|||||:
Db 4 CCACATCCCAACACTT 19

RESULT 2090
ADP49668/C
ID ADP49668 standard; cDNA; 20 BP.
XX
AC ADP49668;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human BAF53 antisense oligonucleotide target region #58.
XX
KW Human; ss; antisense; chromatin; BAF complex; BRG1/brm-associated factor;
KW BAF53; BRG1-associated factor 53kDa; cancer; tumour;
KW actin-related protein; hyperproliferative disorder; chromosome 3.
XX
OS Homo sapiens.
XX
PN US2004110147-A1.
XX
PD 10-JUN-2004.
XX
PF 09-DEC-2002; 2002US-00316243.
XX
PR 09-DEC-2002; 2002US-00316243.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW, Jain R;
XX
WPI; 2004-440336/41.
XX
New oligonucleotide compound that inhibits expression of BAF53, useful
for preparing a composition for treating hyperproliferative disorder,
e.g. cancer.
XX
Example 15; SEQ ID NO 155; 72pp; English.
XX
The invention relates to a compound, having a sequence comprising 8-80 bp
targeted to a nucleic acid encoding BAF53 (a member of the BAF complex
(BRG1/brm-associated factor), BRG1-associated factor 53kDa which is an
actin-related protein), specifically hybridises with the nucleic acid
encoding BAF53 comprising 28001-bp sequence (derived from human
chromosome 3) and inhibits expression of BAF53, i.e. an antisense
oligonucleotide. Also included are inhibiting the expression of BAF53 in
cells or tissues, screening for a modulator of BAF53, a diagnostic method
for identifying a disease state, a kit or assay device comprising the
compound and treating an animal having a disease or condition associated
with BAF53. The oligonucleotide compound is useful for preparing a

SQ Sequence 20 BP; 4 A; 1 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3069 CCACACCCCAACACTT 3084
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Db      17  CACATCCCAACACTT 2
||||| ||||| |||||
RESULT 2091
ADQ09480/c
ID      ADQ09480 standard; DNA; 20 BP.
XX
AC      ADQ09480;
XX
XX
DT      09-SEP-2004 (first entry)
XX
DE      Murine Angiopoietin-2 DNA antisense oligonucleotide #16.
XX
KW      Mouse; Angiopoietin-2; ss; antisense oligonucleotide;
KW      phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;
KW      5-methylcytosine; hyperproliferative disorder; cancer; cytostatic.
XX
OS      Mus musculus.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..20      /*tag= b
FT      /*mod_base= OTHER
FT      /*note= "OTHER= Phosphorothioate backbone. All cytidines
FT      are 5-methylcytidines"
FT      modified_base 1..5      /*tag= a
FT      /*mod_base= OTHER
FT      /*note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT      modified_base 16..20     /*tag= c
FT      /*mod_base= OTHER
FT      /*note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX
US2004115640-A1.
XX
PN      17-JUN-2004.
XX
XX
PF      11-DEC-2002; 2002US-00317803.
XX
XX
PR      11-DEC-2002; 2002US-00317803.
XX
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Myers K, Dobie KW;
XX
XX      WPI; 2004-449380/42.
XX
XX      New oligonucleotide compound that inhibits expression of Angiopoietin-2,
XX      useful for preparing a composition for treating hyperproliferative
XX      disorder, e.g., cancer.
XX
PS      Example 16; SEQ ID NO 116; 102pp; English.
XX
XX      The invention relates to a compound targeted to a nucleic acid molecule
XX      encoding the human Angiopoietin-2 polypeptide. The compound is an
XX      antisense oligonucleotide that specifically hybridizes with the nucleic
XX      acid and inhibits expression of the polypeptide. The antisense
XX      oligonucleotide comprises at least one modified internucleoside linkage
XX      i.e. a phosphorothioate linkage, at least one modified sugar moiety,
XX      preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified
XX      nucleobase comprising a 5-methylcytosine. The antisense compounds are
XX      useful for modulating the expression of the human Angiopoietin-2
XX      polypeptide and in preparation of a composition for treating
XX      hyperproliferative disorders, e.g. cancer. This sequence represents an
XX      antisense oligonucleotide targeted to DNA encoding the murine
XX      Angiopoietin-2 polypeptide of the invention.
XX
SQ      Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;
Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      53 GGCTGCAGGTGCTGAA 68
      ||||| ||||| |||||
Db      18 GGCTGCAGGTGCTGGA 3
      ||||| ||||| |||||

RESULT 2092
ADO81060
ID      ADO81060 standard; DNA; 25 BP.
XX
AC      ADO81060;
XX
XX
DT      29-JUL-2004 (first entry)
XX
DE      Cow prion protein microsatellite locus primer #72.
XX
KW      gene typing; polymorphic microsatellite loci; PML;
KW      disease predisposition; microsatellite marker; prion disease;
KW      cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
KW      milk protein; hormone; transcription factor; pT7-blue-vector; cow;
KW      microsatellite; PCR; primer; ss.
XX
OS      Bos taurus.
XX
PN      DE10236711-A1.
XX
PD      26-FEB-2004.
XX
XX
PF      09-AUG-2002; 2002DE-01036711.
XX
PR      09-AUG-2002; 2002DE-01036711.
XX
XX      (UYHO-) UNIV HOHENHEIM.
PA
XX
PI      Geldermann H, Preuss S, Han Y;
XX
XX      WPI; 2004-215730/21.
XX
XX
PT      Typing genes that contain polymorphic microsatellite loci, useful for
PT      identifying predisposition to disease, by amplification and determining
PT      length of amplicons.
XX
XX
PS      Example 3; Page 28; 64pp; German.
XX
XX      The invention describes a method of typing (M1) a gene (I) that has one
XX      or more polymorphic microsatellite loci (PML). The method comprises: PCR
XX      amplification of at least one DNA region of (I) that includes PML, using
XX      as template a DNA sample containing at least one segment of (I); and
XX      determining the length of the resulting amplicon(s). Also described are:
XX      a method of determining (M2) microsatellite markers (MW) for
XX      predisposition to a disease, associated with a gene that includes one or
XX      more PML; and prediagnosis (M3) of diseases associated with gene that
XX      include PML. The method is used to identify microsatellite markers, in a
XX      disease-related gene, that are associated with a predisposition to
XX      diseases and for prediagnosis of such diseases, especially prion diseases
XX      but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
XX      metabolic diseases; also to type genes that encode milk proteins,
XX      hormones or transcription factors. The method is simpler, quicker and
XX      particularly less expensive than known methods based on sequencing. This
XX      sequence represents a primer used to genotype a region of the cow prion
XX      protein (PrP) comprising a polymorphic microsatellite locus.
XX
SQ      Sequence 25 BP; 0 A; 3 C; 0 G; 22 T; 0 U; 0 Other;
Query Match      0.4%; Score 14.4; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY      3262 TATTTTATTTGCTTGCTCTTTT 3285
      ||||| ||||| ||||| |||||
Db      2 TTTTATTTTATTTTTCCTTTT 25
      ||||| ||||| ||||| |||||
```

Key	modified_base	Location/Qualifiers
FT	1..26	
FT	/*tag= a	
FT	/note= "phosphodiester oligonucleotide"	
XX	WO9720924-A1.	
XX	12-JUN-1997.	
XX	04-DEC-1996;	96WO-EP005388.
XX	04-DEC-1995;	95IT-MI002539.
XX	(SAIC-) SAICOM SRL.	
XX	Scaggiante B, Quadrifoglio F;	
XX	WPI; 1997-319771/29.	
XX	New phosphodiesteric oligonucleotide(s) - which exert a specific and selective cytotoxic effect on tumour cells, for treating both solid and liquid tumours.	
XX	Claim 10; Page 5; 38pp; English.	
XX	Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the generic formula, in the 3'-5' or 5'-3' direction: (Gara')a'-(Gbtb')b'-(Gctc')c'-(Gdtd')d'-(Geff')e'-(Gfff')f'-(Gggg')g'-'N', where: N and N' = T or G, equal or different from each other; x = 0-8, equal or different from each other; a', b', c', d', e', f', and g' = 0-10, equal or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 0-30, equal or different from each other; a''', b''', c''', d''', e''', f''', and g''' = 1-16, equal or different from each other; The oligonucleotides are believed to selectively bind and sequester some proteins which are essential to the viability and growth of tumoural cell line. They have specific and selective cytotoxic activity against tumour cells, and can be used for treating tumours of the liquid type, in particular of lymphoblastic origin, and of solid type, in particular lymphomas. The present phosphodiester oligonucleotide, at a concentration of 15 micromolar, reduced growth of CCRF-CEM tumoural cells by 76%, which is detectable 48 hours after administration. (Updated on 25-MAR-2003 to correct PR field.)	
XX	SQ	Sequence 26 BP; 0 A; 0 C; 2 G; 24 T; 0 U; 0 Other;
XX	Query Match	0.4%; Score 14.4; DB 1; Length 26;
XX	Best Local Similarity	75.0%; Pred. No. 2.3e+03;
XX	Matches	18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	3262	TATTTTATTTGCTTGTCTCTTTT 3285
Db	3	TTTTTTGTTTTTTTGTCTTTT 26
RESULT 2095		
AAAT13806		
ID	AAAT13806	standard; DNA; 26 BP.
XX	AAAT13806;	
XX	27-JUL-2000	(first entry)
XX	Yeast DOG2 stress responsive gene PCR primer SEQ ID NO:5.	
XX	Yeast; stress responsive gene; promoter; brewing; beer; wine; sake;	
XX	bread; oxidative stress; osmotic pressure; stress; glucose starvation;	
XX	PCR primer; ss.	
XX	Saccharomyces cerevisiae.	
XX	JP2000078977-A.	
XX	21-MAR-2000.	

XX Example 5; Page 21; 55pp; English.

XX The invention relates to the determination of the concentration of a

CC nucleic acid target, using a fluorescently labeled probe which produces

CC reduced fluorescence emission when hybridised to the target nucleic acid.

CC The method comprises measuring the reduction in emission caused by

CC hybridisation. The new method is particularly used to quantify target

CC nucleic acids by a real-time polymerase chain reaction, e.g. for

CC quantifying microbial cells in co-cultures or symbiotic systems, for

CC detecting gene mutations or polymorphisms, and for analysing melting

CC curves of target nucleic acids to determine a Tm value. Methods of the

CC invention allow target nucleic acids to be quantified quickly, easily and

CC accurately. Particularly there is no need to remove unbound probe, and no

CC materials are introduced that inhibit amplification by Taq polymerase (so

CC conventional PCR conditions can be used). The specificity of PCR is kept

CC high (amplification of primer dimers is delayed), and the limit of

CC quantitation is reduced. Complex probes are not needed, and amplification

CC can be monitored in real time. The working graph for data analysis

CC (automatically generated by a computer) has a higher correlation

CC coefficient than conventional graphs so more accurate quantitation is

CC possible. The current sequence represents a synthetic

CC deoxyribonucleotide that was used for investigating the base

CC selectivity of a target nucleic acid

XX

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 30;

Best Local Similarity 75.0%; Pred. No. 2.6e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3474 ATATATATATATTTTATGAGTTTTT 3497

Db 1 ATATATATATTTTCTTTT 24

RESULT 2098

ABA97619

ID ABA97619 standard; DNA; 30 BP.

XX ABA97619;

AC ABA97619;

DT 11-APR-2002 (first entry)

XX

DE Poly h nucleotide sequence.

XX

KW ss; fluorochrome; nucleic acid probe; fluorescence.

XX

OS Unidentified.

XX

PN JP2001286300-A.

XX

PD 16-OCT-2001.

XX

PF 20-APR-2000; 2000JP-00120097.

XX

PR 20-APR-1999; 99JP-00111601.

PR 24-AUG-1999; 99JP-00236666.

PR 30-AUG-1999; 99JP-00242693.

PR 01-FEB-2000; 2000JP-00028896.

XX

PR (BIOI-) BIOINDUSTRY KYOKAI SH.

PA (KANK-) KANKYO ENG KK.

PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.

XX

DR WPI; 2002-134193/18.

XX

PT Measurement of nucleic acids, using a nucleic acid probe and analysis of

PT the obtained data.

XX

PS Example 5; Page 17; 34pp; Japanese.

XX

CC This invention relates to a method for measuring nucleic acids using a

CC

CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

CC decreases the fluorescence of the fluorochrome when hybridised with a

CC target nucleic acid, the decrease in the fluorescence is measured. The

CC method can be used for measuring a target nucleic acid

XX

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 30;

Best Local Similarity 75.0%; Pred. No. 2.6e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3474 ATATATATATTTTATGAGTTTTT 3497

Db 1 ATATATATTTTCTTTT 24

RESULT 2099

ABL95892

ID ABL95892 standard; DNA; 30 BP.

XX

AC ABL95892;

DT 19-JUN-2002 (first entry)

XX

DE Probe poly h for assaying nucleic acids.

XX

KW Probe; polymorphism detection; mutation detection; disease diagnosis;

KW microbial identification; ss.

XX

OS Unidentified.

XX

PN WO200208414-A1.

XX

PD 31-JAN-2002.

XX

PF 27-JUN-2001; 2001WO-IB001147.

XX

PR 27-JUN-2000; 2000JP-00193133.

PR 03-AUG-2000; 2000JP-00236115.

PR 26-SEP-2000; 2000JP-00292483.

XX

PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (KANK-) KANKYO ENG CO LTD.

XX

PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;

PI Yokomaku T;

XX

DR WPI; 2002-195876/25.

XX

PS Example 12; Page 60; 152pp; Japanese.

XX

CC The present invention relates to nucleic acid probes, which are useful

CC for assaying nucleic acids by hybridising with a target nucleic acid, in

CC which a single-stranded oligonucleotide is labelled with a fluorescent

CC substance and a quencher in a manner that the fluorescence intensity of

CC the hybridisation reaction system is increased after completion of the

CC hybridisation but no stem loop structure is formed. The probes are useful

CC for assaying nucleic acids and their polymorphism and mutation,

CC particularly useful for e.g. analytical applications, disease diagnosis

CC and microbial identification. The present sequence was used to illustrate

CC the invention

XX

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 30;

Best Local Similarity 75.0%; Pred. No. 2.6e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
QY 3474 ATATATATAATTTATTGAGTTTT 3497
DB 1 ATATATATTTTTCCTTTT 24

RESULT 2100
AAI30470/c
ID AAI30470 standard; DNA; 31 BP.
XX
XX AAI30470;
AC
XX
XX 18-OCT-2001 (first entry)
DT
XX
XX Human single nucleotide polymorphism (SNP) FGFR3 2.
DE
XX
XX Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Variation replace(16,G)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200166800-A2.
PN
XX
XX 13-SEP-2001.
PD
XX
XX 07-MAR-2001; 2001WO-US007268.
PF
XX
XX 07-MAR-2000; 2000US-0187510P.
PR
XX 22-MAY-2000; 2000US-0206129P.
PR
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA
XX
XX Cargill M, Ireland JS, Lander ES;
PI
XX
XX WPI; 2001-522952/57.
DR
XX
XX Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or severity
PT of a particular phenotype or disorder (e.g. diabetes) associated with a
PT particular genotype.
XX
XX Claim 1; Page 87; 145pp; English.
PS
XX
XX The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing
XX
XX Sequence 31 BP; 3 A; 13 C; 12 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 529 CGGCCCATCTCGAGCGGGCTG 552
DB 26 CAGCCCCGCTCGAGGATGGCGG 3

RESULT 2101
AAQ87894
ID AAQ87894 standard; DNA; 32 BP.
XX
XX AAQ87894;
```

```
XX
DT 25-MAR-2003 (revised)
DT 29-NOV-1995 (first entry)
XX
XX Normalised library first strand cDNA synthesis primer.
XX
XX Normalised cDNA library; directionally cloned cDNA library; screening;
KW hybridisation; ss.
KW
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 15..18
FT /tag= a
FT /note= "Characteristic sequence identifier"
XX
XX WO9508647-A1.
PN
XX
XX 30-MAR-1995.
PD
XX
XX 23-SEP-1994; 94WO-US010821.
PF
XX
XX 24-SEP-1993; 93US-00126594.
PR
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
PA
XX
XX Soares MB, Efstratiadis A;
PI
XX
XX WPI; 1995-139615/18.
DR
XX
XX New normalised directional cDNA libraries - used for isolating novel
PT cDNA's, including tissue-specific and development-specific DNA.
PT
XX
XX Disclosure; Page 45; 186pp; English.
PS
XX
XX Human tissues were obtained for construction of a variety of cDNA
CC libraries, including infant brain, adult brain and adult hippocampus.
CC Each of the cDNA libraries had a characteristic sequence identifier,
CC provided by the oligonucleotide utilised to prime first strand cDNA
CC synthesis (see AAQ87894-Q87907 for these primer sequences; all these
CC primers have the PacI restriction site for directional cloning of cDNAs).
CC Each of the libraries was propagated in the form of single-stranded (ss)
CC circles and normalised separately by a novel method. The method
CC comprises: generating fragments complementary to the 3' non-coding
CC sequence of the ss circles in the library to produce partial duplexes;
CC purifying the partial duplexes; melting and reassociating them to
CC appropriate cot; and purifying the unassociated ss circles to generate a
CC normalised cDNA library. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 32 BP; 4 A; 0 C; 0 G; 28 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3311 TTTTCTTGGAGATTATTTT 3334
DB 1 TTTTCTTAAATTTT 24

RESULT 2102
ABQ80395/c
ID ABQ80395 standard; DNA; 33 BP.
XX
XX ABQ80395;
AC
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Probe APC 1-MUT.
DE
XX
XX Probe; target; nanoparticle; detection; DNA sequencing; pathogen;
KW infection; screening; colour change; ss.
KW
XX
```



```

OS Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /*note= "Gold-S'-A"
XX
XX WO2003048769-A1.
XX
XX 12-JUN-2003.
XX
XX 27-NOV-2002; 2002WO-US038069.
XX
XX 30-NOV-2001; 2001US-0334644P.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Storhoff JJ, Fritz BM, Herrmann M;
XX
XX WPI; 2003-617993/58.
XX
XX Detecting target polynucleotide in a sample, by amplifying target,
XX hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle
XX detection system, and determining amount of signal generated due to
XX binding.
XX
XX Example 1; Page 35; 74pp; English.
XX
XX The sequences given in ABQ80394-99 represent probes and targets which
XX were used in the method of the invention for detecting a target
XX polynucleotide in a sample. The method comprises amplifying the target,
XX hybridizing the target to oligonucleotides bound to nanoparticles in a
XX nanoparticle detection system, determining the amount of signal generated
XX as a result of binding, optionally repeating the above steps, and
XX detecting the presence of the target oligonucleotide by analysing for the
XX amount of signal produced after at least one amplification cycle. The
XX method is useful for detecting target polynucleotide in a sample, and for
XX determining the quantity of target polynucleotide in a sample. The method
XX is useful in research and analytical laboratories in DNA sequencing, in
XX the field to detect the presence of specific pathogens, in the doctor's
XX office for quick identification of an infection to assist in prescribing
XX a drug for treatment, and in homes and health centres for inexpensive
XX first-line screening. The method is based on observing colour change with
XX the naked eye, hence the method is cheap, fast, simple, robust, do not
XX require specialized or expensive equipment, and little or no
XX instrumentation is required
XX
XX Sequence 33 BP; 29 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.4; DB 1; Length 33;
XX Best Local Similarity 75.0%; Pred. No. 2.7e+03;
XX Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 3262 TATTTATTGCTTTCCTTTT 3285
XX | ||||| ||||| |||||
XX Db 32 TTTTTCGCTTTTTCCTTTT 9
XX
XX RESULT 2103
XX ABN89412/C
XX ID ABN89412 standard; DNA; 40 BP.
XX
XX AC ABN89412;
XX
XX DT 30-AUG-2002 (first entry)
XX
XX DE Polymorphism detection related oligonucleotide SEQ ID NO:4.
XX
XX KW Polymorphism; detection; mass spectroscopy; ss.
XX
XX OS Synthetic.
XX
XX PN WO200250307-A1.

```

```

XX 27-JUN-2002.
XX
XX 12-DEC-2001; 2001WO-JP010892.
XX
XX 12-DEC-2000; 2000JP-00378091.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Inoko H, Tamiya G, Nakajima K, Kimura N, Nagashima R, Morikawa M;
XX Okamoto K;
XX
XX WPI; 2002-508814/54.
XX
XX Detection of DNA polymorphism by mass spectroscopy for investigation and
XX diagnosis of gene-related diseases.
XX
XX Example 3; Page 28; 34pp; Japanese.
XX
XX The present invention describes a method for detecting polymorphisms in
XX DNA by: (a) preparing a DNA sample from patients containing the DNA
XX region in which the target polymorphism is located; (b) hybridising to an
XX appropriate oligonucleotide fragment, immobilised on a support; and (c)
XX detecting the hybridised target DNA by mass spectroscopy. The method can
XX be used for the investigation and diagnosis of gene-related diseases. The
XX method allows polymorphisms to be detected rapidly and effectively in a
XX large number of specimens. The present sequence represents an
XX oligonucleotide which is used in an example from the present invention
XX
XX Sequence 40 BP; 30 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.4; DB 1; Length 40;
XX Best Local Similarity 65.6%; Pred. No. 2.9e+03;
XX Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 3262 TATTTATTGCTTTCCTTTTTCAGGAGAA 3293
XX | ||||| ||||| ||||| |||||
XX Db 35 TTTTTCGCTTTTTCCTTTTTCAGGAGAA 4
XX
XX RESULT 2104
XX AD041321/C
XX ID AD041321 standard; cDNA; 40 BP.
XX
XX AC AD041321;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Human cDNA probe useful for disease diagnosis #472.
XX
XX ss; probe; human; bacteria; virus; prion; parasite; fungus; drug;
XX allergen; influenza; malaria; yellow fever; multiple sclerosis;
XX Alzheimer's disease; lung cancer; breast cancer; stomach cancer.
XX
XX OS Homo sapiens.
XX
XX PN WO2004046382-A2.
XX
XX PD 03-JUN-2004.
XX
XX PF 21-NOV-2003; 2003WO-GB005102.
XX
XX PR 21-NOV-2002; 2002GB-00027238.
XX
XX (DIAG-) DIAGENIC AS.
XX (JONE/) JONES E L.
XX
XX Sharma P, Sahni NS, Loenneborg A;
XX
XX WPI; 2004-420641/39.
XX
XX Set of oligonucleotide probes, useful for diagnosing breast cancer or
XX Alzheimer's disease, comprising specific number of oligonucleotides.
XX
XX PT

```


PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PS ubiquinone.
XX Disclosure; SEQ ID NO 6971; 872bp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 6 A; 1 C; 2 G; 11 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3463 TATATATATCTATATATAT 3481
Db 2 TTTATATATGTATGTATAT 20
|||||

RESULT 2107
ABD27959
ID ABD27959 standard; DNA; 20 BP.
XX
AC ABD27959;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA497002-derived oligonucleotide SEQ ID 6971.
XX

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiasthmatic; antiallergic; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US011143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX

XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 6971; 763pp; English.

CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiasthmatic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

XX
SQ Sequence 20 BP; 6 A; 1 C; 2 G; 11 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3463 TATATATATCTATATATAT 3481
Db 2 TTTATATATGTATGTATAT 20
|||||

RESULT 2108
ABD27962
ID ABD27962 standard; DNA; 20 BP.
XX
AC ABD27962;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA497002-derived oligonucleotide SEQ ID 6974.
XX

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiasthmatic; antiallergic; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
XX WO200285309-A2.
XX

PD 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013143.
 XX
 XX 24-APR-2001; 2001US-0286036P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 XX WPI; 2003-093058/08.
 DR
 XX Pharmaceutical composition for treating asthma, has antisense
 XX oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 XX Claim 15; SEQ ID NO 6974; 763pp; English.
 PS
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 20 BP; 11 A; 0 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3463 TATATATATCTATATATAT 3481
 DB ||||| ||||| ||||| |||||
 2 TATATATATGAAATATAT 20
 RESULT 2109
 ABZ98662
 ID ABZ98662 standard; DNA; 20 BP.
 XX
 AC ABZ98662;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human tryptase a oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 XX lung inflammation; respiratory disease; ds.
 OS Homo sapiens.
 XX
 XX WO200285308-A2.
 PN
 XX 31-OCT-2002.
 PD
 XX 23-APR-2002; 2002WO-US013135.
 PF
 XX 24-APR-2001; 2001US-0286137P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 XX WPI; 2003-229219/22.
 DR
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 13904; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 2 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2100 GGACACCCCGCTCCAGC 2118
 DB ||||| ||||| ||||| |||||
 2 GGGCTCTCTCCAGCTCCAGC 20
 RESULT 2110
 ABD31693
 ID ABD31693 standard; DNA; 20 BP.
 XX
 AC ABD31693;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human Tryptase a-derived oligonucleotide SEQ ID 13904.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;

AC ADO46030;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #1396.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KW tryptase b; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW asthma; lung allergy; inflammation; inflammatory disease;
KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW acute respiratory distress syndrome; pulmonary hypertension;
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS Homo sapiens.
XX
FN US2004049022-A1.
XX
PD 11-MAR-2004.
XX
XX 25-JUL-2003; 2003US-00627930.
XX
PR 23-APR-2002; 2002WO-US013135.
XX 23-APR-2002; 2002WO-US013143.
XX
XX (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
XX
XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
PI WPI; 2004-293804/27.
XX
DR Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
PS Claim 2; SEQ ID NO 1397; 174pp; English.
XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX

SQ Sequence 20 BP; 2 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2100 GGACACCCCGCTCCAGC 2118
Db 2 GGGCTCTCCAGCTCCAGC 20
Search completed: October 28, 2004, 12:04:30
Job time : 181 secs

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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 11:51:40 ; Search time 103 Seconds

(without alignments)
3.669 Million cell updates/sec

Title: US-10-630-401-10

Perfect score: 3799

Sequence: 1 aaggatggcacagggtggt.....gacacctgttgtaacctg 3799

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 0.5

Searched: 2344 seqs, 49742 residues

Total number of hits satisfying chosen parameters: 4688

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1504 summaries

Database : rgel0.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36.4	1.0	48	1	AR444606
2	35.6	0.9	50	1	E32208
3	35.6	0.9	50	1	E32228
4	35.6	0.9	50	1	I31183
5	35.6	0.9	50	1	I31274
6	34.8	0.9	48	1	AR444607
7	34.6	0.9	46	1	I31434
8	34.4	0.9	44	1	I31337
9	34.4	0.9	44	1	AR444608
10	34.2	0.9	42	1	I31141
11	34.2	0.9	47	1	I31171
12	34.2	0.9	47	1	I31180
13	34.2	0.9	47	1	I31309
14	34.2	0.9	48	1	A0047784
15	34	0.9	47	1	CQ738314
16	33.8	0.9	38	1	BD251663
17	33.8	0.9	38	1	I31286
18	33.8	0.9	38	1	I31485
19	33.8	0.9	38	1	AX028364
20	33.8	0.9	39	1	I31225
21	33.8	0.9	40	1	I31207
22	33.8	0.9	40	1	I31488
23	33.8	0.9	40	1	I31491
24	33.8	0.9	41	1	I31162
25	33.8	0.9	41	1	I31271
26	33.8	0.9	41	1	I31320
27	33.8	0.9	42	1	I31317
28	33.8	0.9	43	1	I31476
29	33.8	0.9	44	1	I31283
30	33.8	0.9	44	1	I31329
31	33.8	0.9	46	1	I31159
32	33.8	0.9	46	1	I31189
33	33.8	0.9	46	1	I31314

c 34	33.6	0.9	45	1	I31452
c 35	33.4	0.9	35	1	I31165
c 36	33	0.9	41	1	AR222935
c 37	32.8	0.9	36	1	I31192
c 38	32.8	0.9	36	1	I31446
c 39	32.8	0.9	37	1	I31228
c 40	32.8	0.9	44	1	AR444609
c 41	32.8	0.9	45	1	I31291
c 42	32.4	0.9	34	1	I31268
c 43	32.4	0.9	35	1	I31277
c 44	32.2	0.8	38	1	E32209
c 45	32.2	0.8	38	1	I31156
c 46	32.2	0.8	39	1	I31174
c 47	32.2	0.8	40	1	I31240
c 48	32.2	0.8	40	1	I31263
c 49	32.2	0.8	42	1	I31422
c 50	32.2	0.8	45	1	I31245
c 51	32	0.8	39	1	AR007163
c 52	31.4	0.8	33	1	I31147
c 53	31.4	0.8	33	1	I31306
c 54	31.4	0.8	34	1	I31198
c 55	31.4	0.8	34	1	I31260
c 56	31.4	0.8	34	1	I31280
c 57	31.4	0.8	34	1	I31410
c 58	31.4	0.8	43	1	I31458
c 59	30.8	0.8	42	1	I31431
c 60	30.6	0.8	31	1	AX248878
c 61	30.6	0.8	31	1	AX248879
c 62	30.6	0.8	31	1	AX248880
c 63	30.6	0.8	31	1	AX248881
c 64	30.6	0.8	42	1	AR5638
c 65	30.6	0.8	42	1	AR033091
c 66	30.4	0.8	32	1	E32203
c 67	30.4	0.8	32	1	I31298
c 68	30.4	0.8	32	1	I31464
c 69	30.4	0.8	42	1	I31428
c 70	29.4	0.8	31	1	I31303
c 71	29.4	0.8	31	1	I31323
c 72	29.4	0.8	31	1	I31359
c 73	29.4	0.8	41	1	I31440
c 74	29.4	0.8	41	1	I31443
c 75	29	0.8	39	1	I31419
c 76	28.8	0.8	32	1	I31494
c 77	28.8	0.8	41	1	AX513919
c 78	28.8	0.8	41	1	AX519258
c 79	28.4	0.7	30	1	I31461
c 80	28.4	0.7	30	1	BD107614
c 81	28	0.7	40	1	MWVIMV26
c 82	27.4	0.7	29	1	AR051257
c 83	27.4	0.7	29	1	I28386
c 84	27.4	0.7	29	1	I31168
c 85	27.4	0.7	29	1	I31326
c 86	26.4	0.7	28	1	A27175
c 87	26.4	0.7	28	1	I31539
c 88	26	0.7	34	1	AR033092
c 89	26	0.7	34	1	BD174950
c 90	25.8	0.7	29	1	E32218
c 91	25.8	0.7	30	1	AR051255
c 92	25.4	0.7	27	1	AR0127802
c 93	25.4	0.7	27	1	I28384
c 94	25.4	0.7	27	1	I31231
c 95	25.4	0.7	27	1	AX175237
c 96	25.4	0.7	27	1	AX175241
c 97	25.4	0.7	27	1	AX175302
c 98	25.4	0.7	27	1	AX189457
c 99	25.4	0.7	27	1	AX189457
c 100	25.2	0.7	30	1	I31503
c 101	25	0.7	25	1	AX482128
c 102	25	0.7	25	1	AX511367
c 103	25	0.7	25	1	AX721728
c 104	24	0.6	24	1	E11483
c 105	24	0.6	24	1	AX482129
c 106	24	0.6	24	1	AX511368

ACCESSION: I31452
ACCESSION: I31165
ACCESSION: AR222935
ACCESSION: I31192
ACCESSION: I31446
ACCESSION: I31228
ACCESSION: AR444609
ACCESSION: I31291
ACCESSION: I31268
ACCESSION: I31277
ACCESSION: E32209
ACCESSION: I31156
ACCESSION: I31174
ACCESSION: I31240
ACCESSION: I31263
ACCESSION: I31422
ACCESSION: I31245
ACCESSION: AR007163
ACCESSION: I31147
ACCESSION: I31306
ACCESSION: I31198
ACCESSION: I31260
ACCESSION: I31280
ACCESSION: I31410
ACCESSION: I31458
ACCESSION: I31431
ACCESSION: AX248878
ACCESSION: AX248879
ACCESSION: AX248880
ACCESSION: AX248881
ACCESSION: AR033091
ACCESSION: E32203
ACCESSION: I31298
ACCESSION: I31464
ACCESSION: I31428
ACCESSION: I31303
ACCESSION: I31323
ACCESSION: I31359
ACCESSION: I31440
ACCESSION: I31443
ACCESSION: I31419
ACCESSION: I31494
ACCESSION: AX513919
ACCESSION: AX519258
ACCESSION: I31461
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ACCESSION: I28386
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ACCESSION: AX482129
ACCESSION: AX511368

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C 108	23.6	0.6	30	1	A29208	ACCESSION:A29208	C 181	18.8	0.5	22	1	AX486835	ACCESSION:AX486835
C 109	23.6	0.6	30	1	A29211	ACCESSION:A29211	C 182	18.8	0.5	23	1	AX926722	ACCESSION:AX926722
C 110	23.4	0.6	25	1	I31234	ACCESSION:I31234	C 183	18.8	0.5	24	1	AR058875	ACCESSION:AR058875
C 111	23.4	0.6	25	1	AX115976	ACCESSION:AX115976	C 184	18.8	0.5	24	1	AR058877	ACCESSION:AR058877
C 112	23.4	0.6	33	1	I31400	ACCESSION:I31400	C 185	18.8	0.5	24	1	AR079580	ACCESSION:AR079580
C 113	22.4	0.6	33	1	I31533	ACCESSION:I31533	C 186	18.8	0.5	24	1	AR079582	ACCESSION:AR079582
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C 115	22.4	0.6	24	1	AX175257	ACCESSION:AX175257	C 188	18.8	0.5	24	1	AR123291	ACCESSION:AR123291
C 116	22.4	0.6	24	1	AX175258	ACCESSION:AX175258	C 189	18.8	0.5	24	1	AR146823	ACCESSION:AR146823
C 117	22.4	0.6	24	1	AX547929	ACCESSION:AX547929	C 190	18.8	0.5	24	1	AR123291	ACCESSION:AR123291
C 118	22.4	0.6	25	1	AR117836	ACCESSION:AR117836	C 191	18.8	0.5	24	1	BD188891	ACCESSION:BD188891
C 119	22.4	0.6	22	1	AR173691	ACCESSION:AR173691	C 192	18.8	0.5	24	1	BD188893	ACCESSION:BD188893
C 120	22.4	0.6	22	1	BD231722	ACCESSION:BD231722	C 193	18.8	0.5	24	1	I33252	ACCESSION:I33252
C 121	22.4	0.6	22	1	BD231723	ACCESSION:BD231723	C 194	18.8	0.5	24	1	I33254	ACCESSION:I33254
C 122	22.4	0.6	22	1	BD270911	ACCESSION:BD270911	C 195	18.8	0.5	24	1	I35517	ACCESSION:I35517
C 123	22.4	0.6	22	1	BD270912	ACCESSION:BD270912	C 196	18.8	0.5	24	1	I35519	ACCESSION:I35519
C 124	22.4	0.6	22	1	AR383046	ACCESSION:AR383046	C 197	18.8	0.5	24	1	I43127	ACCESSION:I43127
C 125	22.4	0.6	22	1	AR383047	ACCESSION:AR383047	C 198	18.8	0.5	24	1	I43129	ACCESSION:I43129
C 126	22.4	0.6	22	1	AR327687	ACCESSION:AR327687	C 199	18.8	0.5	24	1	I92005	ACCESSION:I92005
C 127	22.4	0.6	22	1	AX327688	ACCESSION:AX327688	C 200	18.6	0.5	25	1	I92007	ACCESSION:I92007
C 128	22.4	0.6	22	1	AX812159	ACCESSION:AX812159	C 201	18.6	0.5	25	1	AR177699	ACCESSION:AR177699
C 129	22.4	0.6	28	1	AR020621	ACCESSION:AR020621	C 202	18.6	0.5	25	1	AR028293	ACCESSION:AR028293
C 130	21.8	0.6	25	1	AR117832	ACCESSION:AR117832	C 203	18.4	0.5	25	1	AR434784	ACCESSION:AR434784
C 131	21.4	0.6	23	1	AR127801	ACCESSION:AR127801	C 204	18.4	0.5	20	1	A63570	ACCESSION:A63570
C 132	21.4	0.6	23	1	I31542	ACCESSION:I31542	C 205	18.4	0.5	20	1	AR084543	ACCESSION:AR084543
C 133	21	0.6	21	1	AR173690	ACCESSION:AR173690	C 206	18.4	0.5	20	1	AR123339	ACCESSION:AR123339
C 134	21	0.6	30	1	AR090052	ACCESSION:AR090052	C 207	18.4	0.5	20	1	AR129684	ACCESSION:AR129684
C 135	21	0.6	30	1	AR197087	ACCESSION:AR197087	C 208	18.4	0.5	20	1	E36173	ACCESSION:E36173
C 136	21	0.6	30	1	AR259241	ACCESSION:AR259241	C 209	18.4	0.5	20	1	AX179298	ACCESSION:AX179298
C 137	20.8	0.5	25	1	AX117828	ACCESSION:AX117828	C 210	18.4	0.5	20	1	AX179299	ACCESSION:AX179299
C 138	20.6	0.5	27	1	AR022729	ACCESSION:AR022729	C 211	18.4	0.5	20	1	BD016468	ACCESSION:BD016468
C 139	20.6	0.5	27	1	AR053130	ACCESSION:AR053130	C 212	18.4	0.5	20	1	BD084130	ACCESSION:BD084130
C 140	20.6	0.5	27	1	BD174951	ACCESSION:BD174951	C 213	18.4	0.5	20	1	BD084130	ACCESSION:BD084130
C 141	20.4	0.5	22	1	I31213	ACCESSION:I31213	C 214	18.4	0.5	20	1	BD097545	ACCESSION:BD097545
C 142	20	0.5	20	1	CQ759610	ACCESSION:CQ759610	C 215	18.4	0.5	20	1	BD105781	ACCESSION:BD105781
C 143	20	0.5	20	1	E23735	ACCESSION:E23735	C 216	18.4	0.5	21	1	AX398276	ACCESSION:AX398276
C 144	19.8	0.5	23	1	BD107438	ACCESSION:BD107438	C 217	18.4	0.5	21	1	AX398277	ACCESSION:AX398277
C 145	19.8	0.5	24	1	E32214	ACCESSION:E32214	C 218	18.4	0.5	24	1	AX926721	ACCESSION:AX926721
C 146	19.8	0.5	26	1	AR090987	ACCESSION:AR090987	C 219	18.2	0.5	25	1	AB086601	ACCESSION:AB086601
C 147	19.8	0.5	26	1	AR198022	ACCESSION:AR198022	C 220	18	0.5	18	1	AR071800	ACCESSION:AR071800
C 148	19.8	0.5	26	1	AR260176	ACCESSION:AR260176	C 221	18	0.5	18	1	AX482165	ACCESSION:AX482165
C 149	19.8	0.5	27	1	AX183949	ACCESSION:AX183949	C 222	18	0.5	18	1	AX511404	ACCESSION:AX511404
C 150	19.6	0.5	27	1	AR090230	ACCESSION:AR090230	C 223	18	0.5	18	1	AX721765	ACCESSION:AX721765
C 151	19.6	0.5	28	1	AR197265	ACCESSION:AR197265	C 224	18	0.5	20	1	E05457	ACCESSION:E05457
C 152	19.6	0.5	28	1	AR259419	ACCESSION:AR259419	C 225	18	0.5	22	1	BD192794	ACCESSION:BD192794
C 153	19.4	0.5	21	1	AR007164	ACCESSION:AR007164	C 226	17.8	0.5	21	1	I30547	ACCESSION:I30547
C 154	19.4	0.5	21	1	I31248	ACCESSION:I31248	C 227	17.8	0.5	21	1	AX020772	ACCESSION:AX020772
C 155	19.4	0.5	21	1	AX104715	ACCESSION:AX104715	C 228	17.8	0.5	21	1	AX116107	ACCESSION:AX116107
C 156	19.4	0.5	21	1	AX175255	ACCESSION:AX175255	C 229	17.8	0.5	21	1	AX556883	ACCESSION:AX556883
C 157	19.4	0.5	21	1	AX175256	ACCESSION:AX175256	C 230	17.8	0.5	21	1	BD089174	ACCESSION:BD089174
C 158	19.4	0.5	21	1	AX547768	ACCESSION:AX547768	C 231	17.8	0.5	21	1	AB068223	ACCESSION:AB068223
C 159	19.4	0.5	22	1	BD251661	ACCESSION:BD251661	C 232	17.8	0.5	24	1	AS7514	ACCESSION:AS7514
C 160	19.4	0.5	22	1	BD251661	ACCESSION:BD251661	C 233	17.8	0.5	24	1	AR052980	ACCESSION:AR052980
C 161	19.4	0.5	22	1	AX028362	ACCESSION:AX028362	C 234	17.8	0.5	24	1	AX117030	ACCESSION:AX117030
C 162	19.4	0.5	22	1	AX028362	ACCESSION:AX028362	C 235	17.6	0.5	24	1	BD249753	ACCESSION:BD249753
C 163	19.4	0.5	22	1	AX104718	ACCESSION:AX104718	C 236	17.6	0.5	24	1	AR302333	ACCESSION:AR302333
C 164	19.4	0.5	22	1	AX104718	ACCESSION:AX104718	C 237	17.6	0.5	24	1	AX740251	ACCESSION:AX740251
C 165	19.4	0.5	22	1	AX547771	ACCESSION:AX547771	C 238	17.6	0.5	24	1	AX743827	ACCESSION:AX743827
C 166	19.4	0.5	22	1	AX547771	ACCESSION:AX547771	C 239	17.6	0.5	25	1	AR028294	ACCESSION:AR028294
C 167	19.4	0.5	24	1	AX116747	ACCESSION:AX116747	C 240	17.6	0.5	25	1	AR434781	ACCESSION:AR434781
C 168	19.4	0.5	26	1	A59562	ACCESSION:A59562	C 241	17.6	0.5	25	1	AR434782	ACCESSION:AR434782
C 169	19.4	0.5	26	1	A82434	ACCESSION:A82434	C 242	17.6	0.5	25	1	AR434785	ACCESSION:AR434785
C 170	19.4	0.5	26	1	AR28125	ACCESSION:AR28125	C 243	17.6	0.5	25	1	BD174952	ACCESSION:BD174952
C 171	19.4	0.5	26	1	BD135484	ACCESSION:BD135484	C 244	17.4	0.5	19	1	I31530	ACCESSION:I31530
C 172	19.2	0.5	24	1	BD192781	ACCESSION:BD192781	C 245	17.4	0.5	19	1	AX040467	ACCESSION:AX040467
C 173	19.2	0.5	24	1	E32221	ACCESSION:E32221	C 246	17.4	0.5	19	1	AX040468	ACCESSION:AX040468
C 174	19.2	0.5	19	1	AX482164	ACCESSION:AX482164	C 247	17.4	0.5	19	1	AX132174	ACCESSION:AX132174
C 175	19	0.5	19	1	AX511403	ACCESSION:AX511403	C 248	17.4	0.5	19	1	AR129716	ACCESSION:AR129716
C 176	19	0.5	19	1	AX721764	ACCESSION:AX721764	C 249	17.4	0.5	20	1	I33568	ACCESSION:I33568
C 177	19	0.5	19	1	AR404118	ACCESSION:AR404118	C 250	17.4	0.5	20	1	AX462693	ACCESSION:AX462693
C 178	19	0.5	27	1	AX080281	ACCESSION:AX080281	C 251	17.4	0.5	20	1		
C 179	19	0.5	27	1			C 252	17.4	0.5	20	1		

253	17.4	0.5	21	1	AR126570	ACCESSION:AR126570	326	17	0.4	18	1	AX115187	ACCESSION:AX115187
254	17.4	0.5	21	1	AR126571	ACCESSION:AR126571	327	17	0.4	18	1	AX175253	ACCESSION:AX175253
c 255	17.4	0.5	21	1	AX203572	ACCESSION:AX203572	328	17	0.4	18	1	AX175254	ACCESSION:AX175254
c 256	17.4	0.5	21	1	AX613777	ACCESSION:AX613777	329	17	0.4	18	1	BD087486	ACCESSION:BD087486
257	17.4	0.5	30	1	AR264920	ACCESSION:AR264920	c 330	17	0.4	20	1	CQ818365	ACCESSION:CQ818365
258	17.4	0.5	30	1	AR264926	ACCESSION:AR264926	c 331	17	0.4	20	1	CQ818387	ACCESSION:CQ818387
259	17.4	0.5	30	1	AR478201	ACCESSION:AR478201	c 332	16.8	0.4	20	1	AR010007	ACCESSION:AR010007
260	17.4	0.5	30	1	AR478207	ACCESSION:AR478207	c 333	16.8	0.4	20	1	AR034742	ACCESSION:AR034742
261	17.4	0.5	30	1	BD072865	ACCESSION:BD072865	334	16.8	0.4	20	1	AR058876	ACCESSION:AR058876
262	17.4	0.5	30	1	BD072871	ACCESSION:BD072871	c 335	16.8	0.4	20	1	AR058876	ACCESSION:AR058876
263	17.4	0.5	30	1	BD107492	ACCESSION:BD107492	336	16.8	0.4	20	1	AR079581	ACCESSION:AR079581
264	17.4	0.5	30	1	BD107498	ACCESSION:BD107498	c 337	16.8	0.4	20	1	AR079581	ACCESSION:AR079581
265	17.4	0.5	30	1	BD145024	ACCESSION:BD145024	338	16.8	0.4	20	1	AR123290	ACCESSION:AR123290
266	17.4	0.5	30	1	BD145030	ACCESSION:BD145030	c 339	16.8	0.4	20	1	AR123290	ACCESSION:AR123290
267	17.4	0.5	30	1	BD166025	ACCESSION:BD166025	c 340	16.8	0.4	20	1	AR130163	ACCESSION:AR130163
268	17.4	0.5	30	1	BD166030	ACCESSION:BD166030	c 341	16.8	0.4	20	1	AR177700	ACCESSION:AR177700
c 269	17.4	0.5	31	1	AX248881	ACCESSION:AX248881	342	16.8	0.4	20	1	BD188892	ACCESSION:BD188892
270	17.2	0.5	22	1	A38159	ACCESSION:A38159	c 343	16.8	0.4	20	1	BD188892	ACCESSION:BD188892
271	17.2	0.5	22	1	AR173686	ACCESSION:AR173686	c 344	16.8	0.4	20	1	E32219	ACCESSION:E32219
272	17.2	0.5	23	1	A27197	ACCESSION:A27197	c 345	16.8	0.4	20	1	I24757	ACCESSION:I24757
273	17.2	0.5	23	1	A32939	ACCESSION:A32939	346	16.8	0.4	20	1	I33253	ACCESSION:I33253
274	17.2	0.5	23	1	A33834	ACCESSION:A33834	c 347	16.8	0.4	20	1	I33253	ACCESSION:I33253
275	17.2	0.5	23	1	AR077343	ACCESSION:AR077343	348	16.8	0.4	20	1	I35518	ACCESSION:I35518
276	17.2	0.5	23	1	AR117963	ACCESSION:AR117963	c 349	16.8	0.4	20	1	I35518	ACCESSION:I35518
277	17.2	0.5	23	1	BD231857	ACCESSION:BD231857	350	16.8	0.4	20	1	I43128	ACCESSION:I43128
278	17.2	0.5	23	1	CQ802102	ACCESSION:CQ802102	c 351	16.8	0.4	20	1	I43128	ACCESSION:I43128
279	17.2	0.5	23	1	CQ846562	ACCESSION:CQ846562	352	16.8	0.4	20	1	I92006	ACCESSION:I92006
280	17.2	0.5	23	1	E09110	ACCESSION:E09110	c 353	16.8	0.4	20	1	I92006	ACCESSION:I92006
281	17.2	0.5	23	1	I27518	ACCESSION:I27518	c 354	16.8	0.4	20	1	AR199772	ACCESSION:AR199772
c 282	17.2	0.5	23	1	I44506	ACCESSION:I44506	c 355	16.8	0.4	20	1	AR242049	ACCESSION:AR242049
283	17.2	0.5	23	1	I95684	ACCESSION:I95684	c 356	16.8	0.4	20	1	AX956707	ACCESSION:AX956707
c 284	17.2	0.5	23	1	AR262782	ACCESSION:AR262782	357	16.8	0.4	20	1	DOGKIT1A	ACCESSION:DOGKIT1A
285	17.2	0.5	23	1	AR265406	ACCESSION:AR265406	358	16.8	0.4	21	1	AR074234	ACCESSION:AR074234
286	17.2	0.5	23	1	AR301927	ACCESSION:AR301927	c 359	16.8	0.4	21	1	AR098876	ACCESSION:AR098876
287	17.2	0.5	23	1	AR428817	ACCESSION:AR428817	c 360	16.8	0.4	21	1	I79716	ACCESSION:I79716
c 288	17.2	0.5	23	1	AR438219	ACCESSION:AR438219	c 361	16.8	0.4	21	1	AR301331	ACCESSION:AR301331
289	17.2	0.5	23	1	AR447097	ACCESSION:AR447097	c 362	16.8	0.4	21	1	AX020545	ACCESSION:AX020545
290	17.2	0.5	23	1	AX010545	ACCESSION:AX010545	363	16.8	0.4	21	1	AX032596	ACCESSION:AX032596
291	17.2	0.5	23	1	AX203707	ACCESSION:AX203707	c 364	16.8	0.4	22	1	AR171534	ACCESSION:AR171534
292	17.2	0.5	23	1	AX203708	ACCESSION:AX203708	c 365	16.8	0.4	22	1	BD005554	ACCESSION:BD005554
293	17.2	0.5	23	1	AX357138	ACCESSION:AX357138	c 366	16.8	0.4	22	1	BD107557	ACCESSION:BD107557
294	17.2	0.5	24	1	AX058875	ACCESSION:AR058875	367	16.8	0.4	23	1	BD271420	ACCESSION:BD271420
295	17.2	0.5	24	1	AR058877	ACCESSION:AR058877	368	16.8	0.4	23	1	BD271421	ACCESSION:BD271421
296	17.2	0.5	24	1	AR079580	ACCESSION:AR079580	369	16.8	0.4	23	1	AX074547	ACCESSION:AX074547
297	17.2	0.5	24	1	AR123289	ACCESSION:AR123289	370	16.8	0.4	23	1	AX455018	ACCESSION:AX455018
298	17.2	0.5	24	1	AR123289	ACCESSION:AR123289	371	16.8	0.4	23	1	AX785090	ACCESSION:AX785090
299	17.2	0.5	24	1	AR123291	ACCESSION:AR123291	c 372	16.8	0.4	23	1	AX799210	ACCESSION:AX799210
300	17.2	0.5	24	1	BD188891	ACCESSION:BD188891	c 373	16.8	0.4	24	1	AS7513	ACCESSION:AS7513
301	17.2	0.5	24	1	BD188893	ACCESSION:BD188893	c 374	16.8	0.4	24	1	AS7516	ACCESSION:AS7516
302	17.2	0.5	24	1	I33252	ACCESSION:I33252	c 375	16.8	0.4	24	1	AR052979	ACCESSION:AR052979
303	17.2	0.5	24	1	I33254	ACCESSION:I33254	c 376	16.8	0.4	24	1	AR052982	ACCESSION:AR052982
304	17.2	0.5	24	1	I35517	ACCESSION:I35517	c 377	16.8	0.4	24	1	CQ828722	ACCESSION:CQ828722
305	17.2	0.5	24	1	I35519	ACCESSION:I35519	c 378	16.8	0.4	24	1	E31758	ACCESSION:E31758
306	17.2	0.5	24	1	I43127	ACCESSION:I43127	c 379	16.6	0.4	23	1	AX8768	ACCESSION:AX8768
307	17.2	0.5	24	1	I43129	ACCESSION:I43129	c 380	16.6	0.4	23	1	AR157364	ACCESSION:AR157364
308	17.2	0.5	24	1	I92005	ACCESSION:I92005	c 381	16.6	0.4	23	1	BD195029	ACCESSION:BD195029
309	17.2	0.5	24	1	I92007	ACCESSION:I92007	c 382	16.6	0.4	23	1	CQ799557	ACCESSION:CQ799557
c 310	17	0.4	17	1	E11484	ACCESSION:E11484	c 383	16.6	0.4	23	1	CQ841335	ACCESSION:CQ841335
311	17	0.4	17	1	AR455908	ACCESSION:AR455908	384	16.6	0.4	23	1	CQ841340	ACCESSION:CQ841340
c 312	17	0.4	17	1	AR455910	ACCESSION:AR455910	c 385	16.6	0.4	23	1	AX020199	ACCESSION:AX020199
313	17	0.4	17	1	AX239678	ACCESSION:AX239678	c 386	16.6	0.4	23	1	AX452855	ACCESSION:AX452855
c 314	17	0.4	17	1	AX239680	ACCESSION:AX239680	c 387	16.6	0.4	23	1	AX685107	ACCESSION:AX685107
c 315	17	0.4	18	1	AR071773	ACCESSION:AR071773	c 388	16.6	0.4	23	1	AX794949	ACCESSION:AX794949
c 316	17	0.4	18	1	AR071777	ACCESSION:AR071777	c 389	16.6	0.4	23	1	AX926751	ACCESSION:AX926751
c 317	17	0.4	18	1	AR071778	ACCESSION:AR071778	c 390	16.4	0.4	18	1	AR071772	ACCESSION:AR071772
c 318	17	0.4	18	1	AR071779	ACCESSION:AR071779	c 391	16.4	0.4	18	1	AR071799	ACCESSION:AR071799
c 319	17	0.4	18	1	AR071801	ACCESSION:AR071801	392	16.4	0.4	18	1	E28534	ACCESSION:E28534
c 320	17	0.4	18	1	AR071802	ACCESSION:AR071802	c 393	16.4	0.4	18	1	E28534	ACCESSION:E28534
c 321	17	0.4	18	1	AR071803	ACCESSION:AR071803	394	16.4	0.4	18	1	AR241816	ACCESSION:AR241816
c 322	17	0.4	18	1	AR178165	ACCESSION:AR178165	395	16.4	0.4	18	1	AX355057	ACCESSION:AX355057
323	17	0.4	18	1	AR178166	ACCESSION:AR178166	c 396	16.4	0.4	18	1	AX355057	ACCESSION:AX355057
324	17	0.4	18	1	AR182079	ACCESSION:AR182079	397	16.4	0.4	20	1	AR338196	ACCESSION:AR338196
325	17	0.4	18	1	AR261503	ACCESSION:AR261503	398	16.4	0.4	21	1	AR393666	ACCESSION:AR393666

C 399	16.4	0.4	21	1	AX020767	472	16	0.4	30	1	BD166026	ACCESSION:BD166026
C 400	16.4	0.4	21	1	AX020767	473	16	0.4	30	1	BD166028	ACCESSION:BD166028
C 401	16.4	0.4	23	1	AX020767	474	15.8	0.4	19	1	AR074777	ACCESSION:AR074777
C 402	16.4	0.4	23	1	A73578	C 475	15.8	0.4	19	1	BD192775	ACCESSION:BD192775
C 403	16.2	0.4	21	1	AX38978	476	15.8	0.4	19	1	AX132173	ACCESSION:AX132173
C 404	16.2	0.4	21	1	A25398	477	15.8	0.4	20	1	A80994	ACCESSION:A80994
C 405	16.2	0.4	21	1	A25416	478	15.8	0.4	20	1	A88143	ACCESSION:A88143
C 406	16.2	0.4	21	1	A27176	479	15.8	0.4	20	1	A90110	ACCESSION:A90110
C 407	16.2	0.4	21	1	AR031310	480	15.8	0.4	20	1	A95373	ACCESSION:A95373
C 408	16.2	0.4	21	1	AR084555	C 481	15.8	0.4	20	1	AR070856	ACCESSION:AR070856
C 409	16.2	0.4	21	1	AR084555	C 482	15.8	0.4	20	1	AR074792	ACCESSION:AR074792
C 410	16.2	0.4	21	1	AR084576	C 483	15.8	0.4	20	1	AR117573	ACCESSION:AR117573
C 411	16.2	0.4	21	1	AR121232	C 484	15.8	0.4	20	1	AR125552	ACCESSION:AR125552
C 412	16.2	0.4	21	1	AR121232	C 485	15.8	0.4	20	1	BD190536	ACCESSION:BD190536
C 413	16.2	0.4	21	1	AR121232	C 486	15.8	0.4	20	1	BD250309	ACCESSION:BD250309
C 414	16.2	0.4	21	1	AR121232	C 487	15.8	0.4	20	1	E32215	ACCESSION:E32215
C 415	16.2	0.4	21	1	AR121232	C 488	15.8	0.4	20	1	AR228858	ACCESSION:AR228858
C 416	16.2	0.4	21	1	AR121232	C 489	15.8	0.4	20	1	AR271190	ACCESSION:AR271190
C 417	16.2	0.4	21	1	AR121232	C 490	15.8	0.4	20	1	AX029182	ACCESSION:AX029182
C 418	16.2	0.4	21	1	AR121232	C 491	15.8	0.4	20	1	AX224874	ACCESSION:AX224874
C 419	16.2	0.4	21	1	AR121232	C 492	15.8	0.4	20	1	AX224884	ACCESSION:AX224884
C 420	16.2	0.4	21	1	AR121232	C 493	15.8	0.4	20	1	AX250713	ACCESSION:AX250713
C 421	16.2	0.4	21	1	AR121232	C 494	15.8	0.4	20	1	AX469446	ACCESSION:AX469446
C 422	16.2	0.4	21	1	AR121232	C 495	15.8	0.4	20	1	AX476807	ACCESSION:AX476807
C 423	16.2	0.4	21	1	AR121232	C 496	15.8	0.4	20	1	BD016057	ACCESSION:BD016057
C 424	16.2	0.4	21	1	AR121232	C 497	15.8	0.4	20	1	BD016176	ACCESSION:BD016176
C 425	16.2	0.4	21	1	AR121232	C 498	15.8	0.4	20	1	BD017328	ACCESSION:BD017328
C 426	16.2	0.4	21	1	AR121232	C 499	15.8	0.4	20	1	BD065656	ACCESSION:BD065656
C 427	16.2	0.4	21	1	AR121232	C 500	15.8	0.4	20	1	BD174235	ACCESSION:BD174235
C 428	16.2	0.4	21	1	AR121232	C 501	15.8	0.4	21	1	E14785	ACCESSION:E14785
C 429	16.2	0.4	21	1	AR121232	C 502	15.8	0.4	21	1	BD056548	ACCESSION:BD056548
C 430	16.2	0.4	21	1	AR121232	C 503	15.8	0.4	21	1	AR264925	ACCESSION:AR264925
C 431	16.2	0.4	21	1	AR121232	C 504	15.8	0.4	21	1	AR478206	ACCESSION:AR478206
C 432	16.2	0.4	21	1	AR121232	C 505	15.8	0.4	21	1	BD072870	ACCESSION:BD072870
C 433	16.2	0.4	21	1	AR121232	C 506	15.8	0.4	21	1	BD107497	ACCESSION:BD107497
C 434	16.2	0.4	21	1	AR121232	C 507	15.8	0.4	21	1	BD145029	ACCESSION:BD145029
C 435	16.2	0.4	21	1	AR121232	C 508	15.8	0.4	21	1	BD166029	ACCESSION:BD166029
C 436	16.2	0.4	21	1	AR121232	C 509	15.8	0.4	21	1	AR309630	ACCESSION:AR309630
C 437	16.2	0.4	21	1	AR121232	C 510	15.8	0.4	21	1	BD238391	ACCESSION:BD238391
C 438	16.2	0.4	21	1	AR121232	C 511	15.8	0.4	21	1	AR279817	ACCESSION:AR279817
C 439	16.2	0.4	21	1	AR121232	C 512	15.6	0.4	21	1	AR138717	ACCESSION:AR138717
C 440	16.2	0.4	21	1	AR121232	C 513	15.6	0.4	21	1	AX094910	ACCESSION:AX094910
C 441	16.2	0.4	21	1	AR121232	C 514	15.6	0.4	22	1	A39908	ACCESSION:A39908
C 442	16.2	0.4	21	1	AR121232	C 515	15.6	0.4	22	1	AR036420	ACCESSION:AR036420
C 443	16.2	0.4	21	1	AR121232	C 516	15.6	0.4	22	1	AR048932	ACCESSION:AR048932
C 444	16.2	0.4	21	1	AR121232	C 517	15.6	0.4	22	1	CQ812601	ACCESSION:CQ812601
C 445	16.2	0.4	21	1	AR121232	C 518	15.6	0.4	22	1	I29861	ACCESSION:I29861
C 446	16.2	0.4	21	1	AR121232	C 519	15.6	0.4	22	1	I34465	ACCESSION:I34465
C 447	16.2	0.4	21	1	AR121232	C 520	15.6	0.4	22	1	AX252963	ACCESSION:AX252963
C 448	16.2	0.4	21	1	AR121232	C 521	15.6	0.4	22	1	AX367061	ACCESSION:AX367061
C 449	16.2	0.4	21	1	AR121232	C 522	15.6	0.4	22	1	AX740255	ACCESSION:AX740255
C 450	16.2	0.4	21	1	AR121232	C 523	15.6	0.4	22	1	AX743831	ACCESSION:AX743831
C 451	16.2	0.4	21	1	AR121232	C 524	15.6	0.4	22	1	AX937575	ACCESSION:AX937575
C 452	16.2	0.4	21	1	AR121232	C 525	15.4	0.4	17	1	A95626	ACCESSION:A95626
C 453	16.2	0.4	21	1	AR121232	C 526	15.4	0.4	17	1	AR023742	ACCESSION:AR023742
C 454	16.2	0.4	21	1	AR121232	C 527	15.4	0.4	17	1	AR036967	ACCESSION:AR036967
C 455	16.2	0.4	21	1	AR121232	C 528	15.4	0.4	17	1	BD199067	ACCESSION:BD199067
C 456	16.2	0.4	21	1	AR121232	C 529	15.4	0.4	17	1	BD226525	ACCESSION:BD226525
C 457	16.2	0.4	21	1	AR121232	C 530	15.4	0.4	17	1	CQ623256	ACCESSION:CQ623256
C 458	16.2	0.4	21	1	AR121232	C 531	15.4	0.4	17	1	AR188722	ACCESSION:AR188722
C 459	16.2	0.4	21	1	AR121232	C 532	15.4	0.4	17	1	AR188754	ACCESSION:AR188754
C 460	16.2	0.4	21	1	AR121232	C 533	15.4	0.4	17	1	AR286400	ACCESSION:AR286400
C 461	16.2	0.4	21	1	AR121232	C 534	15.4	0.4	17	1	AR324575	ACCESSION:AR324575
C 462	16.2	0.4	21	1	AR121232	C 535	15.4	0.4	17	1	AR324607	ACCESSION:AR324607
C 463	16.2	0.4	21	1	AR121232	C 536	15.4	0.4	17	1	AR329327	ACCESSION:AR329327
C 464	16.2	0.4	21	1	AR121232	C 537	15.4	0.4	17	1	AR329328	ACCESSION:AR329328
C 465	16.2	0.4	21	1	AR121232	C 538	15.4	0.4	17	1	AR329329	ACCESSION:AR329329
C 466	16.2	0.4	21	1	AR121232	C 539	15.4	0.4	17	1	AR329330	ACCESSION:AR329330
C 467	16.2	0.4	21	1	AR121232	C 540	15.4	0.4	17	1	AR329331	ACCESSION:AR329331
C 468	16.2	0.4	21	1	AR121232	C 541	15.4	0.4	17	1	AR329332	ACCESSION:AR329332
C 469	16.2	0.4	21	1	AR121232	C 542	15.4	0.4	17	1	AR329333	ACCESSION:AR329333
C 470	16.2	0.4	21	1	AR121232	C 543	15.4	0.4	17	1	AR329334	ACCESSION:AR329334
C 471	16.2	0.4	21	1	AR121232	C 544	15.4	0.4	17	1	AR329335	ACCESSION:AR329335

545	15.4	0.4	17	1	AX734179	ACCSSION:AX734179	C 618	15.2	0.4	20	1	AX293956	ACCSSION:AX293956
546	15.4	0.4	17	1	AX738591	ACCSSION:AX738591	C 619	15.2	0.4	20	1	AX452336	ACCSSION:AX452336
547	15.4	0.4	17	1	BD091430	ACCSSION:BD091430	620	15.2	0.4	20	1	AX477161	ACCSSION:AX477161
548	15.4	0.4	18	1	AX241816	ACCSSION:AX241816	621	15.2	0.4	20	1	AX526537	ACCSSION:AX526537
549	15.4	0.4	19	1	A95063	ACCSSION:A95063	622	15.2	0.4	20	1	AX712200	ACCSSION:AX712200
550	15.4	0.4	19	1	AR072218	ACCSSION:AR072218	623	15.2	0.4	20	1	AX787161	ACCSSION:AX787161
551	15.4	0.4	19	1	CQ802798	ACCSSION:CQ802798	624	15.2	0.4	20	1	AX799916	ACCSSION:AX799916
552	15.4	0.4	19	1	I26329	ACCSSION:I26329	625	15.2	0.4	20	1	BD072884	ACCSSION:BD072884
553	15.4	0.4	19	1	AR222435	ACCSSION:AR222435	626	15.2	0.4	20	1	BD072895	ACCSSION:BD072895
554	15.4	0.4	19	1	BD102783	ACCSSION:BD102783	627	15.2	0.4	20	1	BD106032	ACCSSION:BD106032
555	15.4	0.4	20	1	AR373540	ACCSSION:AR373540	628	15.2	0.4	20	1	BD107511	ACCSSION:BD107511
556	15.4	0.4	20	1	AR074776	ACCSSION:AR074776	629	15.2	0.4	20	1	BD107522	ACCSSION:BD107522
557	15.4	0.4	20	1	AR103195	ACCSSION:AR103195	630	15.2	0.4	20	1	BD138221	ACCSSION:BD138221
558	15.4	0.4	20	1	AR199773	ACCSSION:AR199773	631	15.2	0.4	20	1	BD138283	ACCSSION:BD138283
559	15.4	0.4	20	1	AR214196	ACCSSION:AR214196	632	15.2	0.4	20	1	BD145043	ACCSSION:BD145043
560	15.4	0.4	20	1	AR214200	ACCSSION:AR214200	633	15.2	0.4	20	1	BD145054	ACCSSION:BD145054
561	15.4	0.4	20	1	AX370498	ACCSSION:AX370498	634	15.2	0.4	20	1	BD166043	ACCSSION:BD166043
562	15.4	0.4	20	1	AX527818	ACCSSION:AX527818	635	15.2	0.4	20	1	BD166054	ACCSSION:BD166054
563	15.4	0.4	20	1	AX601143	ACCSSION:AX601143	636	15.2	0.4	20	1	DOGH0X7B	ACCSSION:L77371
564	15.4	0.4	20	1	BD144226	ACCSSION:BD144226	637	15.2	0.4	21	1	BD140705	ACCSSION:BD140705
565	15.4	0.4	21	1	AR177588	ACCSSION:AR177588	638	15.2	0.4	21	1	A28676	ACCSSION:A28676
566	15.4	0.4	21	1	CQ788487	ACCSSION:CQ788487	639	15.2	0.4	21	1	AR073030	ACCSSION:AR073030
567	15.4	0.4	21	1	AX146144	ACCSSION:AX146144	640	15.2	0.4	21	1	AR084556	ACCSSION:AR084556
568	15.4	0.4	21	1	AX539564	ACCSSION:AX539564	641	15.2	0.4	21	1	AR084560	ACCSSION:AR084560
569	15.4	0.4	21	1	AX539565	ACCSSION:AX539565	642	15.2	0.4	21	1	AR084593	ACCSSION:AR084593
570	15.4	0.4	21	1	AX955606	ACCSSION:AX955606	643	15.2	0.4	21	1	AR084597	ACCSSION:AR084597
571	15.4	0.4	25	1	AX042549	ACCSSION:AX042549	644	15.2	0.4	21	1	BD250646	ACCSSION:BD250646
572	15.4	0.4	25	1	AX043230	ACCSSION:AX043230	645	15.2	0.4	21	1	BD266134	ACCSSION:BD266134
573	15.4	0.4	30	1	AX351715	ACCSSION:AX351715	646	15.2	0.4	21	1	CQ769152	ACCSSION:CQ769152
574	15.4	0.4	31	1	A08914	ACCSSION:A08914	647	15.2	0.4	21	1	CQ797933	ACCSSION:CQ797933
575	15.4	0.4	35	1	AR029831	ACCSSION:AR029831	648	15.2	0.4	21	1	E08187	ACCSSION:E08187
576	15.4	0.4	41	1	I31440	ACCSSION:I31440	649	15.2	0.4	21	1	I27608	ACCSSION:I27608
577	15.4	0.4	41	1	I31443	ACCSSION:I31443	650	15.2	0.4	21	1	AR279803	ACCSSION:AR279803
578	15.2	0.4	40	1	AR181773	ACCSSION:AR181773	651	15.2	0.4	21	1	AR351501	ACCSSION:AR351501
579	15.2	0.4	20	1	A65910	ACCSSION:A65910	652	15.2	0.4	21	1	AR483457	ACCSSION:AR483457
580	15.2	0.4	20	1	AR050627	ACCSSION:AR050627	653	15.2	0.4	21	1	AR203590	ACCSSION:AR203590
581	15.2	0.4	20	1	AR067440	ACCSSION:AR067440	654	15.2	0.4	21	1	AX226447	ACCSSION:AX226447
582	15.2	0.4	20	1	AR100070	ACCSSION:AR100070	655	15.2	0.4	21	1	AX250034	ACCSSION:AX250034
583	15.2	0.4	20	1	AR117533	ACCSSION:AR117533	656	15.2	0.4	21	1	AX740291	ACCSSION:AX740291
584	15.2	0.4	20	1	AR129685	ACCSSION:AR129685	657	15.2	0.4	22	1	BD140700	ACCSSION:BD140700
585	15.2	0.4	20	1	AR163988	ACCSSION:AR163988	658	15.2	0.4	29	1	AR438517	ACCSSION:AR438517
586	15.2	0.4	20	1	AR170760	ACCSSION:AR170760	659	15.2	0.4	29	1	AX430216	ACCSSION:AX430216
587	15.2	0.4	20	1	AR176139	ACCSSION:AR176139	660	15.2	0.4	29	1	BD165919	ACCSSION:BD165919
588	15.2	0.4	20	1	BD250269	ACCSSION:BD250269	661	15.2	0.4	30	1	I30206	ACCSSION:I30206
589	15.2	0.4	20	1	CQ759158	ACCSSION:CQ759158	662	15.2	0.4	30	1	A79651	ACCSSION:A79651
590	15.2	0.4	20	1	CQ762434	ACCSSION:CQ762434	663	15.2	0.4	37	1	HSOBRI05	ACCSSION:U62489
591	15.2	0.4	20	1	CQ762603	ACCSSION:CQ762603	664	15	0.4	15	1	AR074710	ACCSSION:AR074710
592	15.2	0.4	20	1	CQ763381	ACCSSION:CQ763381	665	15	0.4	15	1	AR074711	ACCSSION:AR074711
593	15.2	0.4	20	1	E12301	ACCSSION:E12301	666	15	0.4	15	1	AR074712	ACCSSION:AR074712
594	15.2	0.4	20	1	E25559	ACCSSION:E25559	667	15	0.4	15	1	AR074713	ACCSSION:AR074713
595	15.2	0.4	20	1	I16675	ACCSSION:I16675	668	15	0.4	15	1	AR127803	ACCSSION:AR127803
596	15.2	0.4	20	1	I18759	ACCSSION:I18759	669	15	0.4	15	1	AX175252	ACCSSION:AX175252
597	15.2	0.4	20	1	I19017	ACCSSION:I19017	670	15	0.4	15	1	AX721631	ACCSSION:AX721631
598	15.2	0.4	20	1	IR9428	ACCSSION:IR9428	671	15	0.4	16	1	AR328668	ACCSSION:AR328668
599	15.2	0.4	20	1	AR199806	ACCSSION:AR199806	672	15	0.4	17	1	AR074719	ACCSSION:AR074719
600	15.2	0.4	20	1	AR208740	ACCSSION:AR208740	673	15	0.4	17	1	AX687933	ACCSSION:AX687933
601	15.2	0.4	20	1	AR211982	ACCSSION:AR211982	674	15	0.4	17	1	AX687934	ACCSSION:AX687934
602	15.2	0.4	20	1	AR214733	ACCSSION:AR214733	675	15	0.4	17	1	AX687935	ACCSSION:AX687935
603	15.2	0.4	20	1	AR225997	ACCSSION:AR225997	676	15	0.4	18	1	AR076354	ACCSSION:AR076354
604	15.2	0.4	20	1	AR228818	ACCSSION:AR228818	677	15	0.4	18	1	BD234297	ACCSSION:BD234297
605	15.2	0.4	20	1	AR264939	ACCSSION:AR264939	678	15	0.4	19	1	AR127806	ACCSSION:AR127806
606	15.2	0.4	20	1	AR304132	ACCSSION:AR304132	679	15	0.4	20	1	AR163975	ACCSSION:AR163975
607	15.2	0.4	20	1	AR305121	ACCSSION:AR305121	680	15	0.4	20	1	AR208748	ACCSSION:AR208748
608	15.2	0.4	20	1	AR309225	ACCSSION:AR309225	681	15	0.4	20	1	AX482068	ACCSSION:AX482068
609	15.2	0.4	20	1	AR399605	ACCSSION:AR399605	682	15	0.4	20	1	AX511307	ACCSSION:AX511307
610	15.2	0.4	20	1	AR478220	ACCSSION:AR478220	683	15	0.4	20	1	AX721667	ACCSSION:AX721667
611	15.2	0.4	20	1	AR489949	ACCSSION:AR489949	684	15	0.4	23	1	S61964	ACCSSION:S61964
612	15.2	0.4	20	1	AR489951	ACCSSION:AR489951	685	14.8	0.4	18	1	AR7890	ACCSSION:AR7890
613	15.2	0.4	20	1	AR489957	ACCSSION:AR489957	686	14.8	0.4	18	1	A89857	ACCSSION:A89857
614	15.2	0.4	20	1	AX035957	ACCSSION:AX035957	687	14.8	0.4	18	1	AR187533	ACCSSION:AR187533
615	15.2	0.4	20	1	AX149223	ACCSSION:AX149223	688	14.8	0.4	18	1	AR190756	ACCSSION:AR190756
616	15.2	0.4	20	1	AX224921	ACCSSION:AX224921	689	14.8	0.4	18	1	AR219474	ACCSSION:AR219474
617	15.2	0.4	20	1			690	14.8	0.4	18	1	AR324047	ACCSSION:AR324047

691	14.8	0.4	18	1	AR325602	ACCESSION:AR325602	764	14.8	0.4	20	1	AX295588	ACCESSION:AX295588
692	14.8	0.4	18	1	AR336934	ACCESSION:AR336934	765	14.8	0.4	20	1	AX295703	ACCESSION:AX295703
693	14.8	0.4	18	1	AR336934	ACCESSION:AR336934	766	14.8	0.4	20	1	AX296579	ACCESSION:AX296579
694	14.8	0.4	18	1	AX733276	ACCESSION:AX733276	767	14.8	0.4	20	1	AX297158	ACCESSION:AX297158
695	14.8	0.4	18	1	AX773292	ACCESSION:AX773292	768	14.8	0.4	20	1	AX355435	ACCESSION:AX355435
696	14.8	0.4	18	1	AX773292	ACCESSION:AX773292	769	14.8	0.4	20	1	AX357565	ACCESSION:AX357565
697	14.8	0.4	18	1	AX822700	ACCESSION:AX822700	770	14.8	0.4	20	1	AX487479	ACCESSION:AX487479
698	14.8	0.4	18	1	AX826340	ACCESSION:AX826340	771	14.8	0.4	20	1	AX487479	ACCESSION:AX487479
699	14.8	0.4	18	1	BD065403	ACCESSION:BD065403	772	14.8	0.4	20	1	AX547172	ACCESSION:AX547172
700	14.8	0.4	19	1	AX1634	ACCESSION:AX1634	773	14.8	0.4	20	1	AX552535	ACCESSION:AX552535
701	14.8	0.4	19	1	AR129286	ACCESSION:AR129286	774	14.8	0.4	20	1	AX613359	ACCESSION:AX613359
702	14.8	0.4	19	1	BD182533	ACCESSION:BD182533	775	14.8	0.4	20	1	AX708866	ACCESSION:AX708866
703	14.8	0.4	19	1	BD196868	ACCESSION:BD196868	776	14.8	0.4	20	1	AX708891	ACCESSION:AX708891
704	14.8	0.4	19	1	BD196931	ACCESSION:BD196931	777	14.8	0.4	20	1	BD014728	ACCESSION:BD014728
705	14.8	0.4	19	1	195651	ACCESSION:195651	778	14.8	0.4	20	1	BD074607	ACCESSION:BD074607
706	14.8	0.4	19	1	AR493086	ACCESSION:AR493086	779	14.8	0.4	20	1	BD074618	ACCESSION:BD074618
707	14.8	0.4	19	1	AX166727	ACCESSION:AX166727	780	14.8	0.4	20	1	BD082094	ACCESSION:BD082094
708	14.8	0.4	19	1	AX353125	ACCESSION:AX353125	781	14.8	0.4	20	1	BD084635	ACCESSION:BD084635
709	14.8	0.4	19	1	AX362970	ACCESSION:AX362970	782	14.8	0.4	20	1	BD088328	ACCESSION:BD088328
710	14.8	0.4	19	1	AX539200	ACCESSION:AX539200	783	14.8	0.4	20	1	BD147172	ACCESSION:BD147172
711	14.8	0.4	19	1	BD023416	ACCESSION:BD023416	784	14.8	0.4	21	1	BD146811	ACCESSION:BD146811
712	14.8	0.4	19	1	BD089758	ACCESSION:BD089758	785	14.8	0.4	21	1	BD223228	ACCESSION:BD223228
713	14.8	0.4	20	1	AB068169	ACCESSION:AB068169	786	14.8	0.4	21	1	BD247285	ACCESSION:BD247285
714	14.8	0.4	20	1	AR214196	ACCESSION:AR214196	787	14.8	0.4	21	1	BD262820	ACCESSION:BD262820
715	14.8	0.4	20	1	AR2029135	ACCESSION:AR2029135	788	14.8	0.4	21	1	BD266093	ACCESSION:BD266093
716	14.8	0.4	20	1	AR036519	ACCESSION:AR036519	789	14.8	0.4	21	1	BD266093	ACCESSION:BD266093
717	14.8	0.4	20	1	AR073957	ACCESSION:AR073957	790	14.8	0.4	21	1	BD266093	ACCESSION:BD266093
718	14.8	0.4	20	1	AR073957	ACCESSION:AR073957	791	14.8	0.4	21	1	BD266093	ACCESSION:BD266093
719	14.8	0.4	20	1	AR074771	ACCESSION:AR074771	792	14.8	0.4	21	1	BD266093	ACCESSION:BD266093
720	14.8	0.4	20	1	AR074785	ACCESSION:AR074785	793	14.8	0.4	21	1	BD266093	ACCESSION:BD266093
721	14.8	0.4	20	1	AR096052	ACCESSION:AR096052	794	1					

837	14.4	0.4	16	1	I33563	ACCSSION:I33563	910	14.4	0.4	18	1	BD086292	ACCSSION:BD086292
838	14.4	0.4	16	1	I33563	ACCSSION:I33563	911	14.4	0.4	18	1	BD172416	ACCSSION:BD172416
839	14.4	0.4	16	1	I38642	ACCSSION:I38642	912	14.4	0.4	18	1	BD172735	ACCSSION:BD172735
840	14.4	0.4	16	1	I38642	ACCSSION:I38642	913	14.4	0.4	18	1	BD173054	ACCSSION:BD173054
841	14.4	0.4	16	1	I51790	ACCSSION:I51790	914	14.4	0.4	18	1	BD173373	ACCSSION:BD173373
842	14.4	0.4	16	1	I84399	ACCSSION:I84399	915	14.4	0.4	19	1	AR131366	ACCSSION:AR131366
843	14.4	0.4	16	1	AR204607	ACCSSION:AR204607	916	14.4	0.4	19	1	CQ785575	ACCSSION:CQ785575
844	14.4	0.4	16	1	AR307317	ACCSSION:AR307317	C 917	14.4	0.4	19	1	E09395	ACCSSION:E09395
845	14.4	0.4	16	1	AR328417	ACCSSION:AR328417	C 918	14.4	0.4	19	1	AR482127	ACCSSION:AR482127
846	14.4	0.4	16	1	AR328446	ACCSSION:AR328446	C 919	14.4	0.4	19	1	AX117795	ACCSSION:AX117795
847	14.4	0.4	16	1	AR328669	ACCSSION:AR328669	C 920	14.4	0.4	19	1	AX131096	ACCSSION:AX131096
848	14.4	0.4	16	1	AX067878	ACCSSION:AX067878	C 921	14.4	0.4	19	1	BD001771	ACCSSION:BD001771
849	14.4	0.4	16	1	AX135452	ACCSSION:AX135452	C 922	14.4	0.4	20	1	AR020466	ACCSSION:AR020466
850	14.4	0.4	16	1	BD002055	ACCSSION:BD002055	C 923	14.4	0.4	20	1	AR026501	ACCSSION:AR026501
851	14.4	0.4	16	1	BD016424	ACCSSION:BD016424	C 924	14.4	0.4	20	1	AR063688	ACCSSION:AR063688
852	14.4	0.4	17	1	AR046263	ACCSSION:AR046263	C 925	14.4	0.4	20	1	AR116436	ACCSSION:AR116436
853	14.4	0.4	17	1	AR057459	ACCSSION:AR057459	C 926	14.4	0.4	20	1	AR130803	ACCSSION:AR130803
854	14.4	0.4	17	1	AR057807	ACCSSION:AR057807	C 927	14.4	0.4	20	1	BD233551	ACCSSION:BD233551
855	14.4	0.4	17	1	AR115217	ACCSSION:AR115217	C 928	14.4	0.4	20	1	I25851	ACCSSION:I25851
856	14.4	0.4	17	1	AR115565	ACCSSION:AR115565	C 929	14.4	0.4	20	1	I43488	ACCSSION:I43488
857	14.4	0.4	17	1	CQ617262	ACCSSION:CQ617262	C 930	14.4	0.4	20	1	AR208766	ACCSSION:AR208766
858	14.4	0.4	17	1	CQ617263	ACCSSION:CQ617263	C 931	14.4	0.4	20	1	AR435720	ACCSSION:AR435720
859	14.4	0.4	17	1	CQ617265	ACCSSION:CQ617265	C 932	14.4	0.4	20	1	AR475721	ACCSSION:AR475721
860	14.4	0.4	17	1	CQ617266	ACCSSION:CQ617266	C 933	14.4	0.4	20	1	AX006846	ACCSSION:AX006846
861	14.4	0.4	17	1	CQ623255	ACCSSION:CQ623255	C 934	14.4	0.4	20	1	AX078019	ACCSSION:AX078019
862	14.4	0.4	17	1	CQ623257	ACCSSION:CQ623257	C 935	14.4	0.4	20	1	AX304783	ACCSSION:AX304783
863	14.4	0.4	17	1	I53315	ACCSSION:I53315	C 936	14.4	0.4	20	1	AX040665	ACCSSION:AX040665
864	14.4	0.4	17	1	AR190295	ACCSSION:AR190295	C 937	14.4	0.4	20	1	AX494234	ACCSSION:AX494234
865	14.4	0.4	17	1	AR325248	ACCSSION:AR325248	C 938	14.4	0.4	20	1	AX553634	ACCSSION:AX553634
866	14.4	0.4	17	1	AR327351	ACCSSION:AR327351	C 939	14.4	0.4	20	1	AX740160	ACCSSION:AX740160
867	14.4	0.4	17	1	AR293330	ACCSSION:AR293330	C 940	14.4	0.4	20	1	AX785898	ACCSSION:AX785898
868	14.4	0.4	17	1	AR458325	ACCSSION:AR458325	C 941	14.4	0.4	20	1	AX926289	ACCSSION:AX926289
869	14.4	0.4	17	1	AR458326	ACCSSION:AR458326	C 942	14.4	0.4	20	1	AX926579	ACCSSION:AX926579
870	14.4	0.4	17	1	AR458328	ACCSSION:AR458328	C 943	14.4	0.4	20	1	BD074593	ACCSSION:BD074593
871	14.4	0.4	17	1	AR458329	ACCSSION:AR458329	C 944	14.4	0.4	25	1	BD244864	ACCSSION:BD244864
872	14.4	0.4	17	1	AR464318	ACCSSION:AR464318	C 945	14.4	0.4	25	1	AX043454	ACCSSION:AX043454
873	14.4	0.4	17	1	AR464320	ACCSSION:AR464320	C 946	14.4	0.4	26	1	AG3569	ACCSSION:AG3569
874	14.4	0.4	17	1	AX216365	ACCSSION:AX216365	C 947	14.4	0.4	26	1	E33560	ACCSSION:E33560
875	14.4	0.4	17	1	AX217982	ACCSSION:AX217982	C 948	14.4	0.4	30	1	AR264927	ACCSSION:AR264927
876	14.4	0.4	17	1	AX272813	ACCSSION:AX272813	C 949	14.4	0.4	30	1	AR478208	ACCSSION:AR478208
877	14.4	0.4	17	1	AX273076	ACCSSION:AX273076	C 950	14.4	0.4	30	1	BD072872	ACCSSION:BD072872
878	14.4	0.4	17	1	AX273311	ACCSSION:AX273311	C 951	14.4	0.4	30	1	BD107499	ACCSSION:BD107499
879	14.4	0.4	17	1	AX530932	ACCSSION:AX530932	C 952	14.4	0.4	30	1	BD145031	ACCSSION:BD145031
880	14.4	0.4	17	1	AX530934	ACCSSION:AX530934	C 953	14.4	0.4	30	1	BD166031	ACCSSION:BD166031
881	14.4	0.4	17	1	AX530935	ACCSSION:AX530935	C 954	14.4	0.4	32	1	AR051291	ACCSSION:AR051291
882	14.4	0.4	17	1	AX530936	ACCSSION:AX530936	C 955	14.4	0.4	32	1	I16939	ACCSSION:I16939
883	14.4	0.4	17	1	AX634548	ACCSSION:AX634548	C 956	14.4	0.4	32	1	I45733	ACCSSION:I45733
884	14.4	0.4	17	1	AX634866	ACCSSION:AX634866	C 957	14.4	0.4	40	1	BD170449	ACCSSION:BD170449
885	14.4	0.4	17	1	AX687337	ACCSSION:AX687337	C 958	14.4	0.4	40	1	CQ820328	ACCSSION:CQ820328
886	14.4	0.4	17	1	AX687398	ACCSSION:AX687398	C 959	14.4	0.4	44	1	AR038858	ACCSSION:AR038858
887	14.4	0.4	17	1	AX734671	ACCSSION:AX734671	C 960	14.4	0.4	19	1	A37552	ACCSSION:A37552
888	14.4	0.4	17	1	AX759120	ACCSSION:AX759120	C 961	14.2	0.4	19	1	A42357	ACCSSION:A42357
889	14.4	0.4	17	1	AX762817	ACCSSION:AX762817	C 962	14.2	0.4	19	1	A44390	ACCSSION:A44390
890	14.4	0.4	18	1	A34808	ACCSSION:A34808	C 963	14.2	0.4	19	1	A47177	ACCSSION:A47177
891	14.4	0.4	18	1	A47305	ACCSSION:A47305	C 964	14.2	0.4	19	1	A56651	ACCSSION:A56651
892	14.4	0.4	18	1	AR7891	ACCSSION:AR7891	C 965	14.2	0.4	19	1	AR0372	ACCSSION:AR0372
893	14.4	0.4	18	1	AR9858	ACCSSION:AR9858	C 966	14.2	0.4	19	1	AR111775	ACCSSION:AR111775
894	14.4	0.4	18	1	AR035673	ACCSSION:AR035673	C 967	14.2	0.4	19	1	AR179815	ACCSSION:AR179815
895	14.4	0.4	18	1	AR104208	ACCSSION:AR104208	C 968	14.2	0.4	19	1	BD266251	ACCSSION:BD266251
896	14.4	0.4	18	1	AR134314	ACCSSION:AR134314	C 969	14.2	0.4	19	1	CQ800200	ACCSSION:CQ800200
897	14.4	0.4	18	1	AR165360	ACCSSION:AR165360	C 970	14.2	0.4	19	1	I46926	ACCSSION:I46926
898	14.4	0.4	18	1	AR175407	ACCSSION:AR175407	C 971	14.2	0.4	19	1	I84730	ACCSSION:I84730
899	14.4	0.4	18	1	AR410785	ACCSSION:AR410785	C 972	14.2	0.4	19	1	AR193516	ACCSSION:AR193516
900	14.4	0.4	18	1	AR439149	ACCSSION:AR439149	C 973	14.2	0.4	19	1	AR254165	ACCSSION:AR254165
901	14.4	0.4	18	1	AR473169	ACCSSION:AR473169	C 974	14.2	0.4	19	1	AR292967	ACCSSION:AR292967
902	14.4	0.4	18	1	AX352818	ACCSSION:AX352818	C 975	14.2	0.4	19	1	AR294648	ACCSSION:AR294648
903	14.4	0.4	18	1	AX362663	ACCSSION:AX362663	C 976	14.2	0.4	19	1	AX081351	ACCSSION:AX081351
904	14.4	0.4	18	1	AX683709	ACCSSION:AX683709	C 977	14.2	0.4	19	1	AX128989	ACCSSION:AX128989
905	14.4	0.4	18	1	AX697638	ACCSSION:AX697638	C 978	14.2	0.4	19	1	AX128990	ACCSSION:AX128990
906	14.4	0.4	18	1	AX773279	ACCSSION:AX773279	C 979	14.2	0.4	19	1	AX129129	ACCSSION:AX129129
907	14.4	0.4	18	1	AX773295	ACCSSION:AX773295	C 980	14.2	0.4	19	1	AX129366	ACCSSION:AX129366
908	14.4	0.4	18	1	BD065404	ACCSSION:BD065404	C 981	14.2	0.4	19	1	AX129367	ACCSSION:AX129367
909	14.4	0.4	18	1	BD075556	ACCSSION:BD075556	C 982	14.2	0.4	19	1	AX129652	ACCSSION:AX129652

983	14.2	0.4	19	1	AX130617	ACCESSION:AX130617	CI056	14.2	0.4	20	1	I28186	ACCESSION:I28186
984	14.2	0.4	19	1	AX131319	ACCESSION:AX131319	1057	14.2	0.4	20	1	I33357	ACCESSION:I33357
985	14.2	0.4	19	1	AX132490	ACCESSION:AX132490	CI058	14.2	0.4	20	1	I33959	ACCESSION:I33959
C 986	14.2	0.4	19	1	AX204959	ACCESSION:AX204959	1059	14.2	0.4	20	1	I75371	ACCESSION:I75371
987	14.2	0.4	19	1	AX283191	ACCESSION:AX283191	CI060	14.2	0.4	20	1	I84306	ACCESSION:I84306
988	14.2	0.4	19	1	AX283247	ACCESSION:AX283247	CI061	14.2	0.4	20	1	I88636	ACCESSION:I88636
989	14.2	0.4	19	1	AX384647	ACCESSION:AX384647	CI062	14.2	0.4	20	1	AR182775	ACCESSION:AR182775
C 990	14.2	0.4	19	1	AX474023	ACCESSION:AX474023	CI063	14.2	0.4	20	1	AR198529	ACCESSION:AR198529
C 991	14.2	0.4	19	1	AX513754	ACCESSION:AX513754	1064	14.2	0.4	20	1	AR207423	ACCESSION:AR207423
C 992	14.2	0.4	19	1	AX544866	ACCESSION:AX544866	CI065	14.2	0.4	20	1	AR208741	ACCESSION:AR208741
993	14.2	0.4	19	1	AX928387	ACCESSION:AX928387	1066	14.2	0.4	20	1	AR211282	ACCESSION:AR211282
994	14.2	0.4	19	1	AX956746	ACCESSION:AX956746	CI067	14.2	0.4	20	1	AR217715	ACCESSION:AR217715
C 995	14.2	0.4	19	1	BD002098	ACCESSION:BD002098	CI068	14.2	0.4	20	1	AR217726	ACCESSION:AR217726
C 996	14.2	0.4	19	1	BD002141	ACCESSION:BD002141	CI069	14.2	0.4	20	1	AR217729	ACCESSION:AR217729
C 997	14.2	0.4	19	1	BD008057	ACCESSION:BD008057	CI070	14.2	0.4	20	1	AR221053	ACCESSION:AR221053
C 998	14.2	0.4	19	1	AB067988	ACCESSION:AB067988	CI071	14.2	0.4	20	1	AR223313	ACCESSION:AR223313
C 999	14.2	0.4	20	1	A32748	ACCESSION:A32748	CI072	14.2	0.4	20	1	AR223403	ACCESSION:AR223403
CI000	14.2	0.4	20	1	A47852	ACCESSION:A47852	CI073	14.2	0.4	20	1	AR224513	ACCESSION:AR224513
1001	14.2	0.4	20	1	A63042	ACCESSION:A63042	1074	14.2	0.4	20	1	AR225072	ACCESSION:AR225072
1002	14.2	0.4	20	1	A97518	ACCESSION:A97518	CI075	14.2	0.4	20	1	AR231256	ACCESSION:AR231256
1003	14.2	0.4	20	1	AR012029	ACCESSION:AR012029	CI076	14.2	0.4	20	1	AR242698	ACCESSION:AR242698
1004	14.2	0.4	20	1	AR062662	ACCESSION:AR062662	CI077	14.2	0.4	20	1	AR243570	ACCESSION:AR243570
CI005	14.2	0.4	20	1	AR062829	ACCESSION:AR062829	CI078	14.2	0.4	20	1	AR255972	ACCESSION:AR255972
CI006	14.2	0.4	20	1	AR076718	ACCESSION:AR076718	CI079	14.2	0.4	20	1	AR268291	ACCESSION:AR268291
CI007	14.2	0.4	20	1	AR079558	ACCESSION:AR079558	CI080	14.2	0.4	20	1	AR272010	ACCESSION:AR272010
1008	14.2	0.4	20	1	AR104765	ACCESSION:AR104765	1081	14.2	0.4	20	1	AR279110	ACCESSION:AR279110
1009	14.2	0.4	20	1	AR105587	ACCESSION:AR105587	1082	14.2	0.4	20	1	AR299882	ACCESSION:AR299882
CI010	14.2	0.4	20	1	AR108646	ACCESSION:AR108646	CI083	14.2	0.4	20	1	AR300855	ACCESSION:AR300855
1011	14.2	0.4	20	1	AR116480	ACCESSION:AR116480	CI084	14.2	0.4	20	1	AR311304	ACCESSION:AR311304
CI012	14.2	0.4	20	1	AR122482	ACCESSION:AR122482	1085	14.2	0.4	20	1	AR312921	ACCESSION:AR312921
CI013	14.2	0.4	20	1	AR122500	ACCESSION:AR122500	CI086	14.2	0.4	20	1	AR314131	ACCESSION:AR314131
CI014	14.2	0.4	20	1	AR122507	ACCESSION:AR122507	CI087	14.2	0.4	20	1	AR314261	ACCESSION:AR314261
1015	14.2	0.4	20	1	AR123249	ACCESSION:AR123249	CI088	14.2	0.4	20	1	AR314448	ACCESSION:AR314448
1016	14.2	0.4	20	1	AR127702	ACCESSION:AR127702	1089	14.2	0.4	20	1	AR315253	ACCESSION:AR315253
CI017	14.2	0.4	20	1	AR129756	ACCESSION:AR129756	1090	14.2	0.4	20	1	AR316159	ACCESSION:AR316159
CI018	14.2	0.4	20	1	AR142705	ACCESSION:AR142705	CI091	14.2	0.4	20	1	AR342815	ACCESSION:AR342815
CI019	14.2	0.4	20	1	AR162412	ACCESSION:AR162412	CI092	14.2	0.4	20	1	AR361086	ACCESSION:AR361086
CI020	14.2	0.4	20	1	AR163862	ACCESSION:AR163862	CI093	14.2	0.4	20	1	AR366100	ACCESSION:AR366100
1021	14.2	0.4	20	1	AR163934	ACCESSION:AR163934	1094	14.2	0.4	20	1	AR370587	ACCESSION:AR370587
CI022	14.2	0.4	20	1	AR164041	ACCESSION:AR164041	CI095	14.2	0.4	20	1	AR382073	ACCESSION:AR382073
CI023	14.2	0.4	20	1	AR174372	ACCESSION:AR174372	CI096	14.2	0.4	20	1	AR382084	ACCESSION:AR382084
CI024	14.2	0.4	20	1	AR177628	ACCESSION:AR177628	CI097	14.2	0.4	20	1	AR382087	ACCESSION:AR382087
CI025	14.2	0.4	20	1	BD181148	ACCESSION:BD181148	CI098	14.2	0.4	20	1	AR382950	ACCESSION:AR382950
CI026	14.2	0.4	20	1	BD181159	ACCESSION:BD181159	CI099	14.2	0.4	20	1	AR408461	ACCESSION:AR408461
CI027	14.2	0.4	20	1	BD181162	ACCESSION:BD181162	CI100	14.2	0.4	20	1	AR437052	ACCESSION:AR437052
CI028	14.2	0.4	20	1	BD196159	ACCESSION:BD196159	1101	14.2	0.4	20	1	AR437053	ACCESSION:AR437053
1029	14.2	0.4	20	1	BD235060	ACCESSION:BD235060	CI102	14.2	0.4	20	1	AR437098	ACCESSION:AR437098
CI030	14.2	0.4	20	1	BD230252	ACCESSION:BD230252	CI103	14.2	0.4	20	1	AR451291	ACCESSION:AR451291
1031	14.2	0.4	20	1	BD272738	ACCESSION:BD272738	1104	14.2	0.4	20	1	AR488805	ACCESSION:AR488805
1032	14.2	0.4	20	1	CQ762181	ACCESSION:CQ762181	CI105	14.2	0.4	20	1	AR492019	ACCESSION:AR492019
CI033	14.2	0.4	20	1	CQ762365	ACCESSION:CQ762365	1106	14.2	0.4	20	1	AR492377	ACCESSION:AR492377
1034	14.2	0.4	20	1	CQ762759	ACCESSION:CQ762759	CI107	14.2	0.4	20	1	AR492685	ACCESSION:AR492685
CI035	14.2	0.4	20	1	CQ762890	ACCESSION:CQ762890	1108	14.2	0.4	20	1	AX080337	ACCESSION:AX080337
1036	14.2	0.4	20	1	CQ763511	ACCESSION:CQ763511	CI109	14.2	0.4	20	1	AX080338	ACCESSION:AX080338
CI037	14.2	0.4	20	1	CQ764464	ACCESSION:CQ764464	CI110	14.2	0.4	20	1	AX148837	ACCESSION:AX148837
CI038	14.2	0.4	20	1	CQ764591	ACCESSION:CQ764591	1111	14.2	0.4	20	1	AX149220	ACCESSION:AX149220
CI039	14.2	0.4	20	1	CQ779747	ACCESSION:CQ779747	1112	14.2	0.4	20	1	AX167126	ACCESSION:AX167126
CI040	14.2	0.4	20	1	CQ779749	ACCESSION:CQ779749	1113	14.2	0.4	20	1	AX224922	ACCESSION:AX224922
1041	14.2	0.4	20	1	CQ786731	ACCESSION:CQ786731	1114	14.2	0.4	20	1	AX224927	ACCESSION:AX224927
1042	14.2	0.4	20	1	CQ819706	ACCESSION:CQ819706	CI115	14.2	0.4	20	1	AX295702	ACCESSION:AX295702
1043	14.2	0.4	20	1	CQ821690	ACCESSION:CQ821690	1116	14.2	0.4	20	1	AX296663	ACCESSION:AX296663
CI044	14.2	0.4	20	1	E02948	ACCESSION:E02948	1117	14.2	0.4	20	1	AX298596	ACCESSION:AX298596
1045	14.2	0.4	20	1	E04077	ACCESSION:E04077	CI118	14.2	0.4	20	1	AX298894	ACCESSION:AX298894
CI046	14.2	0.4	20	1	E11000	ACCESSION:E11000	1119	14.2	0.4	20	1	AX317742	ACCESSION:AX317742
CI047	14.2	0.4	20	1	E13769	ACCESSION:E13769	CI120	14.2	0.4	20	1	AX342778	ACCESSION:AX342778
CI048	14.2	0.4	20	1	E29869	ACCESSION:E29869	1121	14.2	0.4	20	1	AX356852	ACCESSION:AX356852
CI049	14.2	0.4	20	1	E30661	ACCESSION:E30661	CI122	14.2	0.4	20	1	AX462663	ACCESSION:AX462663
1050	14.2	0.4	20	1	E31396	ACCESSION:E31396	1123	14.2	0.4	20	1	AX462663	ACCESSION:AX462663
1051	14.2	0.4	20	1	E37366	ACCESSION:E37366	1124	14.2	0.4	20	1	AX487048	ACCESSION:AX487048
1052	14.2	0.4	20	1	E39123	ACCESSION:E39123	1125	14.2	0.4	20	1	AX488257	ACCESSION:AX488257
1053	14.2	0.4	20	1	E59332	ACCESSION:E59332	1126	14.2	0.4	20	1	AX589229	ACCESSION:AX589229
CI054	14.2	0.4	20	1	I12350	ACCESSION:I12350	CI127	14.2	0.4	20	1	AX658511	ACCESSION:AX658511
1055	14.2	0.4	20	1	I20664	ACCESSION:I20664	1128	14.2	0.4	20	1	AX665329	ACCESSION:AX665329

c1129	14.2	0.4	20	1	AX719302	ACCESSION:AX719302	c1202	14	0.4	20	1	AX149325	ACCESSION:AX149325
c1130	14.2	0.4	20	1	AX743793	ACCESSION:AX743793	c1203	14	0.4	20	1	AX613800	ACCESSION:AX613800
c1131	14.2	0.4	20	1	AX776233	ACCESSION:AX776233	c1204	14	0.4	20	1	BD013149	ACCESSION:BD013149
c1132	14.2	0.4	20	1	AX804534	ACCESSION:AX804534	c1205	14	0.4	20	1	BD167763	ACCESSION:BD167763
c1133	14.2	0.4	20	1	AX923443	ACCESSION:AX923443	c1206	14	0.4	22	1	AX107369	ACCESSION:AX107369
c1134	14.2	0.4	20	1	AX938959	ACCESSION:AX938959	c1207	14	0.4	22	1	AX546922	ACCESSION:AX546922
c1135	14.2	0.4	20	1	AX958421	ACCESSION:AX958421	c1208	14	0.4	22	1	AX184223	ACCESSION:AX184223
c1136	14.2	0.4	20	1	AX962209	ACCESSION:AX962209	c1209	14	0.4	39	1	I31174	ACCESSION:I31174
c1137	14.2	0.4	20	1	BD016082	ACCESSION:BD016082	c1210	14	0.4	44	1	I31337	ACCESSION:I31337
c1138	14.2	0.4	20	1	BD016201	ACCESSION:BD016201	c1211	13.8	0.4	17	1	AR046263	ACCESSION:AR046263
c1139	14.2	0.4	20	1	BD017353	ACCESSION:BD017353	c1212	13.8	0.4	17	1	I53315	ACCESSION:I53315
c1140	14.2	0.4	20	1	BD074637	ACCESSION:BD074637	c1213	13.8	0.4	17	1	AO2372	ACCESSION:AO2372
c1141	14.2	0.4	20	1	BD081247	ACCESSION:BD081247	c1214	13.8	0.4	17	1	AO6173	ACCESSION:AO6173
c1142	14.2	0.4	20	1	BD123453	ACCESSION:BD123453	c1215	13.8	0.4	17	1	AR039211	ACCESSION:AR039211
c1143	14.2	0.4	20	1	BD140699	ACCESSION:BD140699	c1216	13.8	0.4	17	1	AR046566	ACCESSION:AR046566
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c1145	14.2	0.4	23	1	BD271421	ACCESSION:BD271421	c1218	13.8	0.4	17	1	BD234970	ACCESSION:BD234970
c1146	14.2	0.4	23	1	AR409907	ACCESSION:AR409907	c1219	13.8	0.4	17	1	BD241250	ACCESSION:BD241250
c1147	14.2	0.4	30	1	AR264929	ACCESSION:AR264929	c1220	13.8	0.4	17	1	BD241618	ACCESSION:BD241618
c1148	14.2	0.4	30	1	AR478210	ACCESSION:AR478210	c1221	13.8	0.4	17	1	BD253988	ACCESSION:BD253988
c1149	14.2	0.4	30	1	BD072869	ACCESSION:BD072869	c1222	13.8	0.4	17	1	BD253989	ACCESSION:BD253989
c1150	14.2	0.4	30	1	BD072874	ACCESSION:BD072874	c1223	13.8	0.4	17	1	BD254375	ACCESSION:BD254375
c1151	14.2	0.4	30	1	BD107496	ACCESSION:BD107496	c1224	13.8	0.4	17	1	BD254495	ACCESSION:BD254495
c1152	14.2	0.4	30	1	BD107501	ACCESSION:BD107501	c1225	13.8	0.4	17	1	BD254752	ACCESSION:BD254752
c1153	14.2	0.4	30	1	BD145028	ACCESSION:BD145028	c1226	13.8	0.4	17	1	Q6617474	ACCESSION:Q6617474
c1154	14.2	0.4	30	1	BD145033	ACCESSION:BD145033	c1227	13.8	0.4	17	1	Q6617930	ACCESSION:Q6617930
c1155	14.2	0.4	30	1	BD166033	ACCESSION:BD166033	c1228	13.8	0.4	17	1	Q6618036	ACCESSION:Q6618036
c1156	14.2	0.4	30	1	BD166129	ACCESSION:BD166129	c1229	13.8	0.4	17	1	Q6618038	ACCESSION:Q6618038
c1157	14.2	0.4	31	1	AX248879	ACCESSION:AX248879	c1230	13.8	0.4	17	1	Q6623102	ACCESSION:Q6623102
c1158	14.2	0.4	38	1	AR222444	ACCESSION:AR222444	c1231	13.8	0.4	17	1	Q6623258	ACCESSION:Q6623258
c1159	14.2	0.4	42	1	I31428	ACCESSION:I31428	c1232	13.8	0.4	17	1	Q6623261	ACCESSION:Q6623261
c1160	14	0.4	14	1	BD185612	ACCESSION:BD185612	c1233	13.8	0.4	17	1	Q6623347	ACCESSION:Q6623347
c1161	14	0.4	14	1	BD185613	ACCESSION:BD185613	c1234	13.8	0.4	17	1	Q6623985	ACCESSION:Q6623985
c1162	14	0.4	14	1	E32202	ACCESSION:E32202	c1235	13.8	0.4	17	1	Q6623986	ACCESSION:Q6623986
c1163	14	0.4	14	1	I31524	ACCESSION:I31524	c1236	13.8	0.4	17	1	Q6624607	ACCESSION:Q6624607
c1164	14	0.4	14	1	AX175251	ACCESSION:AX175251	c1237	13.8	0.4	17	1	Q6624974	ACCESSION:Q6624974
c1165	14	0.4	15	1	AR241795	ACCESSION:AR241795	c1238	13.8	0.4	17	1	Q6625121	ACCESSION:Q6625121
c1166	14	0.4	16	1	BD234638	ACCESSION:BD234638	c1239	13.8	0.4	17	1	Q6806745	ACCESSION:Q6806745
c1167	14	0.4	16	1	AR230234	ACCESSION:AR230234	c1240	13.8	0.4	17	1	I53618	ACCESSION:I53618
c1168	14	0.4	16	1	AR328665	ACCESSION:AR328665	c1241	13.8	0.4	17	1	I54420	ACCESSION:I54420
c1169	14	0.4	17	1	AR057463	ACCESSION:AR057463	c1242	13.8	0.4	17	1	AR187317	ACCESSION:AR187317
c1170	14	0.4	17	1	AR115221	ACCESSION:AR115221	c1243	13.8	0.4	17	1	AR187357	ACCESSION:AR187357
c1171	14	0.4	17	1	BD241576	ACCESSION:BD241576	c1244	13.8	0.4	17	1	AR188717	ACCESSION:AR188717
c1172	14	0.4	17	1	BD272846	ACCESSION:BD272846	c1245	13.8	0.4	17	1	AR188718	ACCESSION:AR188718
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c1174	14	0.4	17	1	AX634556	ACCESSION:AX634556	c1247	13.8	0.4	17	1	AR190226	ACCESSION:AR190226
c1175	14	0.4	17	1	AX687746	ACCESSION:AX687746	c1248	13.8	0.4	17	1	AR190240	ACCESSION:AR190240
c1176	14	0.4	17	1	AX687747	ACCESSION:AX687747	c1249	13.8	0.4	17	1	AR190291	ACCESSION:AR190291
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c1178	14	0.4	17	1	AX687749	ACCESSION:AX687749	c1251	13.8	0.4	17	1	AR190307	ACCESSION:AR190307
c1179	14	0.4	17	1	AX687932	ACCESSION:AX687932	c1252	13.8	0.4	17	1	AR192109	ACCESSION:AR192109
c1180	14	0.4	17	1	AX687936	ACCESSION:AX687936	c1253	13.8	0.4	17	1	AR261711	ACCESSION:AR261711
c1181	14	0.4	17	1	AX688344	ACCESSION:AX688344	c1254	13.8	0.4	17	1	AR286089	ACCESSION:AR286089
c1182	14	0.4	17	1	AX688345	ACCESSION:AX688345	c1255	13.8	0.4	17	1	AR286406	ACCESSION:AR286406
c1183	14	0.4	17	1	AX688346	ACCESSION:AX688346	c1256	13.8	0.4	17	1	AR286407	ACCESSION:AR286407
c1184	14	0.4	17	1	AX688347	ACCESSION:AX688347	c1257	13.8	0.4	17	1	AR286445	ACCESSION:AR286445
c1185	14	0.4	17	1	AX728804	ACCESSION:AX728804	c1258	13.8	0.4	17	1	AR286463	ACCESSION:AR286463
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c1191	14	0.4	18	1	AX453148	ACCESSION:AX453148	c1264	13.8	0.4	17	1	AR324608	ACCESSION:AR324608
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c1196	14	0.4	20	1	AR126637	ACCESSION:AR126637	c1269	13.8	0.4	17	1	AR327329	ACCESSION:AR327329
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c1199	14	0.4	20	1	Q6818386	ACCESSION:Q6818386	c1272	13.8	0.4	17	1	AR329331	ACCESSION:AR329331
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1276	13.8	0.4	17	1	AR398397	1349	13.8	0.4	17	1	AX783665
1277	13.8	0.4	17	1	AR398435	1350	13.8	0.4	17	1	BD002054
1278	13.8	0.4	17	1	AR398453	1351	13.8	0.4	17	1	BD067798
1279	13.8	0.4	17	1	AR402298	1352	13.8	0.4	17	1	BD104450
1280	13.8	0.4	17	1	AR433738	1353	13.8	0.4	17	1	DOGP36202
1281	13.8	0.4	17	1	AR433961	1354	13.8	0.4	18	1	A88187
1282	13.8	0.4	17	1	AR433962	1355	13.8	0.4	18	1	AX0154
1283	13.8	0.4	17	1	AR433963	1356	13.8	0.4	18	1	AX0829
1284	13.8	0.4	17	1	AR433964	1357	13.8	0.4	18	1	AX0911
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1286	13.8	0.4	17	1	AR458933	1359	13.8	0.4	18	1	AR062605
1287	13.8	0.4	17	1	AR459001	1360	13.8	0.4	18	1	AR078582
1288	13.8	0.4	17	1	AR459101	1361	13.8	0.4	18	1	AR080699
1289	13.8	0.4	17	1	AR464165	1362	13.8	0.4	18	1	AR082993
1290	13.8	0.4	17	1	AR464321	1363	13.8	0.4	18	1	AR104708
1291	13.8	0.4	17	1	AR464410	1364	13.8	0.4	18	1	AR105530
1292	13.8	0.4	17	1	AR465048	1365	13.8	0.4	18	1	AR119310
1293	13.8	0.4	17	1	AR465049	1366	13.8	0.4	18	1	AR121140
1294	13.8	0.4	17	1	AR465049	1367	13.8	0.4	18	1	AR123192
1295	13.8	0.4	17	1	AR465670	1368	13.8	0.4	18	1	AR138072
1296	13.8	0.4	17	1	AR466037	1369	13.8	0.4	18	1	AR145511
1297	13.8	0.4	17	1	AR466184	1370	13.8	0.4	18	1	AR162682
1298	13.8	0.4	17	1	AR482439	1371	13.8	0.4	18	1	AR178738
1299	13.8	0.4	17	1	AR482751	1372	13.8	0.4	18	1	AR226623
1300	13.8	0.4	17	1	AR483119	1373	13.8	0.4	18	1	BD227742
1301	13.8	0.4	17	1	AX009041	1374	13.8	0.4	18	1	BD250528
1302	13.8	0.4	17	1	AX216115	1375	13.8	0.4	18	1	BD250528
1303	13.8	0.4	17	1	AX216149	1376	13.8	0.4	18	1	BD250528
1304	13.8	0.4	17	1	AX217295	1377	13.8	0.4	18	1	BD250528
1305	13.8	0.4	17	1	AX227292	1378	13.8	0.4	18	1	BD250528
1306	13.8	0.4	17	1	AX227304	1379	13.8	0.4	18	1	BD250528
1307	13.8	0.4	17	1	AX227310	1380	13.8	0.4	18	1	BD250528
1308	13.8	0.4	17	1	AX225317	1381	13.8	0.4	18	1	BD250528
1309	13.8	0.4	17	1	AX325318	1382	13.8	0.4	18	1	BD250528
1310	13.8	0.4	17	1	AX422231	1383	13.8	0.4	18	1	BD250528
1311	13.8	0.4	17	1	AX423119	1384	13.8	0.4	18	1	BD250528
1312	13.8	0.4	17	1	AX423120	1385	13.8	0.4	18	1	BD250528
1313	13.8	0.4	17	1	AX475039	1386	13.8	0.4	18	1	BD250528
1314	13.8	0.4	17	1	AX530931	1387	13.8	0.4	18	1	BD250528
1315	13.8	0.4	17	1	AX530944	1388	13.8	0.4	18	1	BD250528
1316	13.8	0.4	17	1	AX530945	1389	13.8	0.4	18	1	BD250528
1317	13.8	0.4	17	1	AX531999	1390	13.8	0.4	18	1	BD250528
1318	13.8	0.4	17	1	AX544529	1391	13.8	0.4	18	1	BD250528
1319	13.8	0.4	17	1	AX544984	1392	13.8	0.4	18	1	BD250528
1320	13.8	0.4	17	1	AX578222	1393	13.8	0.4	18	1	BD250528
1321	13.8	0.4	17	1	AX578223	1394	13.8	0.4	18	1	BD250528
1322	13.8	0.4	17	1	AX649233	1395	13.8	0.4	18	1	BD250528
1323	13.8	0.4	17	1	AX671977	1396	13.8	0.4	18	1	BD250528
1324	13.8	0.4	17	1	AX671977	1397	13.8	0.4	18	1	BD250528
1325	13.8	0.4	17	1	AX67732	1398	13.8	0.4	18	1	BD250528
1326	13.8	0.4	17	1	AX687796	1399	13.8	0.4	18	1	BD250528
1327	13.8	0.4	17	1	AX687852	1400	13.8	0.4	18	1	BD250528
1328	13.8	0.4	17	1	AX688383	1401	13.8	0.4	18	1	BD250528
1329	13.8	0.4	17	1	AX688727	1402	13.8	0.4	18	1	BD250528
1330	13.8	0.4	17	1	AX690707	1403	13.8	0.4	18	1	BD250528
1331	13.8	0.4	17	1	AX722945	1404	13.8	0.4	18	1	BD250528
1332	13.8	0.4	17	1	AX722971	1405	13.8	0.4	18	1	BD250528
1333	13.8	0.4	17	1	AX724318	1406	13.8	0.4	18	1	BD250528
1334	13.8	0.4	17	1	AX727665	1407	13.8	0.4	18	1	BD250528
1335	13.8	0.4	17	1	AX729266	1408	13.8	0.4	18	1	BD250528
1336	13.8	0.4	17	1	AX734014	1409	13.8	0.4	18	1	BD250528
1337	13.8	0.4	17	1	AX734582	1410	13.8	0.4	18	1	BD250528
1338	13.8	0.4	17	1	AX735612	1411	13.8	0.4	18	1	BD250528
1339	13.8	0.4	17	1	AX735612	1412	13.8	0.4	18	1	BD250528
1340	13.8	0.4	17	1	AX737215	1413	13.8	0.4	18	1	BD250528
1341	13.8	0.4	17	1	AX737594	1414	13.8	0.4	18	1	BD250528
1342	13.8	0.4	17	1	AX753829	1415	13.8	0.4	18	1	BD250528
1343	13.8	0.4	17	1	AX753829	1416	13.8	0.4	18	1	BD250528
1344	13.8	0.4	17	1	AX759942	1417	13.8	0.4	18	1	BD250528
1345	13.8	0.4	17	1	AX760079	1418	13.8	0.4	18	1	BD250528
1346	13.8	0.4	17	1	AX761940	1419	13.8	0.4	18	1	BD250528
1347	13.8	0.4	17	1	AX782224	1420	13.8	0.4	18	1	BD250528
1348	13.8	0.4	17	1	AX782224	1421	13.8	0.4	18	1	BD250528
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1350	13.8	0.4	17	1	AX782224	1423	13.8	0.4	18	1	BD250528
1351	13.8	0.4	17	1	AX782224	1424	13.8	0.4	18	1	BD250528
1352	13.8	0.4	17	1	AX782224	1425	13.8	0.4	18	1	BD250528
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1356	13.8	0.4	17	1	AX782224	1429	13.8	0.4	18	1	BD250528
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1360	13.8	0.4	17	1	AX782224	1433	13.8	0.4	18	1	BD250528
1361	13.8	0.4	17	1	AX782224	1434	13.8	0.4	18	1	BD250528
1362	13.8	0.4	17	1	AX782224	1435	13.8	0.4	18	1	BD250528
1363	13.8	0.4	17	1	AX782224	1436	13.8	0.4	18	1	BD250528
1364	13.8	0.4	17	1	AX782224	1437	13.8	0.4	18	1	BD250528
1365	13.8	0.4	17	1	AX782224	1438	13.8	0.4	18	1	BD250528
1366	13.8	0.4	17	1	AX782224	1439	13.8	0.4	18	1	BD250528
1367	13.8	0.4	17	1	AX782224	1440	13.8	0.4	18	1	BD250528
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1369	13.8	0.4	17	1	AX782224	1442	13.8	0.4	18	1	BD250528
1370	13.8	0.4	17	1	AX782224	1443	13.8	0.4	18	1	BD250528
1371	13.8	0.4	17	1	AX782224	1444	13.8	0.4	18	1	BD250528
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1373	13.8	0.4	17	1	AX782224	1446	13.8	0.4	18	1	BD250528
1374	13.8	0.4	17	1	AX782224	1447	13.8	0.4	18	1	BD250528
1375	13.8	0.4	17	1	AX782224	1448	13.8	0.4	18	1	BD250528
1376	13.8	0.4	17	1	AX782224	1449	13.8	0.4	18	1	BD250528
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1378	13.8	0.4	17	1	AX782224	1451	13.8	0.4	18	1	BD250528
1379	13.8	0.4	17	1	AX782224	1452	13.8	0.4	18	1	BD250528
1380	13.8	0.4	17	1	AX782224	1453	13.8	0.4	18	1	BD250528
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1382	13.8	0.4	17	1	AX782224	1455	13.8	0.4	18	1	BD250528
1383	13.8	0.4	17	1	AX782224	1456	13.8	0.4	18	1	BD250528
1384	13.8	0.4	17	1	AX782224	1457	13.8	0.4	18	1	BD250528
1385	13.8	0.4	17	1	AX782224	1458	13.8	0.4	18	1	BD250528
1386	13.8	0.4	17	1	AX782224	1459	13.8	0.4	18	1	BD250528
1387	13.8	0.4	17	1	AX782224	1460	13.8	0.4	18	1	BD250528
1388	13.8	0.4	17	1	AX782224	1461	13.8	0.4	18	1	BD250528
1389	13.8	0									

[illegible]

LOCUS	I31180		47 bp	DNA	linear	PAT 06-FEB-1999
DEFINITION	Sequence 92 from patent US 5582979.					
ACCESSION	I31180					
VERSION	I31180.1	GI:1821971				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 47)					
AUTHORS	Weber,J.L.					
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same					
JOURNAL	Patent: US 5582979-A 92 10-DEC-1996;					
FEATURES	Location/Qualifiers					
source	1..47					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	0.9%; Score 34.2; DB 1; Length 47;					
Best Local Similarity	83.0%; Pred. No.9.2;					
Matches	39; Conservative 0; Mismatches 8; Indels 0; Gaps 0;					
Qy	2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGGCTGT 2364					
Db	47 TGT 1					
RESULT 13						
I31309/c						
LOCUS	I31309		47 bp	DNA	linear	PAT 06-FEB-1997
DEFINITION	Sequence 221 from patent US 5582979.					
ACCESSION	I31309					
VERSION	I31309.1	GI:1822100				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 47)					
AUTHORS	Weber,J.L.					
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same					
JOURNAL	Patent: US 5582979-A 221 10-DEC-1996;					
FEATURES	Location/Qualifiers					
source	1..47					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	0.9%; Score 34.2; DB 1; Length 47;					
Best Local Similarity	83.0%; Pred. No.9.2;					
Matches	39; Conservative 0; Mismatches 8; Indels 0; Gaps 0;					
Qy	2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGGCTGT 2364					
Db	47 TGT 1					
RESULT 14						
AU047784/c						
LOCUS	AU047784		48 bp	DNA	linear	STS 22-APR-1999
DEFINITION	Rattus norvegicus, OTSUKA clone, 303d01, microsatellite sequence, sequence tagged site.					
ACCESSION	AU047784					
VERSION	AU047784.1	GI:4632419				
KEYWORDS	STS.					
SOURCE	Rattus norvegicus (Norway rat)					
ORGANISM	Rattus norvegicus					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.						
REFERENCE	1 (sites)					
AUTHORS	Watanabe,T.K., Hishigaki,H., Okuno,S., Mizoguchi,A., Oga,K., Tsuji,I.A., Ono,T., Yamasaki,Y., Kanemoto,N., Takahashi,E., Irie,Y., Nakamura,Y., Takagi,Y. and Taniqami,A.					

TITLE The large-scale mapping of rat microsatellite markers
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 48)
AUTHORS Watanabe,T.K.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-1998) Takeshi K Watanabe, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 483-10, Kagasuno, Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan
(B-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888,
Fax:+81-886-37-1035)

FEATURES Location/Qualifiers
source
1..48
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="Brown Norway"
/db_xref="taxon:10116"
/clone="303d01"
/cell_type="hepatocyte"
/tissue_type="liver"
/note="303d01F=5'-TTACAGGACAATTGTGCGGT-3',
303d01R=5'-GTGTGTGTGTGCTGCCTCACAAT-3'"

Query Match 0.9%; Score 34.2; DB 1; Length 48;
Best Local Similarity 90.0%; Pred.No.9.4;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2312 TTGTCGTGTGTGTGTGTGGCTGTGTGTGTGTGTGTG 2351
|||||
Db 48 TTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 9
|||||

RESULT 15
CQ738314
LOCUS CQ738314 47 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 24248 from Patent WO02068579.
ACCESSION CQ738314
VERSION CQ738314.1 GI:42338865
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 24248 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES Location/Qualifiers
source
1..47
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 34; DB 1; Length 47;
Best Local Similarity 88.1%; Pred.No.9.8;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 170 GAGATGACGAAGACGGGGAGACGAGGCTGAGGACACAGTGT 211
|||||
Db 1 GAGATGACAAAGACGCTGGAGCAAGGCTGAAGACACAAAGTG 42
|||||

RESULT 16
BD251663/c
LOCUS BD251663 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Selection of animal based on character imprinted by parent.
ACCESSION BD251663
VERSION BD251663.1 GI:33061433
KEYWORDS JP 2002535963-A/183.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

Thu Oct 28 12:48:19 2004

[illegible]

RESULT 53

source
1. .31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 30.6; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 17;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1928 ACTGCACACACACCTGTACATGATCATGCG 1958
1 ACTGCACACACACCTGTACATGATCATGCG 31
|||||
|||||

Db 1 ACTGCACACACACCTGTACATGATCATGCG 31
|||||
|||||

RESULT 61
AX248879
LOCUS AX248879 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 958 from Patent WO0166800.
ACCESSION AX248879
VERSION AX248879.1 GI:15863502
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 958 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES
Location/Qualifiers
1. .31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 30.6; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 17;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 527 ACCGCCCATCTCTGCAGCGGGCTCGCGGC 557
1 ACCGCCCATCTCTGCAGCGGGCTCGCGGC 31
|||||
|||||

Db 1 ACCGCCCATCTCTGCAGCGGGCTCGCGGC 31
|||||
|||||

RESULT 62
AX248880
LOCUS AX248880 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 959 from Patent WO0166800.
ACCESSION AX248880
VERSION AX248880.1 GI:15863503
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 959 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES
Location/Qualifiers
1. .31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 30.6; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 17;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 642 GCACGTGGAGTGAATGGCAGCAAGTGGGC 672
|||||
|||||

Db 642 GCACGTGGAGTGAATGGCAGCAAGTGGGC 672
|||||
|||||

source
1 GCACGTGGAGTGAATGGCAGCAAGTGGGC 31
|||||
|||||

RESULT 63
AX248881
LOCUS AX248881 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 960 from Patent WO0166800.
ACCESSION AX248881
VERSION AX248881.1 GI:15863504
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 960 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES
Location/Qualifiers
1. .31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 30.6; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 17;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1407 CTGCACGACGCGCGCGCTGTACGTGCTG 1437
1 CTGCACGACGCGCGCGCTGTACGTGCTG 31
|||||
|||||

Db 1 CTGCACGACGCGCGCGCTGTACGTGCTG 31
|||||
|||||

RESULT 64
A45638
LOCUS A45638 42 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 32 from Patent WO9520044.
ACCESSION A45638
VERSION A45638.1 GI:2300036
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE
AUTHORS Barton, C.H., White, J.K. and Blackwell, J.M.
TITLE NATURAL RESISTANCE ASSOCIATED MACROPHAGE PROTEIN AND USES THEREOF
JOURNAL Patent: WO 9520044-A 32 27-JUL-1995;
LYNXVALE LTD (GB)

COMMENT
Other publication CA 2181544 950727
Other publication ZA 9500444 950927
Other publication AU 1422595 950808.

FEATURES
Location/Qualifiers
1. .42
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.8%; Score 30.6; DB 1; Length 42;
Best Local Similarity 89.2%; Pred. No. 23;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
6 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 42
|||||
|||||

Db 6 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 42
|||||
|||||

RESULT 65
AR033091
LOCUS AR033091 42 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 32 from patent US 5869247.
ACCESSION AR033091
VERSION AR033091.1 GI:5948696

<hr/>					
KEYWORDS	Unknown.				
SOURCE	ORGANISM	Unknown.			
	Unclassified.				
REFERENCE	1 (bases 1 to 42)				
AUTHORS	Barton,C.Howard., White,J.Katie. and Blackwell,J.Mary.				
TITLE	Natural resistance associated macrophage protein and uses thereof				
JOURNAL	Patent: US 589247-A 32 09-FEB-1999;				
FEATURES	Location/Qualifiers				
source	1..42				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.8%; Score 30.6; DB 1; Length 42;				
Best Local Similarity	89.2%; Pred. No.23;				
Matches	33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;				
Qy	2315 GTCTGTGTTGGTGTGCCTGTGTGTGTGTGTGTG 2351				
Db	6 GTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTG 42				
<hr/>					
RESULT 66					
E32203/c					
LOCUS	E32203 32 bp DNA linear PAT 18-JUN-2001				
DEFINITION	Method for isolating satellite sequence.				
ACCESSION	E32203				
VERSION	E32203.1 GI:13021740				
KEYWORDS	JP 2000060559-A/5.				
SOURCE	Haliotis discus discus				
ORGANISM	Haliotis discus discus				
	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;				
	Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.				
REFERENCE	1 (bases 1 to 32)				
AUTHORS	Hideaki,T. and Masashi,S.				
TITLE	Method for isolating satellite sequence				
JOURNAL	Patent: JP 2000060559-A 5 29-FEB-2000;				
COMMENT	NATL INST OF AGRICULTURAL RESOURCES				
	OS Haliotis discus discus				
	PN JP 2000060559-A/5				
	PD 29-FEB-2000				
	PF 18-AUG-1998 JP 1998232153				
	PR				
	PI HIDEAKI TAKAHASHI,WASASHI SEKINO				
	PC C12N15/09,C12Q1/68,C12N15/00				
	CC				
	FH Key Location/Qualifiers				
	FT source 1..32				
	/organism='Haliotis discus discus'.				
FEATURES	Location/Qualifiers				
source	1..32				
	/organism="Haliotis discus discus"				
	/mol_type="genomic DNA"				
	/sub_species="discus"				
	/db_xref="taxon:91233"				
Query Match	0.8%; Score 30.4; DB 1; Length 32;				
Best Local Similarity	96.9%; Pred. No. 19;				
Matches	31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	2318 TGTGTGTGTGTGTGTGCCTGTGTGTGTGTGTGTG 2349				
Db	32 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1				
<hr/>					
RESULT 67					
I31298/c					
LOCUS	I31298 32 bp DNA linear PAT 06-FEB-1997				
DEFINITION	Sequence 210 from patent US 5582979.				
ACCESSION	I31298				
VERSION	I31298.1 GI:1822089				
KEYWORDS					
SOURCE	Unknown.				
Query Match	0.8%; Score 30.4; DB 1; Length 42;				
Best Local Similarity	96.9%; Pred. No.25;				
Matches	31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	2319 GTGTGTGTGTGTGTGCCTGTGTGTGTGTGTGTG 2350				
Db	32 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1				
<hr/>					
RESULT 68					
I31464/c					
LOCUS	I31464 32 bp DNA linear PAT 06-FEB-1997				
DEFINITION	Sequence 376 from patent US 5582979.				
ACCESSION	I31464				
VERSION	I31464.1 GI:1822255				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
	Unclassified.				
REFERENCE	1 (bases 1 to 32)				
AUTHORS	Weber,J.L.				
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same				
JOURNAL	Patent: US 5582979-A 376 10-DEC-1996;				
FEATURES	Location/Qualifiers				
source	1..32				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.8%; Score 30.4; DB 1; Length 32;				
Best Local Similarity	96.9%; Pred. No.19;				
Matches	31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	2319 GTGTGTGTGTGTGTGCCTGTGTGTGTGTGTGTG 2350				</

Query Match 0.7%; Score 28.4; DB 1; Length 30;

[illegible]

REFERENCE 1 (bases 1 to 27)


```

TITLE      Therapeutically useful synthetic oligonucleotides
JOURNAL    Patent: WO 0144465-A 5 21-JUN-2001;
           Bioniche Life Sciences Inc. (CA)
FEATURES
  source
    1..27
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
  Query Match
    0.7%; Score 25.4; DB 1; Length 27;
  Best Local Similarity
    96.3%; Pred. No. 68;
  Matches
    26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGTGTGTGTGT 2344
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 98
AX175302
LOCUS      AX175302
DEFINITION Sequence 66 from Patent WO0144465.
ACCESSION AX175302
VERSION   AX175302.1 GI:14598670
KEYWORDS
SOURCE    synthetic construct
          artificial sequences.
ORGANISM
REFERENCE
AUTHORS   Phillips,N.C. and Filion,M.C.
TITLE     Therapeutically useful synthetic oligonucleotides
JOURNAL   Patent: WO 0144465-A 66 21-JUN-2001;
           Bioniche Life Sciences Inc. (CA)
FEATURES
  source
    1..27
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
  Query Match
    0.7%; Score 25.4; DB 1; Length 27;
  Best Local Similarity
    96.3%; Pred. No. 68;
  Matches
    26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGCGTGTGTGTGTG 2345
Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGTG 27

RESULT 100
AX1503/c
LOCUS      I31503
DEFINITION Sequence 415 from patent US 5582979.
ACCESSION I31503
VERSION   I31503.1 GI:1822294
KEYWORDS
SOURCE    Unknown.
          Unclassified.
          1 (bases 1 to 30)
          Weber,J.L.
          Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
          method of using the same
          Patent: US 5582979-A 415 10-DEC-1996;
          Location/Qualifiers
            1..30
            /organism="unknown"
            /mol_type="unassigned DNA"
  Query Match
    0.7%; Score 25.2; DB 1; Length 30;
  Best Local Similarity
    90.0%; Pred. No. 79;
  Matches
    27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGTGTGTGTGTG 2347
Db 30 TGTGTGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 101
AX482128
LOCUS      AX482128
DEFINITION Sequence 105 from Patent EP1225233.
ACCESSION AX482128
VERSION   AX482128.1 GI:22316850
KEYWORDS
SOURCE    synthetic construct
          synthetic construct
          artificial sequences.
ORGANISM
REFERENCE
AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
TITLE     Means and methods for treatment evaluation
JOURNAL   Patent: EP 1225233-A 105 24-JUL-2002;
           Amsterdam Support Diagnostics B.V. (NL)
FEATURES
  source
    1..25
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="5'TAG019GENE"
  Query Match
    0.7%; Score 25; DB 1; Length 25;
  Best Local Similarity
    100.0%; Pred. No. 71;
  Matches
    25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GTGACCGAGGACACGTGTGTGAAGA 1672
Db 1 GTGACCGAGGACACGTGTGTGAAGA 25

RESULT 102
AX511367
LOCUS      AX511367
DEFINITION Sequence 105 from Patent WO02059558.
ACCESSION AX511367
VERSION   AX511367.1 GI:23392244
KEYWORDS
```

```

SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS     van der Kuyl,A.C. and Cornelissen,M.
TITLE       Means and methods for treatment evaluation
JOURNAL     Patent: WO 02059558-A 105 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="5'TAG019GENE"

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GTGACCGAGGACAACTGTGATGAAGA 1672
      ||||||||||||||||||||||||
Db 1 GTGACCGAGGACAACTGTGATGAAGA 25

RESULT 103
LOCUS      AX7211728          25 bp      DNA      linear      PAT 07-MAY-2003
DEFINITION Sequence 107 from Patent EP1298221.
ACCESSION  AX7211728
VERSION     AX7211728.1 GI:30422319
KEYWORDS
ORGANISM    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS     van der Kuyl,A.C. and Cornelissen,M.
TITLE       Means and methods for treatment evaluation
JOURNAL     Patent: EP 1298221-A 107 02-APR-2003;
            PrimaGen Holding B.V. (NL)
FEATURES
source
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="primer 5'TAG019GENE"

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GTGACCGAGGACAACTGTGATGAAGA 1672
      ||||||||||||||||||||||||
Db 1 GTGACCGAGGACAACTGTGATGAAGA 25

RESULT 104
LOCUS      E11483          24 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Primer for gaining probe which is for screening human Tie gene.
ACCESSION  E11483
VERSION     E11483.1 GI:22025119
KEYWORDS    JP 1996143598-A/1.
SOURCE      unidentified
            unidentified
            unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS     Yasunaga,K., Suda,T., Iwama,A., Kurozumi,K., Shimizu,Y., Nakada,S.
            and Masuyasu,Y.
TITLE       ANTI-TIE MONOCLONAL ANTIBODY AND HYBRIDOMA
JOURNAL     Patent: JP 1996143598-A 1 04-JUN-1996;
            YAMANOUCHI PHARMACEUT CO LTD
COMMENT     OS None
            OC Artificial sequences.

PN JP 1996143598-A/1
PD 04-JUN-1996
PF 17-NOV-1994 JP 1994308249
PI YASUNAGA KUNIO, SUDA TOSHIO, IWAMA ATSUSHI, KUROZUMI KOICHI,
    SHIMIZU YASUAKI, NAKADA SUSUMU, MASUYASU YASUHIKO PC
C07K16/28 C12N5/10 C12P21/08 G01N33/53 G01N33/53, PC
G01N33/577//C12N15/02,
PC (C12P21/08,C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No; Location/Qualifiers
FH Key
FT source
1..24
/organism='Artificial sequences'.
FEATURES
source
1..24
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1622 GGGACCTGGCTGCCCGCAATGTGC 1645
      ||||||||||||||||||||||||
Db 1 GGGACCTGGCTGCCCGCAATGTGC 24

RESULT 105
LOCUS      AX482129          24 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 106 from Patent EPI225233.
ACCESSION  AX482129
VERSION     AX482129.1 GI:22316951
KEYWORDS    synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS     van der Kuyl,A.C. and Cornelissen,M.
TITLE       Means and methods for treatment evaluation
JOURNAL     Patent: EP 1225233-A 106 24-JUL-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="3'TAG019GENE"

Query Match      0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 ACACAGCAGCTGTACATGATCATG 1956
      ||||||||||||||||||||||||
Db 24 ACACAGCAGCTGTACATGATCATG 1

RESULT 106
LOCUS      AX511368          24 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 106 from Patent WO02059558.
ACCESSION  AX511368
VERSION     AX511368.1 GI:23392245
KEYWORDS    synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE 1
```

AUTHORS van der Kuyl, A.C. and Cornelissen, M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: WO 02059558-A 106 01-AUG-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3'TAG019GENE"

Query Match 0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 ACACAGCCTGTACATGATCATG 1956
Db 24 ACACAGCCTGTACATGATCATG 1

RESULT 107
A29208/c
LOCUS A29208 30 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 108 from Patent EP1298221.
ACCESSION AX721729
VERSION AX721729.1 GI:30422320
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van der Kuyl, A.C. and Cornelissen, M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1298221-A 108 02-APR-2003;
PrimaGen Holding B.V. (NL)
FEATURES
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/note="primer 3'TAG019GENE"

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Best Local Similarity 100.0%; Pred. No. 90;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 ACACAGCCTGTACATGATCATG 1956
Db 24 ACACAGCCTGTACATGATCATG 1

RESULT 108
A29208/c
LOCUS A29208 30 bp DNA linear PAT 30-JUN-1995
DEFINITION DNA probe from patent WO9111459.
ACCESSION A29208
VERSION A29208.1 GI:1248929
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van der Kuyl, A.C. and Cornelissen, M.
TITLE EXTRACELLULAR FORM OF THE HUMAN FIBROBLAST GROWTH FACTOR RECEPTOR
JOURNAL Patent: WO 9111459-A 2 08-AUG-1991;
FEATURES
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Query Match 0.6%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.3e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1963 TGCTGGCATGCGCGCCCTCCAGAGGCC 1992
Db 30 TGCTGGCATGCGCGCCCTCCAGAGGCC 1

RESULT 109
A29211/c
LOCUS A29211 30 bp DNA linear PAT 30-JUN-1995
DEFINITION Oligonucleotide OAB984 from patent WO9111459.
ACCESSION A29211
VERSION A29211.1 GI:1248932
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS
TITLE EXTRACELLULAR FORM OF THE HUMAN FIBROBLAST GROWTH FACTOR RECEPTOR
JOURNAL Patent: WO 9111459-A 6 08-AUG-1991;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.3e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1963 TGCTGGCATGCGCGCCCTCCAGAGGCC 1992
Db 30 TGCTGGCATGCGCGCCCTCCAGAGGCC 1

RESULT 110
I31234/c
LOCUS I31234 25 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 146 from patent US 5582979.
ACCESSION I31234
VERSION I31234.1 GI:1822025
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 146 10-DEC-1996;
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGT 2342
Db 25 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 111
AX115976
LOCUS AX115976 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1099 from Patent WO0129262.
ACCESSION AX115976
VERSION AX115976.1 GI:14032918
KEYWORDS synthetic construct
SOURCE synthetic construct


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ACCESSION AX175258
VERSION AX175258.1 GI:14598626
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 22 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
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        1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
Query Match 0.6%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2319 GTGTGTGTGTGTGCGTGTGTGT 2342
Db 1 GTGTGTGTGTGTGTGTGTGTGT 24

RESULT 117
AX547929
LOCUS AX547929 24 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 1068 from Patent WO02053141.
ACCESSION AX547929
VERSION AX547929.1 GI:25813073
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 1068 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
    source
        1..24
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic Sequence"
Query Match 0.6%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGCGTGTGTGT 2341
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 118
AX117836/c
LOCUS AX117836 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2959 from Patent WO0129262.
ACCESSION AX117836
VERSION AX117836.1 GI:14034787
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2959 28-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
    Location/Qualifiers
        1
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"
Query Match 0.6%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2319 GTGTGTGTGTGTGCGTGTGTGT 2342
Db 24 GTGTGTGTGTGTGTGTGTGTGT 1

RESULT 119
ARI173691/c
LOCUS ARI173691 22 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 8 from patent US 6306591.
ACCESSION ARI173691
VERSION ARI173691.1 GI:17914011
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Cockett,N.E. and Beaver,J.E.
TITLE Screening for the molecular defect causing spider lamb syndrome in sheep
JOURNAL Patent: US 6306591-A 8 23-OCT-2001;
Location/Qualifiers
    source
        1..22
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1985 AGAGGCCCCACCTTCAAGCAGCT 2006
Db 22 AGAGGCCCCACCTTCAAGCAGCT 1

RESULT 120
BD231722
LOCUS BD231722 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Low oxygen culturing of cells.
ACCESSION BD231722
VERSION BD231722.1 GI:33041492
KEYWORDS JP 2002530067-A/21.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Ceste,M., Doyle,J., Wold,B.J., Morrison,S.J. and Anderson,D.
TITLE Low oxygen culturing of cells
JOURNAL Patent: JP 2002530067-A 21 17-SEP-2002;
CALIFORNIA INSTITUTE OF TECHNOLOGY
COMMENT
    PS Artificial Sequence
    PN JP 2002530067-A/21
    PD 17-SEP-2002
    PF 18-NOV-1999 JP 2000582533
    PR 18-NOV-1998 US 09/195569, 22-OCT-1999 US 09/425462 PI
    MARIE CESTE, JOHN DOYLE, BARBARA J WOLD, SEAN J MORRISON, DAVID PI
    ANDERSON
    PC C12N15/09, C12N5/06, C12N5/10, C12Q1/02, C12N15/00, C12N5/00, C12N5/
    CC Description of Artificial Sequence:Forward PCR primer for CC
    FGPR3
    PH Key Location/Qualifiers
    FT source 1..22
    /organism='Artificial Sequence'

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FEATURES
  source
    Location/Qualifiers
      1..22
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 0.6%; Score 22; DB 1; Length 22;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ATCTCGGAGATGACGAGAC 183
Db 1 ATCTCGGAGATGACGAGAC 22

RESULT 121
BD231723/c
LOCUS BD231723 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Low oxygen culturing of cells.
ACCESSION BD231723
VERSION BD231723.1 GI:33041493
KEYWORDS JP 2002530067-A/22.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Ceste,M., Doyle,J., Wold,B.J., Morrison,S.J. and Anderson,D.
TITLE Low oxygen culturing of cells
JOURNAL Patent: JP 2002530067-A 22 17-SEP-2002;
CALIFORNIA INSTITUTE OF TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2002530067-A/22
PD 17-SEP-2002
PF 18-NOV-1999 JP 2000582533
PR 18-NOV-1998 US 09/195569, 22-OCT-1999 US 09/425462 PI
MARIE CESTE, JOHN DOYLE, BARBARA J WOLD, SEAN J MORRISON, DAVID PI
ANDERSON
PC C12N5/09, C12N5/06, C12N5/10, C12Q1/02, C12N15/00, C12N5/00, C12N5/
PC 00
CC Description of Artificial Sequence: Reverse PCR primer for CC

FEATURES
  source
    Location/Qualifiers
      1..22
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 0.6%; Score 22; DB 1; Length 22;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GAGACAAAGTTGGCAGCATCC 487
Db 22 GAGACAAAGTTGGCAGCATCC 1

RESULT 122
BD270911
LOCUS BD270911 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Low oxygen culturing of central nervous system progenitor cells.
ACCESSION BD270911
VERSION BD270911.1 GI:33080679
KEYWORDS JP 2002530068-A/21.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Ceste,M., Doyle,J., Wold,B.J., McKay,R. and Studer,L.
TITLE Low oxygen culturing of central nervous system progenitor cells
JOURNAL Patent: JP 2002530068-A 21 17-SEP-2002;

FEATURES
  source
    Location/Qualifiers
      1..22
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 0.6%; Score 22; DB 1; Length 22;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GAGACAAAGTTGGCAGCATCC 487
Db 22 GAGACAAAGTTGGCAGCATCC 1

RESULT 123
BD270912/c
LOCUS BD270912 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Low oxygen culturing of central nervous system progenitor cells.
ACCESSION BD270912
VERSION BD270912.1 GI:33080680
KEYWORDS JP 2002530068-A/22.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Ceste,M., Doyle,J., Wold,B.J., McKay,R. and Studer,L.
TITLE Low oxygen culturing of central nervous system progenitor cells
JOURNAL Patent: JP 2002530068-A 22 17-SEP-2002;
CALIFORNIA INSTITUTE OF TECHNOLOGY, THE UNITED STATES OF AMERICA
COMMENT OS Artificial Sequence
PN JP 2002530068-A/22
PD 17-SEP-2002
PF 18-NOV-1999 JP 2000582534
PR 18-NOV-1998 US 09/195569, 22-OCT-1999 US 09/425462 PI
MARIE CESTE, JOHN DOYLE, BARBARA J WOLD, RON MCKAY, LORENZ STUDER PC
C12N5/06, A61K35/30, C12N5/10, C12N5/09, C12N5/00, C12N5/00, C12N5/
PC 00
CC Description of Artificial Sequence: Reverse PCR primer for CC

FEATURES
  source
    Location/Qualifiers
      1..22
        /organism="synthetic construct"
        /mol_type="genomic DNA"
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Query Match
  Best Local Similarity 0.6%; Score 22; DB 1; Length 22;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GAGACAAAGTTGGCAGCATCC 487
Db 22 GAGACAAAGTTGGCAGCATCC 1

RESULT 124

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CALIFORNIA INSTITUTE OF TECHNOLOGY, THE UNITED STATES OF AMERICA
OS Artificial Sequence
PN JP 2002530068-A/21
PD 17-SEP-2002
PF 18-NOV-1999 JP 2000582534
PR 18-NOV-1998 US 09/195569, 22-OCT-1999 US 09/425462 PI
MARIE CESTE, JOHN DOYLE, BARBARA J WOLD, RON MCKAY, LORENZ STUDER PC
C12N5/06, A61K35/30, C12N5/10, C12N5/09, C12N5/00, C12N5/00, C12N5/
PC 00
CC Description of Artificial Sequence: Forward PCR primer for CC

FEATURES
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    Location/Qualifiers
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Query Match
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  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ATCTCGGAGATGACGAGAC 183
Db 1 ATCTCGGAGATGACGAGAC 22

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RESULT 123
BD270912/c
LOCUS BD270912 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Low oxygen culturing of central nervous system progenitor cells.
ACCESSION BD270912
VERSION BD270912.1 GI:33080680
KEYWORDS JP 2002530068-A/22.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Ceste,M., Doyle,J., Wold,B.J., McKay,R. and Studer,L.
TITLE Low oxygen culturing of central nervous system progenitor cells
JOURNAL Patent: JP 2002530068-A 22 17-SEP-2002;
CALIFORNIA INSTITUTE OF TECHNOLOGY, THE UNITED STATES OF AMERICA
COMMENT OS Artificial Sequence
PN JP 2002530068-A/22
PD 17-SEP-2002
PF 18-NOV-1999 JP 2000582534
PR 18-NOV-1998 US 09/195569, 22-OCT-1999 US 09/425462 PI
MARIE CESTE, JOHN DOYLE, BARBARA J WOLD, RON MCKAY, LORENZ STUDER PC
C12N5/06, A61K35/30, C12N5/10, C12N5/09, C12N5/00, C12N5/00, C12N5/
PC 00
CC Description of Artificial Sequence: Reverse PCR primer for CC

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FEATURES
  source
    Location/Qualifiers
      1..22
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Query Match
  Best Local Similarity 0.6%; Score 22; DB 1; Length 22;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GAGACAAAGTTGGCAGCATCC 487
Db 22 GAGACAAAGTTGGCAGCATCC 1

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RESULT 124

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AR383046
LOCUS       AR383046               22 bp    DNA             linear      PAT 18-DEC-2003
DEFINITION   Sequence 21 from patent US 6610540.
ACCESSION   AR383046
VERSION     AR383046.1 GI:40091859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Csete,M., Doyle,J., Wold,B.J., McKay,R. and Studer,L.
TITLE      Low oxygen culturing of central nervous system progenitor cells
JOURNAL    Patent: US 6610540-A 21 26-AUG-2003;
FEATURES    Location/Qualifiers
  source    1..22
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ATCTCGGAGATGACGAAGAC 183
  |||||
Db 1 ATCTCGGAGATGACGAAGAC 22

RESULT 125
LOCUS       AR383047/c            22 bp    DNA             linear      PAT 18-DEC-2003
DEFINITION   Sequence 22 from patent US 6610540.
ACCESSION   AR383047
VERSION     AR383047.1 GI:40091860
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Csete,M., Doyle,J., Wold,B.J., McKay,R. and Studer,L.
TITLE      Low oxygen culturing of central nervous system progenitor cells
JOURNAL    Patent: US 6610540-A 22 26-AUG-2003;
FEATURES    Location/Qualifiers
  source    1..22
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ATCTCGGAGATGACGAAGAC 183
  |||||
Db 1 ATCTCGGAGATGACGAAGAC 22

RESULT 126
LOCUS       AR327687            22 bp    DNA             linear      PAT 07-JAN-2002
DEFINITION   Sequence 23 from Patent WO0183715.
ACCESSION   AR327687
VERSION     AR327687.1 GI:18098018
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM   synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Inoue,K., Kim,D., Gu,Y. and Ishii,M.
TITLE      Method for inducing differentiation of embryonic stem cells into
            functioning cells
JOURNAL    Patent: WO 03062405-A 47 31-JUL-2003;
            Inoue, Kazutomo (JP) ; Yugengaisha Okuma Contactlens Kenkyujo (JP)
FEATURES    Location/Qualifiers
  source    1..22
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide Primer"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

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FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ATCTCGGAGATGACGAAGAC 183
  |||||
Db 1 ATCTCGGAGATGACGAAGAC 22

RESULT 127
LOCUS       AX327688/c            22 bp    DNA             linear      PAT 07-JAN-2002
DEFINITION   Sequence 24 from Patent WO0183715.
ACCESSION   AX327688
VERSION     AX327688.1 GI:18098019
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM   synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Lee,S.H., Lumelsky,N., Studer,L. and McKay,R.D.
TITLE      Derivation of midbrain dopaminergic neurons from embryonic stem
            cells
JOURNAL    Patent: WO 0183715-A 24 08-NOV-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) ;
            Lee, Sang-Hun (KR) ; Lumelsky, Nadya (US) ; Studer, Lorenz (US) ;
            McKay, Ron D. G. (US)
FEATURES    Location/Qualifiers
  source    1..22
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GAGAACAAAGTTGGCAGCATCC 487
  |||||
Db 22 GAGAACAAAGTTGGCAGCATCC 1

RESULT 128
LOCUS       AX812159            22 bp    DNA             linear      PAT 02-DEC-2003
DEFINITION   Sequence 47 from Patent WO03062405.
ACCESSION   AX812159
VERSION     AX812159.1 GI:38635795
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM   synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Inoue,K., Kim,D., Gu,Y. and Ishii,M.
TITLE      Method for inducing differentiation of embryonic stem cells into
            functioning cells
JOURNAL    Patent: WO 03062405-A 47 31-JUL-2003;
            Inoue, Kazutomo (JP) ; Yugengaisha Okuma Contactlens Kenkyujo (JP)
FEATURES    Location/Qualifiers
  source    1..22
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide Primer"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ATCTCTGGGAGATGACGAAGAC 183
|||||
Db 1 ATCTCTGGGAGATGACGAAGAC 22

RESULT 129
LOCUS AR020621/c
DEFINITION Sequence 5 from patent US 5789182.
ACCESSION AR020621
VERSION AR020621.1 GI:3975236
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yayon,A., Ornitz,D.M., Klagesbrun,M., Leder,P. and Planagan,J.G.
TITLE System for assaying binding to a heparin-binding growth factor receptor
JOURNAL Patent: US 5789182-A 5 04-AUG-1998;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 22; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1348 GAGATGGAGATGATGAAGATGA 1369
|||||
Db 28 GAGATGGAGATGATGAAGATGA 7

RESULT 130
LOCUS AX117832/c
DEFINITION Sequence 2955 from Patent WO0129262.
ACCESSION AX117832
VERSION AX117832.1 GI:14034783
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2955 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTGTGTGTGTG 2341
|||||
Db 25 CCGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 131
LOCUS AR127801/c
DEFINITION Sequence 22 from patent US 6180777.
ACCESSION AR127801
VERSION AR127801.1 GI:14114396

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Horn,T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 22 30-JAN-2001;
FEATURES Location/Qualifiers
source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GGTGTGTGTGTGTGTGTGTGTGTG 2341
|||||
Db 23 GGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 132
LOCUS I31542/c
DEFINITION Sequence 454 from patent US 5582979.
ACCESSION I31542
VERSION I31542.1 GI:1822333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 454 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGT 2340
|||||
Db 23 TGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 133
LOCUS AR173690
DEFINITION Sequence 7 from patent US 6306591.
ACCESSION AR173690
VERSION AR173690.1 GI:17914010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cockett,N.E. and Beever,J.E.
TITLE Screening for the molecular defect causing spider lamb syndrome in sheep
JOURNAL Patent: US 6306591-A 7 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1425 CCTGTACGTGCTGGTGGAGTA 1445
|||||
Db 1 CCTGTACGTGCTGGTGGAGTA 21

RESULT 134
AR090052/c
LOCUS AR090052 30 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 172 from patent US 5994076.
ACCESSION AR090052
VERSION AR090052.1 GI:10016807
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 172 30-NOV-1999;
FEATURES Location/Qualifiers
source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 2.6e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1572 CCAGTGGCCCGGGCATGGAGTACTTGG 1600
|||||
Db 29 CCAAGTGGCTAAGGGCATGGAGTCTTGG 1

RESULT 135
AR197087/c
LOCUS AR197087 30 bp DNA PAT 20-APR-2002
DEFINITION Sequence 172 from patent US 6352829.
ACCESSION AR197087
VERSION AR197087.1 GI:20246936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 172 05-MAR-2002;
FEATURES Location/Qualifiers
source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 2.6e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1572 CCAGTGGCCCGGGCATGGAGTACTTGG 1600
|||||
Db 29 CCAAGTGGCTAAGGGCATGGAGTCTTGG 1

RESULT 136
AR259241/c
LOCUS AR259241 30 bp DNA PAT 20-DEC-2002
DEFINITION Sequence 172 from patent US 6489455.
ACCESSION AR259241
VERSION AR259241.1 GI:27309752
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 30)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 172 03-DEC-2002;
FEATURES Location/Qualifiers
source
1..30
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 2.6e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1572 CCAGTGGCCCGGGCATGGAGTACTTGG 1600
|||||
Db 29 CCAAGTGGCTAAGGGCATGGAGTCTTGG 1

RESULT 137
AX117828/c
LOCUS AX117828 25 bp DNA PAT 11-MAY-2001
DEFINITION Sequence 2951 from Patent WO0129262.
ACCESSION AX117828
VERSION AX117828.1 GI:14034779
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2951 26-APR-2001;
FEATURES Location/Qualifiers
source
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.5%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 2.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTGTGTGTGTGT 2340
|||||
Db 24 CCGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 138
AR002279/c
LOCUS AR002279 27 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 18 from patent US 5741645.
ACCESSION AR002279
VERSION AR002279.1 GI:3963833
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE Gene sequence for spinocerebellar ataxia type 1 and method for diagnosis
JOURNAL Patent: US 5741645-A 18 21-APR-1998;
FEATURES Location/Qualifiers
source
1..27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 20.6; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 2.6e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;


```

ORGANISM      unidentified
REFERENCE      1 (bases 1 to 20)
AUTHORS        Jun,S., Eriko,T., Chika,H., Akihiro,I., Masahiro,T. and Hiroshi,H.
TITLE          Immortalized human papilla pili cell and method for evaluating hair
JOURNAL        Growth stimulants with the use of the same
                Patent: JP 199089565-A 24 06-APR-1999;
                SHISEIDO CO LTD
COMMENT        OS Unidentified
                PN JP 199089565-A/24
                PD 06-APR-1999
                PF 19-SEP-1997 JP 1997271927
                PR
                PI JUN SUZUKI, ERIKO TAKEOKA, CHIKA HAMADA, AKIHIRO ISHINO, PI
                MASAHIRO TAJIMA,
                PI HIROSHI HANDA
                PC C12N5/10,A61K7/06, C12N15/09, C12P21/02, C12Q1/02, C12N5/10, PC
                C12R1/91),
                PC (C12P21/02, C12R1/91), C12N5/00, C12N15/00, (C12N5/00, C12R1/91) CC
                Strandedness: Single;
                CC Topology: Linear;
                FH Key Location/Qualifiers
                FT source 1..20
                FT Location/Qualifiers
                FT /organism='Unidentified'.
                FT 1..20
                FT /organism='unidentified'
                FT /mol_type='genomic DNA'
                FT /db_xref='taxon:32644'

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1297 AAGATGCTGAAGACGATGC 1316
DB      20 AAGATGCTGAAGACGATGC 1

RESULT 144
LOCUS      BD107438      27 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Novel microsatellite DNA of pears.
ACCESSION      BD107438
VERSION      BD107438.1 GI:23202256
KEYWORDS      JP 2002034562-A/47.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 27)
AUTHORS        Yamamoto,T., Sawamura,Y., Matsuda,N. and Hayashi,K.
TITLE          Novel microsatellite DNA of pears
JOURNAL        Patent: JP 2002034562-A 47 05-FEB-2002;
COMMENT        OS Artificial Sequence
                PN JP 2002034562-A/47
                PD 05-FEB-2002
                PF 21-JUL-2000 JP 2000220340
                PR TOSHIYA YAMAMOTO, YUTAKA SAWAMURA, NAGAO MATSUDA, KENKI HAYASHI
                PC C12N15/09, C12N15/00
                CC Description of Artificial Sequence: Primer
                CC 1
                FH Key Location/Qualifiers
                FT modified base (1)..(2).
                FT Location/Qualifiers
                FT 1..27
                FT /organism='synthetic construct'
                FT /mol_type='genomic DNA'
                FT /db_xref='taxon:32630'

Query Match      0.5%; Score 20; DB 1; Length 27;
Best Local Similarity 79.2%; Pred. No. 3.1e+02;
Matches 19; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2332 TCGTGTGTGTGTGTGTGTGCACA 2355
DB      27 TGTGTGTGTGTGTGTGTGTGVMVM 4

RESULT 145
LOCUS      AX116678      23 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 1801 from Patent WO0129262.
ACCESSION      AX116678
VERSION      AX116678.1 GI:14033620
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1
AUTHORS        Picoult-Newburg,L. and Pohl,M.
TITLE          Genotyping reagents, kits and methods of use thereof
JOURNAL        Patent: WO 0129262-A 1801 26-APR-2001;
                Orchid Biosciences, Inc. (US)
FEATURES      Location/Qualifiers
                source 1..23
                source /organism='synthetic construct'
                source /mol_type='unassigned DNA'
                source /db_xref='taxon:32630'
                source /note='Primer'

Query Match      0.5%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2311 TTTGTCTGTGTGTGTGTGTGTG 2333
DB      1 TTTTGTGTGTGTGTGTGTGTGTG 23

RESULT 146
LOCUS      E32214/c      24 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION      E32214
VERSION      E32214.1 GI:13021823
KEYWORDS      JP 2000060559-A/16.
SOURCE      Haliotis discus discus
ORGANISM      Haliotis discus discus
                Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
                Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Hideaki,T. and Masashi,S.
TITLE          Method for isolating satellite sequence
JOURNAL        Patent: JP 2000060559-A 16 29-FEB-2000;
                NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT        OS Haliotis discus discus
                PN JP 2000060559-A/16
                PD 29-FEB-2000
                PF 18-AUG-1998 JP 1998232153
                PR
                PR HIDEAKI TAKAHASHI, MASASHI SEKINO
                PC C12N15/09, C12Q1/68, C12N15/00
                CC
                CC Key Location/Qualifiers
                FT source 1..24
                FT /organism='Haliotis discus discus'.
                FT Location/Qualifiers
                FT 1..24
                FT /organism='Haliotis discus discus'
                FT /mol_type='genomic DNA'
                FT /sub_species='discus'
                FT /db_xref='taxon:91233'

Query Match      0.5%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 3e+02;

```



```
QY 1765 GAGGCCTTTGACCGAGCTCTACAC 1790
||||| ||||| ||||| |||||
Db 27 GAGGCATTATTGACCGGATCTACAC 2

RESULT 152
AR197265/c
LOCUS AR197265 28 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 350 from patent US 6352829.
ACCESSION AR197265
VERSION AR197265.1 GI:20247114
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 350 05-MAR-2002;
FEATURES
source
Location/Qualifiers
1..28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 19.6; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1765 GAGGCCTTTGACCGAGCTCTACAC 1790
||||| ||||| ||||| |||||
Db 27 GAGGCATTATTGACCGGATCTACAC 2

RESULT 153
AR259419/c
LOCUS AR259419 28 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 350 from patent US 6489455.
ACCESSION AR259419
VERSION AR259419.1 GI:27309930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 350 03-DEC-2002;
FEATURES
source
Location/Qualifiers
1..28
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 19.6; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1765 GAGGCCTTTGACCGAGCTCTACAC 1790
||||| ||||| ||||| |||||
Db 27 GAGGCATTATTGACCGGATCTACAC 2

RESULT 154
AR007164
LOCUS AR007164 21 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 16 from patent US 5750371.
ACCESSION AR007164
VERSION AR007164.1 GI:3966648
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Senoo,M., Watanabe,T. and Igarashi,K.

TITLE Water-soluble mutein of FGF receptor, DNA and production thereof
JOURNAL Patent: US 5750371-A 16 12-MAY-1998;
FEATURES
source
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1345 TCTGAGATGGAGATGATGAAG 1365
||||| ||||| ||||| |||||
Db 1 TCAGAGATGGAGATGATGAAG 21

RESULT 155
I31248/c
LOCUS I31248 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 160 from patent US 5582979.
ACCESSION I31248
VERSION I31248.1 GI:1822039
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Weber,J.L.
TITLE length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 160 10-DEC-1996;
FEATURES
source
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGTGT 2338
||||| ||||| ||||| |||||
Db 21 TGTGTGTGTGTGTGTTGTGT 1

RESULT 156
AX104715
LOCUS AX104715 21 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 907 from Patent WO0122972.
ACCESSION AX104715
VERSION AX104715.1 GI:13920912
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 907 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGTGT 2338
||||| ||||| ||||| |||||
```

```
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 157
AX175255
LOCUS AX175255 21 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 19 from Patent WO0144465.
ACCESSION AX175255
VERSION AX175255.1 GI:14598623
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 19 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGT 2338
|||||
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 160
BD251661
LOCUS BD251661 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Selection of animal based on character imprinted by parent.
ACCESSION BD251661
VERSION BD251661.1 GI:33061431
KEYWORDS JP 2002535963-A/181.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Andersson,L., Georges,M., Spincemaille,G. and Nezer,C.D.A.
TITLE Selection of animal based on character imprinted by parent
JOURNAL Patent: JP 2002535963-A 181 29-OCT-2002;
UNIVERSITY OF LIège,MELICA HB, SEGHERS GENTEC NV
COMMENT OS Sus scrofa (pig)
PN JP 2002535963-A/181
PD 29-OCT-2002
PF 16-DEC-1999 JP 2000588390
PR 16-DEC-1998 EP 98204291.3
PI LEIF ANDERSSON,MICHEL GEORGES,GEERT SPINCHEMAILLE, PI CARINE
DANIELLE ANDREE NEZER
PC C12N15/09,A01K67/027,C12N5/06,C12Q1/68,C12N15/00,C12N5/00 CC
/notes="Microsatellite"
FH Key
FT source
1. .22
Location/Qualifiers
/organism="Sus scrofa (pig)".
FEATURES
source
1. .22
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"

Query Match 0.5%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATATA 2844
|||||
Db 1 ATATATATATATATATATATA 21

RESULT 161
BD251661/C
LOCUS BD251661/C 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Selection of animal based on character imprinted by parent.
ACCESSION BD251661
VERSION BD251661.1 GI:33061431
KEYWORDS JP 2002535963-A/181.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 157
AX175255
LOCUS AX175255 21 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 19 from Patent WO0144465.
ACCESSION AX175255
VERSION AX175255.1 GI:14598623
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 19 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGT 2338
|||||
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 158
AX175256
LOCUS AX175256 21 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 20 from Patent WO0144465.
ACCESSION AX175256
VERSION AX175256.1 GI:14598624
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 20 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2339
|||||
Db 1 GTGTGTGTGTGTGTGTGTGT 21

RESULT 159
AX547768
LOCUS AX547768 21 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 907 from Patent WO20053141.
ACCESSION AX547768
VERSION AX547768.1 GI:25812912
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
```


[illegible]

LEIF ANDERSONSON,JAMES KIYAS,ELISABETTA GIUFFRA,GARY JON PI					
EVANS,RICHARD WALES,	PI	GRAHAM STUART PLASTOW			
PC	C12Q1/68				
CC	Strandedness:	Single;			
CC	Topology:	Linear;			
CC	Primer				
FH	Key	Location/Qualifiers			
FT	source	1. .26			
FEATURES					
source					
Query Match 0.5%; Score 19.4; DB 1; Length 26;					
Best Local Similarity 80.0%; Pred. No. 3.6e+02;					
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;					
Qy	1796	AGAGTGACGTCGTCTGGTCTTTGGGGT 1820			
Db	2	AAAGTGAYGTCGTCTCATSGGAT 26			
RESULT 173					
BD192781/c					
LOCUS					
DEFINITION					
Generation, characterization and isolation of neuroepithelial stem cells and lineage restricted intermediate precursor.					
ACCESSION					
BD192781.1 GI:33002520					
VERSION					
JP 2002513291-A/8.					
KEYWORDS					
Staphylococcus aureus					
SOURCE					
ORGANISM					
Staphylococcus aureus					
Bacteria; Firmicutes; Bacillales; Staphylococcus.					
REFERENCE					
Rao,M.S., Proschel,M.M. and Mujtaba,T.					
Generation, characterization and isolation of neuroepithelial stem cells and lineage restricted intermediate precursor					
TITLE					
Patent: JP 2002513291-A 8 08-MAY-2002;					
JOURNAL					
UNIVERSITY OF UTAH RESEARCH FOUNDATION					
COMMENT					
PN JP 2002513291-A/8					
PD 08-MAY-2002					
PF 07-MAY-1998 JP 1998548581					
PR 07-MAY-1997 US 08/852744,06-MAY-1998 US 09/073881 PT					
MAHENDRA S RAO,MARGOT MAYER PROSCHEL,TAHMINA MUJTABA PC					
C12N5/06,C12N5/08					
CC Strandedness: Single;					
CC Topology: Linear;					
FH Key					
Location/Qualifiers.					
FEATURES					
source					
Query Match 0.5%; Score 19.2; DB 1; Length 24;					
Best Local Similarity 87.5%; Pred. No. 3.5e+02;					
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;					
Qy	984	GAAAGGCCTGGGCTCCCCACCGT 1007			
Db	24	GAAAGGCCTGGGCTCGCCACCGT 1			
RESULT 174					
E32221/c					
LOCUS					
DEFINITION					
Method for isolating satellite sequence.					
ACCESSION					
E32221					
VERSION					
E32221.1 GI:13021846					
KEYWORDS					
JP 2000060559-A/23.					
PAT 18-JUN-2003					

SOURCE Haliotis discus discus
ORGANISM Haliotis discus discus
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hideaki.T. and Masashi.S.
TITLE Method for isolating satellite sequence
JOURNAL Patent: JP 2000060559-A 23 29-FEB-2000;
NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT OS Haliotis discus discus
PN JP 2000060559-A/23
PD 29-FEB-2000
PF 18-AUG-1998 JP 1998232153
PR
PI HIDEAKI TAKAHASHI,MASASHI SEKINO
CC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..24
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Query Match 0.5%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2328 TGTGTCGTGTGTGTGTGTGTGTG 2351
DB 24 TGCATGCATGTGTGTGTGTGTGTGTG 1
RESULT 175
AX482164
LOCUS AX482164 19 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 141 from Patent EP1225233.
ACCESSION AX482164
VERSION AX482164.1 GI:22316886
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1225233-A 141 24-JUL-2002;
Amsterdam Support Diagnostics B.V. (NL)
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/db_xref="taxon:32630"
/note="5'TAG019GENE-2"
Query Match 0.5%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1702 CACAACCTCGACTACTACA 1720
DB 1 CACAACCTCGACTACTACA 19
RESULT 176
AX511403
LOCUS AX511403 19 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 141 from Patent WO202059558.
ACCESSION AX511403
VERSION AX511403.1 GI:23392280

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: WO 02059558-A 141 01-AUG-2002;
Amsterdam Support Diagnostics B.V. (NL)
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/db_xref="taxon:32630"
/note="5'TAG019GENE-2"
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Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1702 CACAACCTCGACTACTACA 1720
DB 1 CACAACCTCGACTACTACA 19
RESULT 177
AX721764
LOCUS AX721764 19 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 143 from Patent EP1298221.
ACCESSION AX721764
VERSION AX721764.1 GI:30422355
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1298221-A 143 02-APR-2003;
PrimaGen Holding B.V. (NL)
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/db_xref="taxon:32630"
/note="5'TAG019GENE-2"
Query Match 0.5%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1702 CACAACCTCGACTACTACA 1720
DB 1 CACAACCTCGACTACTACA 19
RESULT 178
AR404118/c
LOCUS AR404118 24 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6627733.
ACCESSION AR404118
VERSION AR404118.1 GI:40152138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson,J.D., Rutter,W.J. and Edman,J.C.
TITLE Receptor tyrosine kinase with a discoidin-type binding domain
JOURNAL Patent: US 6627733-A 3 30-SEP-2003;
FEATURES
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/organism="unknown"

Thu Oct 28 12:48:19 2004

/mol_type="genomic DNA"

Query Match 0.5%; Score 19; DB 1; Length 24;
Best Local Similarity 69.6%; Pred. No. 3.7e+02;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1618 CACAGGACCTGGCTCCGCCAA 1640
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Db 24 CAYCGSAYCTGGCYGCGSAA 2

RESULT 179
AX080281/c 27 bp DNA linear PAT 22-FEB-2001
LOCUS
DEFINITION Sequence 8 from Patent WO0107632.
ACCESSION AX080281
VERSION AX080281.1 GI:13159750

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Perez, P. and Garcia, D.
TITLE Method for obtaining isogenic transgenic lines
JOURNAL Patent: WO 0107632-A 8 01-FEB-2001;
Rhobio (FR)

FEATURES
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1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic construct"

Query Match 0.5%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 4.1e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3639 GGCAGCTGTCCTTGTGCTGCAG 3665
|||||
Db 27 GAGCAGCTGAAGCTGATGCTGCAG 1

RESULT 180
BD192780 22 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor.

ACCESSION BD192780
VERSION BD192780.1 GI:33002519
KEYWORDS JP 2002513291-A/7.
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus

REFERENCE 1
AUTHORS Rao, M.S., Proschel, M.M. and Mujtaba, T.
TITLE Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor
JOURNAL Patent: JP 2002513291-A 7 08-MAY-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION

COMMENT
FN JP 2002513291-A/7
PD 08-MAY-2002
PF 07-MAY-1998 JP 1998548581
PR 07-MAY-1997 US 08/952744, 06-MAY-1998 US 09/073881 PI
MAHENDRA S RAO, MARGOT WAYER PROSCHEL, TAHMINA MUJTABA PC
C12N5/06, C12N5/08
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.

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/organism="Staphylococcus aureus"
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Query Match 0.5%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 409 AGCTGTGTCATGGAACGCTGG 430
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Db 1 AGCTGTGTCATGGAACGCTGG 22

RESULT 181
AX486835/c 22 bp DNA linear PAT 16-AUG-2002
LOCUS
DEFINITION Sequence 4135 from Patent WO02053728.
ACCESSION AX486835
VERSION AX486835.1 GI:22320983

KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans

REFERENCE 1
AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 4135 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
Location/Qualifiers

FEATURES
source
1. .22
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

Query Match 0.5%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2322 TGTGTGTGTGTGCGTGTGTGTG 2343
|||||
Db 22 TGTACGTGTGTGCGTGTGTGTG 1

RESULT 182
AX926722 23 bp DNA linear PAT 19-DEC-2003
LOCUS
DEFINITION Sequence 5 from Patent WO03085133.
ACCESSION AX926722
VERSION AX926722.1 GI:40247008

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Nagaraju, J.G.
TITLE Novel fissr-pcr primers and method of identifying genotyping
diverse genomes of plant and animal systems including rice
varieties, a kit thereof
JOURNAL Patent: WO 03085133-A 5 16-OCT-2003;
Centre for DNA Fingerprinting and Diagnostics, Centre for; the
Department of Biotechnology, Ministry of Science & Technology (IN)
Location/Qualifiers

FEATURES
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1. .23
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="A novel FISSR-PCR primer for genotyping eukaryotes"

Query Match 0.5%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 3.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 GTCTGTGTGTGTGTGTGTGCT 2336
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Db 2 GTATGTGTGTGTGTGTGTGTG 23


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RESULT 183
AR058875/c
LOCUS AR058875 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5837835.
ACCESSION AR058875
VERSION AR058875.1 GI:5984452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-P5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 7 17-NOV-1998;
FEATURES Location/Qualifiers
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Query Match 0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred.No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 22 TATATATAAAATATATATA 1

RESULT 186
AR079582/c
LOCUS AR079582 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 9 from patent US 5965720.
ACCESSION AR079582
VERSION AR079582.1 GI:10006326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-P5' phosphoramidates
JOURNAL Patent: US 5965720-A 9 12-OCT-1999;
FEATURES Location/Qualifiers
source
1..24
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred.No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 22 TATATATAAAATATATATA 1

RESULT 187
AR123289/c
LOCUS AR123289 24 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6169170.
ACCESSION AR123289
VERSION AR123289.1 GI:14108255
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-P5' phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 7 02-JAN-2001;
FEATURES Location/Qualifiers
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1..24
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred.No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 22 TATATATAAAATATATATA 1

RESULT 188
AR123291/c
LOCUS AR123291 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 7 from patent US 5965720.
ACCESSION AR079580
VERSION AR079580.1 GI:10006324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-P5' phosphoramidates
```

PN	JP 2003012688-A/7
PD	15-JAN-2003
PF	12-JUN-2002 JP 2002171743
PR	18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI
SERGBI	M GRAYZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02, C12Q1/68	
CC	Strandedness: Both;
CC	Topology: Linear;
CC	Oligonucleotide N3', to P5' phosphoramidate: synthesis and CC compound;
CC	hybridization and nuclease tolerant characteristics FH Key Location/Qualifiers
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Best Local Similarity	90.9%; Pred. No. 3.9e+02;
Matches	20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	2823 TATATATACATATATATATA 2844
Db	22 TATATATAAATATATATA 1
RESULT 191	
BD188893/c	
LOCUS	BD188893 24 bp DNA linear PAT 17-JUL-2003
DEFINITION	Oligonucleotide N3' to p5' phosphoramidate: synthesis and compound;
ACCESSION	BD188893
VERSION	BD188893.1 GI:32998632
KEYWORDS	JP 2003012688-A/9.
SOURCE	unidentified
ORGANISM	unclassified
REFERENCE	1 (bases 1 to 24)
AUTHORS	Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE	Oligonucleotide N3' to p5' phosphoramidate: synthesis and compound
JOURNAL	hybridization and nuclease tolerant characteristics Patent: JP 2003012688-A 9 15-JAN-2003; LYNX THERAPEUTICS INC
COMMENT	OS Unidentified PN JP 2003012688-A/9 PD 15-JAN-2003 PF 12-JUN-2002 JP 2002171743 PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI SERGBI M GRAYZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC C07H19/16//C12Q1/02, C12Q1/68 CC Strandedness: Both; CC Topology: Linear; CC /note= 'where the intersubunit bond is 'np'' CC /note= CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' FH Key Location/Qualifiers FT misc feature 1..2 FT misc feature 3..4 FT misc feature 5..6 FT misc feature 7..8 FT misc feature 9..10 FT misc feature 15..16 FT misc feature 17..18

REFERENCE
AUTHORS
1 (bases 1 to 24)
Gryaznov, S.M.; Schultz, R.G. and Chen, J.-K.

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TITLE      Oligonucleotide N3', fwdarw.p5', phosphoramidates: hybridization and
JOURNAL    nuclease resistance properties
PATENT     Patent: US 5631135-A 7 20-MAY-1997;
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Query Match      0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2823 TATATATACATATATATATATA 2844
Db      22 TATATATAAAATATATATATA 1

RESULT 197
LOCUS    143129          24 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 9 from patent US 5631135.
ACCESSION 143129
VERSION   143129.1 GI:2468373
KEYWORDS .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS  Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE    Oligonucleotide N3', fwdarw.p5', phosphoramidates: hybridization and
JOURNAL  nuclease resistance properties
PATENT   Patent: US 5631135-A 9 20-MAY-1997;
FEATURES Location/Qualifiers
SOURCE   1..24
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Query Match      0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2823 TATATATACATATATATATATA 2844
Db      22 TATATATAAAATATATATATA 1

RESULT 198
LOCUS    143129          24 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION Sequence 7 from patent US 5726297.
ACCESSION 192005
VERSION   192005.1 GI:3936475
KEYWORDS .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS  Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE    Oligodeoxyribonucleotide N3', P5', phosphoramidates
JOURNAL  Patent: US 5726297-A 7 10-MAR-1998;
FEATURES Location/Qualifiers
SOURCE   1..24
         /organism="unknown"
         /mol_type="unassigned DNA"

Query Match      0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2823 TATATATACATATATATATATA 2844
Db      22 TATATATAAAATATATATATA 1

TITLE      Oligonucleotide N3', fwdarw.p5', phosphoramidates: hybridization and
JOURNAL    nuclease resistance properties
PATENT     Patent: US 5631135-A 7 20-MAY-1997;
FEATURES   Location/Qualifiers
SOURCE     1..24
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2823 TATATATACATATATATATATA 2844
Db      22 TATATATAAAATATATATATA 1

RESULT 199
LOCUS    192007/c          24 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION Sequence 9 from patent US 5726297.
ACCESSION 192007
VERSION   192007.1 GI:3936477
KEYWORDS .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS  Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE    Oligodeoxyribonucleotide N3', P5', phosphoramidates
JOURNAL  Patent: US 5726297-A 9 10-MAR-1998;
FEATURES Location/Qualifiers
SOURCE   1..24
         /organism="unknown"
         /mol_type="unassigned DNA"

Query Match      0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2823 TATATATACATATATATATATA 2844
Db      22 TATATATAAAATATATATATA 1

RESULT 200
LOCUS    AR177699          20 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 39 from patent US 6312949.
ACCESSION AR177699
VERSION   AR177699.1 GI:17920054
KEYWORDS .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS  Sakurada,K., Palmer,T. and Gage,F.H.
TITLE    Regulation of tyrosine hydroxylase expression
JOURNAL  Patent: US 6312949-A 39 06-NOV-2001;
FEATURES Location/Qualifiers
SOURCE   1..20
         /organism="unknown"
         /mol_type="unassigned DNA"

Query Match      0.5%; Score 18.6; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1345 TCTGAGATGGAGATGATGAA 1364
Db      1 TCNGAGATGGAGTGTGAA 20

RESULT 201
LOCUS    AR028293          25 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5858662.
ACCESSION AR028293
VERSION   AR028293.1 GI:5940266
KEYWORDS .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS  Keating,M.T. and Morris,C.A.
TITLE    Diagnosis of Williams syndrome and Williams syndrome cognitive
JOURNAL  profile by analysis of the presence or absence of a LIM-kinase gene
PATENT   Patent: US 5858662-A 3 12-JAN-1999;
FEATURES Location/Qualifiers
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source      1. .25
/organism="unknown"
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Query Match      0.5%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGCGCCGGGACGTGC 1702
      |||||
Db 1 GACTTTGGGCTGGCTCGAGACATGC 25

RESULT 202
AR434784
LOCUS      AR434784
DEFINITION Sequence 1207 from patent US 6656700.
ACCESSION AR434784
VERSION AR434784.1 GI:40197627
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Gu, Y. and Shannon, M.E.
TITLE      Isoforms of human pregnancy-associated protein-E
JOURNAL      Patent: US 6656700-A 1207 02-DEC-2003;
FEATURES
SOURCE      1. .25
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.5%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2321 GTGTGTGTGTGCGTGTGTGTGTG 2345
      |||||
Db 1 GTGTGTGTGTGTGAGTGTGTATTG 25

RESULT 203
A63570
LOCUS      A63570
DEFINITION Sequence 11 from Patent WO9720924.
ACCESSION A63570
VERSION A63570.1 GI:3717225
KEYWORDS      unidentified
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1
AUTHORS      Scaggiante, B. and Quadrioglio, F.
TITLE      A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMORAL
JOURNAL      AGENTS
COMMENT      Patent: WO 9720924-A 11 12-JUN-1997;
              SAICOM S R L (IT)
              Other publication IT MI952539 19970604
              Other publication AU 1175497 19970627.
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGTGT 2338
      |||||
Db 1 GTGTGTGTGTGTGTGTGTGTGTGT 20

RESULT 204
AR084543
LOCUS      AR084543
DEFINITION Sequence 32 from patent US 5981185.
ACCESSION AR084543
VERSION AR084543.1 GI:10011314
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE      Oligonucleotide repeat arrays
JOURNAL      Patent: US 5981185-A 32 09-NOV-1999;
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SOURCE      Location/Qualifiers
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Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGTGT 2338
      |||||
Db 20 GTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 205
AR123339
LOCUS      AR123339
DEFINITION Sequence 5 from patent US 6169176.
ACCESSION AR123339
VERSION AR123339.1 GI:14108305
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Bruice, T.C. and Dev, A.P.
TITLE      Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL      Patent: US 6169176-A 5 02-JAN-2001;
FEATURES
SOURCE      Location/Qualifiers
              1. .20
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Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGT 2337
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Db 20 TGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 206
AR129684
LOCUS      AR129684
DEFINITION Sequence 88 from patent US 6187545.
ACCESSION AR129684
VERSION AR129684.1 GI:14117581
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS      McKay, R., Butler, M.M., Wyatt, J. and Cowsett, L.M.
TITLE      Antisense modulation of pepck-cytosolic expression
JOURNAL      Patent: US 6187545-A 88 13-FEB-2001;
FEATURES
SOURCE      Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGT 2338
DB 20 GTGTGTGTGTGTGTGTGTGTGT 1

RESULT 207
E36173
LOCUS      20 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Upstream regulatory sequence of melanocortin-1 receptor gene and
utilization thereof.
ACCESSION  E36173
VERSION     E36173.1 GI:18626400
KEYWORDS   JP 2000166563-A/15.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Moro,O., Ifuku,O. and Ideta,T.
TITLE     Upstream regulatory sequence of melanocortin-1 receptor gene and
utilization thereof
JOURNAL    Patent: JP 2000166563-A 15 20-JUN-2000;
SHISEIDO CO LTD
COMMENT    OS Homo sapiens (human)
PN JP 2000166563-A/15
PD 20-JUN-2000
PF 04-DEC-1998 JP 1998345881
PR
PI OSAMU MORO, OJI IFUKU, TATSURO IDETA
PC C12N15/09, C12N5/10, C12Q1/66, C12Q1/68, C07K14/705, (C12N15/09,
C12R1:91),
PC C12N15/00, C12N5/00, (C12N15/00, C12R1:91)
CC
FH Key      Location/Qualifiers
FT source   1..20
FEATURES   Location/Qualifiers
source      1..20
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2842
DB 20 TATATATATATATATATA 1

RESULT 209
AX179298
LOCUS      20 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION Sequence 1 from Patent WO0141813.
ACCESSION  AX179298
VERSION     AX179298.1 GI:14598969
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS   Linnik,M.D. and Mcnealy,P.A.
TITLE     Methods of treating lupus based on antibody affinity and screening
methods and compositions for use thereof
JOURNAL    Patent: WO 0141813-A 1 14-JUN-2001;
LA JOLLA PHARMACEUTICAL COMPANY (CA)
FEATURES   Location/Qualifiers
source      1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGT 2338
DB 1 GTGTGTGTGTGTGTGTGTGTGT 20

RESULT 210
AX179299/c
LOCUS      20 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0141813.
ACCESSION  AX179299
VERSION     AX179299.1 GI:14598970
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1

```

AUTHORS Linnik,M.D. and Mcnealy,P.A.
 TITLE Methods of treating lupus based on antibody affinity and screening
 JOURNAL Methods and compositions for use thereof
 PATENT: WO 0141813-A 2 14-JUN-2001;
 LA JOLLA PHARMACEUTICAL COMPANY (CA)
 FEATURES Location/Qualifiers
 source
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGGTG 2337
 DB 20 TGTGTGTGTGTGTGTGTG 1

RESULT 211
 BD016468
 LOCUS 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION Method for regulating telomeric length.
 ACCESSION BD016468
 VERSION JP 2001231567-A/9.
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 1 (bases 1 to 20)
 Ota.K. and Shibata,T.
 Method for regulating telomeric length
 Patent: JP 2001231567-A 9 28-AUG-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, JAPAN SCIENCE AND
 TECHNOLOGY CORP
 COMMENT OS Artificial Sequence
 PN JP 2001231567-A/9
 PD 28-AUG-2001
 PF 18-FEB-2000 JP 2000041929
 PI KUNIKAZU OTA, TAKEHIKO SHIBATA
 PC C12N15/09,A61K35/76,A61K38/00,A61K48/00,A61P35/00,A61P43/00,
 PC C07H21/00,
 PC C07K14/395,C12N9/16,C12N15/00,A61K37/02
 CC Description of Artificial Sequence: synthetic DNA FH Key
 Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

FEATURES source
 1..20
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGCGGTG 2338
 DB 1 GTGTGTGTGTGTGTGTG 20

RESULT 212
 BD084130
 LOCUS 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION Polymorphisms and new genes in the region of the human
 hemochromatosis gene.
 ACCESSION BD084130
 VERSION BD084130.1 GI:22629740
 KEYWORDS JP 2001525663-A/18.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
 Tsuchihashi,Z. and Wolff,R.K.
 TITLE Polymorphisms and new genes in the region of the human
 hemochromatosis gene
 JOURNAL Patent: JP 2001525663-A 18 11-DEC-2001;
 PROGENITOR INC
 COMMENT OS Homo sapiens (human)
 PN JP 2001525663-A/18
 PD 11-DEC-2001
 PF 30-SEP-1997 JP 1998516815
 PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
 JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
 WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
 C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
 and new genes in the region of the human CC hemochromatosis gene
 PH Key Location/Qualifiers
 FT source 1..20
 /organism='Homo sapiens (human)'.
 FEATURES source
 1..20
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATAT 2843
 DB 1 ATATATATATATATATATAT 20

RESULT 213
 BD084130/c
 LOCUS 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION Polymorphisms and new genes in the region of the human
 hemochromatosis gene.
 ACCESSION BD084130
 VERSION BD084130.1 GI:22629740
 KEYWORDS JP 2001525663-A/18.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 20)
 Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
 Tsuchihashi,Z. and Wolff,R.K.
 TITLE Polymorphisms and new genes in the region of the human
 hemochromatosis gene
 JOURNAL Patent: JP 2001525663-A 18 11-DEC-2001;
 PROGENITOR INC
 COMMENT OS Homo sapiens (human)
 PN JP 2001525663-A/18
 PD 11-DEC-2001
 PF 30-SEP-1997 JP 1998516815
 PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
 JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
 WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
 C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
 and new genes in the region of the human CC hemochromatosis gene
 PH Key Location/Qualifiers
 FT source 1..20
 /organism='Homo sapiens (human)'.
 FEATURES source
 1..20
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.7e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATAT 2843
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Db 20 ATATATATATATATAT 1

RESULT 214
BD097545
LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for regulating telomeric length.
ACCESSION BD097545
VERSION BD097545.1 GI:22643119
KEYWORDS WO 0160996-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Ota,K. and Shibata,T.
TITLE Method for regulating telomeric length
JOURNAL Patent: WO 0160996-A 9 23-AUG-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, JAPAN SCIENCE AND
TECHNOLOGY CORP, KUNIHRO OTA, TAKEHIKO SHIBATA
COMMENT OS Artificial Sequence
FN WO 0160996-A/9
PD 23-AUG-2001
PF 14-FEB-2001 WO 2001JP001024
PI 18-FEB-2000 JP OOP 41929
PR KUNIHRO OTA, TAKEHIKO SHIBATA
PC C12N15/09,A61K35/76,A61K38/00,A61K48/00,A61P35/00,A61P43/00,
PC C07H21/00,
PC C07K14/395,C12N9/16
CC Description of Artificial Sequence:synthetic DNA FH Key
FT source 1..20
PT Location/Qualifiers

FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
||||| ||||||| ||||||| |||||||
Db 20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 215
BD105781/c
LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Conjugates of biologically stable polymers and polynucleotides for
treating systemic lupus erythematosus.
ACCESSION BD105781
VERSION BD105781.1 GI:22651355
KEYWORDS JP 2001354569-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Conrad,M.J. and Coutts,S.
TITLE Conjugates of biologically stable polymers and polynucleotides for
treating systemic lupus erythematosus
JOURNAL Patent: JP 2001354569-A 6 25-DEC-2001;
LA JOLLA PHARMACEUTICAL CO
COMMENT OS Artificial Sequence
FN JP 2001354569-A/6
PD 25-DEC-2001
PF 04-APR-2001 JP 2001106534
PR 16-JAN-1990 US 466138,13-MAR-1990 US 494118 PI

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
||||| ||||||| ||||||| |||||||
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 216
AX398276/c
LOCUS 21 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 1 from Patent WO0220543.
ACCESSION AX398276
VERSION AX398276.1 GI:21261077
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Sinha,N.
TITLE Synthesis for oligonucleotide synthesis
JOURNAL Patent: WO 0220543-A 1 14-MAR-2002;
Avecia Biotechnology, Inc. (US)
FT source 1..21
PT Location/Qualifiers

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Sequence prepared in Example 4"

Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
||||| ||||||| ||||||| |||||||
Db 20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 217
AX398277
LOCUS 21 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 2 from Patent WO0220543.
ACCESSION AX398277
VERSION AX398277.1 GI:21261078
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Sinha,N.
TITLE Synthesis for oligonucleotide synthesis
JOURNAL Patent: WO 0220543-A 2 14-MAR-2002;
Avecia Biotechnology, Inc. (US)
FT source 1..21
PT Location/Qualifiers

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Sequence prepared in Example 4"

Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
||||| ||||||| ||||||| |||||||
Db 20 GTGTGTGTGTGTGTGTGTGT 1


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Query Match          0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
DB 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 218
AX926721/c          24 bp DNA linear PAT 19-DEC-2003
LOCUS               Sequence 4 from Patent WO03085133.
DEFINITION          AX926721
ACCESSION            AX926721
VERSION              AX926721.1 GI:40247005
KEYWORDS             synthetic construct
SOURCE               synthetic construct
ORGANISM              artificial sequences.
REFERENCE            1
AUTHORS               Nagai, J.G.
TITLE                Novel fssr-pcr primers and method of identifying genotyping
                    diverse genomes of plant and animal systems including rice
                    varieties, a kit thereof
JOURNAL              Patent: WO 03085133-A 4 16-OCT-2003;
                    Centre for DNA Fingerprinting and Diagnostics, Centre for; the
                    Department of Biotechnology, Ministry of Science & Technology (IN)
FEATURES              Location/Qualifiers
                    source
                    1..24
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="A novel FISSR-PCR primer for genotyping eukaryotes"

Query Match          0.5%; Score 18.4; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTGTGT 2354
DB 24 GTGTGTGTGTGTGTGTGTGT 5

RESULT 219
AB086601            25 bp DNA linear SYN 21-MAY-2003
LOCUS               Synthetic construct DNA, forward primer for Japanese flounder
DEFINITION          Microsatellite sequence Pol1189TUF.
ACCESSION            AB086601
VERSION              AB086601.1 GI:28804453
KEYWORDS             synthetic construct
SOURCE               synthetic construct
ORGANISM              artificial sequences.
REFERENCE            1
AUTHORS               Coimbra, M.R.M., Kobayashi, K., Koresutsu, S., Hasegawa, O., Ohara, E.,
                    Ozaki, A., Sakamoto, T., Naruse, K. and Okamoto, N.
TITLE                A genetic linkage map of the Japanese flounder, (Paralichthys
                    olivaceus)
JOURNAL              Unpublished
REFERENCE            2 (bases 1 to 25)
AUTHORS               Coimbra, M.R.M., Kobayashi, K., Koresutsu, S., Hasegawa, O., Ohara, E.,
                    Ozaki, A., Sakamoto, T., Naruse, K. and Okamoto, N.
TITLE                Direct Submission
JOURNAL              Submitted (14-JUN-2002) Nobuaki Okamoto, Tokyo University of
                    Fisheries, Department of Aquatic Biosciences; 4-5-7 Konan,
                    Minato-Ku, Tokyo 108-8477, Japan
                    (E-mail:nokamoto@tokyo-u-fish.ac.jp, Tel:81-3-5463-0547,
                    Fax:81-3-5463-0552)
FEATURES              Location/Qualifiers
                    source
                    1..25
                    /organism="synthetic construct"

/misc_feature
/mol_type="genomic DNA"
/db_xref="taxon:32630"
1..25
/note="forward primer for Japanese flounder microsatellite
sequence Pol1189TUF"

Query Match          0.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 4.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2331 GTGCGTGTGTGTGTGTGTGTGCA 2353
DB 2 GTGTGTGTGTGTGTGTGTGTGCA 24

RESULT 220
AR071800/c          18 bp DNA linear PAT 18-FEB-2000
LOCUS               Sequence 29 from patent US 5912147.
DEFINITION          AR071800
ACCESSION            AR071800
VERSION              AR071800.1 GI:7222688
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM              Unclassified.
REFERENCE            1 (bases 1 to 18)
AUTHORS               Stoler, D., Basik, M. and Anderson, G.
TITLE                Rapid means of quantitating genomic instability
JOURNAL              Patent: US 5912147-A 29 15-JUN-1999;
                    Location/Qualifiers
                    source
                    1..18
                    /organism="unknown"
                    /mol_type="unassigned DNA"

Query Match          0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTGTGTG 2333
DB 18 TCTGTGTGTGTGTGTGTGTG 1

RESULT 221
AX482165/c          18 bp DNA linear PAT 17-AUG-2002
LOCUS               Sequence 142 from Patent EP125233.
DEFINITION          AX482165
ACCESSION            AX482165
VERSION              AX482165.1 GI:22316987
KEYWORDS             synthetic construct
SOURCE               synthetic construct
ORGANISM              artificial sequences.
REFERENCE            1
AUTHORS               van der Kuy, A.C. and Cornelissen, M.
TITLE                Means and methods for treatment evaluation
JOURNAL              Patent: EP 125233-A 142 24-JUL-2002;
                    Amsterdam Support Diagnostics B.V. (NL)
                    Location/Qualifiers
                    source
                    1..18
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="3'TAG019GENE-2"

Query Match          0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1888 AAGCTGCTGAAGGAGGCGC 1905
DB 18 AAGCTGCTGAAGGAGGCGC 1

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RESULT 222
AX511404/c
LOCUS AX511404 18 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 142 from Patent WO02059558.
ACCESSION AX511404
VERSION AX511404.1 GI:233922281
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1.
AUTHORS van der Kuyt,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: WO 02059558-A 142 01-AUG-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3'TAG019GENE-2"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1888 AAGCTGCTGAAGGAGGCG 1905
|||||
Db 18 AAGCTGCTGAAGGAGGCG 1

RESULT 223
AX721765/c
LOCUS AX721765 18 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 144 from Patent EPI298221.
ACCESSION AX721765
VERSION AX721765.1 GI:30422356
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1.
AUTHORS van der Kuyt,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1298221-A 144 02-APR-2003;
PrimaGen Holding B.V. (NL)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer 3'TAG019GENE-2"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1888 AAGCTGCTGAAGGAGGCG 1905
|||||
Db 18 AAGCTGCTGAAGGAGGCG 1

RESULT 224
E05497
LOCUS E05497 20 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer for detecting polymorphism of Oryza sativa and Zea
maize.
ACCESSION E05497
VERSION E05497.1 GI:2173685
KEYWORDS JP 1993244995-A/7
SOURCE synthetic construct
ORGANISM synthetic construct

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artificial sequences.
1 (bases 1 to 20)
AUTHORS Komatsu,Y. and Kikuchi,Y.
TITLE NEW PRIMER
JOURNAL Patent: JP 1993244995-A 7 24-SEP-1993;
KYOWA HAKKO KOGYO CO LTD
COMMENT OC Artificial gene
OS Zea maize
PN JP 1993244995-A/7
PD 24-SEP-1993
PF 24-SEP-1991 JP 1991243122
PI KOMATSU YUKI, KIKUCHI YASUHIRO
PC C12Q1/68,C12N15/11;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGC 2352
|||||
Db 2 GTGTGTGTGTGTGTGC 19

RESULT 225
BD192794
LOCUS BD192794 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor.
ACCESSION BD192794
VERSION BD192794.1 GI:33002533
KEYWORDS JP 2002513291-A/21.
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
REFERENCE
1 (bases 1 to 22)
AUTHORS Rao,M.S., Proschel,M.M. and Mujtaba,T.
TITLE Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor
JOURNAL Patent: JP 2002513291-A 21 08-MAY-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION
COMMENT PN JP 2002513291-A/21
PD 08-MAY-2002
PF 07-MAY-1998 JP 1998548581
PR 07-MAY-1997 US 08/852744 06-MAY-1998 US 09/073881 PI
MAHENDRA S RAO,MARGOT MAYER PROSCHEL,TAHMINA MUJTABA PC
C12N5/06,C12N5/08
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
1..22
/organism="Staphylococcus aureus"
/mol_type="genomic DNA"
/db_xref="taxon:1280"
Query Match 0.5%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1347 TGAGATGGAGATGATGAA 1364
|||||
Db 5 TGAGATGGAGATGATGAA 22

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RESULT 226
LOCUS      I30547
DEFINITION Sequence 10 from patent US 5580969.
ACCESSION  I30547
VERSION     I30547.1 GI:1821338
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.-H.
TITLE     Antisense oligonucleotides directed against human ICAM-1 RNA
JOURNAL   Patent: US 5580969-A 10 03-DEC-1996;
FEATURES   Location/Qualifiers
source     1..21
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTCGCTGT 2338
      |||||
Db 21 TGTGTGTGTGTGTGTGTGT 1

RESULT 227
LOCUS      AX020772
DEFINITION Sequence 272 from Patent W09934016.
ACCESSION  AX020772
VERSION     AX020772.1 GI:10044471
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Vidar,B.Z.
TITLE     A method for identifying and characterizing cells and tissues
JOURNAL   Patent: WO 9934016-A 272 08-JUL-1999;
GENENA LTD (IL); VIDAR BEN ZION (IL)
FEATURES   Location/Qualifiers
source     1..21
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1798 AGTGACGCTGTCGTCCTTGGG 1818
      |||||
Db 21 AGTGATGTCGTGTCCTATGGG 1

RESULT 228
LOCUS      AX116107
DEFINITION Sequence 1230 from Patent W00129262.
ACCESSION  AX116107
VERSION     AX116107.1 GI:14033049
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS   Picoult-Newburg,L. and Pohl,M.
TITLE     Genotyping reagents, kits and methods of use thereof

JOURNAL   Patent: WO 0129262-A 1230 26-APR-2001;
FEATURES   Location/Qualifiers
source     1..21
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="Primer"

Query Match      0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2320 TGTGTGTGTGTGTCGCTGTGT 2340
      |||||
Db 1 TCTGTGTGTGTGTGCTGTGT 21

RESULT 229
LOCUS      AX556883
DEFINITION Sequence 10 from Patent W002058723.
ACCESSION  AX556883
VERSION     AX556883.1 GI:25899981
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS   Vicari,A.P., Caux,C. and Laface,D.
TITLE     Chemokines as adjuvants of immune response
JOURNAL   Patent: WO 02058723-A 10 01-AUG-2002;
Schering Corporation (US)
FEATURES   Location/Qualifiers
source     1..21
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="Primer"

Query Match      0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTCGCTGTG 2339
      |||||
Db 21 GTGTGTGTGAGTGTGAGTGTG 1

RESULT 230
LOCUS      BD089174
DEFINITION A method of arraying genome clone.
ACCESSION  BD089174
VERSION     BD089174.1 GI:22634784
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Soeda,E.
TITLE     A method of arraying genome clone
JOURNAL   Patent: JP 2001321190-A 1418 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
COMMENT    OS Artificial Sequence
          PN JP 2001321190-A/1418
          PD 20-NOV-2001
          PF 12-MAR-2001 JP 2001068285
          PI EIICHI SOEDA
          PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
          PC C12N15/00,
          PC C12N15/00
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KEYWORDS	unidentified	identified	unclassified.
SOURCE	unidentified	identified	unclassified.
ORGANISM	unidentified	identified	unclassified.
REFERENCE	1		
AUTHORS	Masucci, M.G.		
TITLE	IMMUNE-EVADING PROTEINS		
JOURNAL	Patent: WO 9632483-A 6 17-OCT-1996;		
COMMENT	MASUCCI MARIA GRAZIA (SE)		
FEATURES	Other publication AU 5284296 961030.		
source	Location/Qualifiers		
	1. .24		
	/organism="unidentified"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32644"		
Query Match	0.5%;	Score 17.8; DB 1; Length 24;	
Best Local Similarity	90.5%;	Pred. No. 5.1e+02;	
Matches	19; Conservative	0; Mismatches	2; Indels
			0; Gaps
			0;
QY	2103 CACCCCGAGCTCCAGTCTCTC 2123		
Db	4 CACCCGACCTCCAGTCTCTC 24		
RESULT 233			
AR052980			
LOCUS	AR052980	24 bp DNA	linear PAT 29-SEP-1999
DEFINITION	Sequence 10 from patent US 5833991.		
ACCESSION	AR052980		
VERSION	AR052980.1 GI:5977842		
KEYWORDS	Glycine-containing sequences conferring invisibility to the immune		
SOURCE	system		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 24)		
AUTHORS	Masucci, M.G.		
TITLE	Glycine-containing sequences conferring invisibility to the immune		
JOURNAL	Patent: US 5833991-A 10-NOV-1998;		
FEATURES	Location/Qualifiers		
source	1. .24		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	0.5%;	Score 17.8; DB 1; Length 24;	
Best Local Similarity	90.5%;	Pred. No. 5.1e+02;	
Matches	19; Conservative	0; Mismatches	2; Indels
			0; Gaps
			0;
QY	2103 CACCCCGAGCTCCAGTCTCTC 2123		
Db	4 CACCCGACCTCCAGTCTCTC 24		
RESULT 234			
AR052980			
LOCUS	AX117030	24 bp DNA	linear PAT 11-MAY-2001
DEFINITION	Sequence 2153 from Patent WO0129262.		
ACCESSION	AX117030		
VERSION	AX117030.1 GI:14033972		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Picoult-Newburg, L. and Pohl, M.		
TITLE	Genotyping reagents, kits and methods of use thereof		
JOURNAL	Patent: WO 0129262-A 2153 26-APR-2001;		
FEATURES	Orchid Biosciences, Inc (US)		
source	Location/Qualifiers		
	1. .24		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		

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REFERENCE
AUTHORS      Hilberg,P., Brandtetter,I., Bette,P., Kleemann,R. and van Meel,J.
TITLE        Pharmacological composition for the treatment of disorders of
              non-human mammals
JOURNAL       Patent: WO 03030910-A 7 17-APR-2003;
              Boehringer Ingelheim International GmbH (DE)
FEATURES     Location/Qualifiers
               ..24
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"
               /note="Primer"

Query Match          0.5%;   Score 17.6;   DB 1;   Length 24;
Best Local Similarity 83.3%;   Pred. NO. 5.4e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY .    1945 TACATGATCATCGGGAGTGTCTGG 1968
         |||

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Db 1 TACATGATCATGGTCAAGTGTGG 24

RESULT 239
AR028294/c
LOCUS AR028294 25 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5858662.
ACCESSION AR028294
VERSION AR028294.1 GI:5940267
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Keating,M.T. and Morris,C.A.
TITLE Diagnosis of Williams syndrome and Williams syndrome cognitive profile by analysis of the presence or absence of a LIM-kinase gene
JOURNAL Patent: US 5858662-A 4 12-JAN-1999;
FEATURES Location/Qualifiers
1..25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1744 CCGTGAAGTGGATGGCGCTGAG 1767
|||||
Db 24 CCAGTCAAGTGGATGGCTCCGGAG 1

RESULT 240
AR434781
LOCUS AR434781 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1204 from patent US 6656700.
ACCESSION AR434781
VERSION AR434781.1 GI:40197624
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1204 02-DEC-2003;
FEATURES Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGGCGTGTGTGT 2342
|||||
Db 1 GAGTGTGTGTGTGTGAGTGTGTAT 24

RESULT 241
AR434782
LOCUS AR434782 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1205 from patent US 6656700.
ACCESSION AR434782
VERSION AR434782.1 GI:40197625
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1208 02-DEC-2003;
FEATURES Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2322 TGTGTGTGTGTGTGTGTGTGTGTG 2345
|||||
Db 1 TGTGTGTGTGTGTGTGTGTGTATTT 24

RESULT 244
BD174952

JOURNAL Patent: US 6656700-A 1205 02-DEC-2003;
FEATURES Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGGCGTGTGTGT 2342
|||||
Db 1 GAGTGTGTGTGTGTGAGTGTGTAT 24

RESULT 242
AR434783
LOCUS AR434783 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1206 from patent US 6656700.
ACCESSION AR434783
VERSION AR434783.1 GI:40197626
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1206 02-DEC-2003;
FEATURES Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2321 GTGTGTGTGTGTGGCGTGTGTGT 2344
|||||
Db 2 GTGTGTGTGTGTGAGTGTGTATTT 25

RESULT 243
AR434785
LOCUS AR434785 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1208 from patent US 6656700.
ACCESSION AR434785
VERSION AR434785.1 GI:40197628
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1208 02-DEC-2003;
FEATURES Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2322 TGTGTGTGTGTGTGTGTGTGTGTG 2345
|||||
Db 1 TGTGTGTGTGTGTGTGTGTATTT 24

RESULT 244
BD174952

[illegible]

JOURNAL Patent: US 6656700-A 1205 02-DEC-2003;
FEATURES
source

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2319 GTGTGTTGTGGTGGCTGTGT 2342
| | | | | | | | | |
DB 1 GAGTGTTGTGTTGTGAGTGTAT 24
| | | | | | | | | |

RESULT 242
AR434783
LOCUS AR434783 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1206 from patent US 6656700.
ACCESSION AR434783
VERSION AR434783.1 GI:40197626
KEYWORDS
SOURCE Unknown.

REFERENCE
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1206 02-DEC-2003;
FEATURES Location/Qualifiers
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source /organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2321 GTGTGTTGTGGTGGCTGTGT 2344
| | | | | | | | | |
DB 2 GTGTGTTGTGTTGTGAGTGTATT 25
| | | | | | | | | |

RESULT 243
AR434785
LOCUS AR434785 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1208 from patent US 6656700.
ACCESSION AR434785
VERSION AR434785.1 GI:40197628
KEYWORDS
SOURCE Unknown.

REFERENCE
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1208 02-DEC-2003;
FEATURES Location/Qualifiers
1..25
source /organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2322 TGTGTGTGTGCGTGTGTGTG 2345
| | | | | | | | | |
DB 1 TGTGTGTTGTGAGTGTATT 24
| | | | | | | | | |

RESULT 244
BD174952

JOURNAL Patent: US 6656700-A 1205 02-DEC-2003;
FEATURES
source

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2319 GTGTGTTGTGGTGGCTGTGT 2342
| | | | | | | | | |
DB 1 GAGTGTTGTGTTGTGAGTGTAT 24
| | | | | | | | | |

RESULT 241
AR434782
LOCUS AR434782 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1205 from patent US 6656700.
ACCESSION AR434782
VERSION AR434782.1 GI:40197625
KEYWORDS
SOURCE Unknown.

REFERENCE
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E

LOCUS BD174952 19 bp DNA linear PAT 18-MAR-2003
DEFINITION Method for examining flat epithelial cell.
ACCESSION BD174952
KEYWORDS BD174952.1 GI:29120646
VERSION JP 2002272474-A/3.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Okamoto,T.
TITLE Method for examining flat epithelial cell
JOURNAL Patent: JP 2002272474-A 3 24-SEP-2002;
ZERIA PHARMACEUTICALS CO LTD
COMMENT OS Artificial Sequence
PN JP 2002272474-A/3
PD 24-SEP-2002
PF 22-MAR-2001 JP 2001083352
PI TETSUJI OKAMOTO
PC C12N15/09,A61K45/00,A61P35/00,C12Q1/68,C12Q1/68,G01N33/15, PC
G01N33/50,
CC G01N33/50,G01N33/50,G01N33/574,C12N15/00
CC FGPR3 mutagenic oligonucleotide
FH Key Location/Qualifiers
FT source 1..19
FEATURES
source Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1855 CCGTACCCCGGATCCCTG 1873
Db 1 CCGTACCCCGGATCCCTG 19
RESULT 245
I31530/c
LOCUS I31530 19 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 442 from patent US 5582979.
ACCESSION I31530
VERSION I31530.1 GI:1822321
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 442 10-DEC-1996;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGTGCGT 2336
Db 19 TGTGTGTGTGTGTGTGTGT 1
RESULT 246
AX040467/c
LOCUS AX040467 19 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 7 from Patent WO0063365.

ACCESSION AX040467
VERSION AX040467.1 GI:11230259
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Belotserkovskii,B., Reddy,G. and Zarling,D.
TITLE Locked nucleic acid hybrids and methods of use
JOURNAL Patent: WO 0063365-A 7 26-OCT-2000;
Pangene Corporation (US)
FEATURES
source Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Z-DNA"
Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGCGT 2336
Db 19 TGTGTGTGTGTGTGTGTGT 1
RESULT 247
AX040468
LOCUS AX040468 19 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 8 from Patent WO0063365.
ACCESSION AX040468
VERSION AX040468.1 GI:11230260
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Belotserkovskii,B., Reddy,G. and Zarling,D.
TITLE Locked nucleic acid hybrids and methods of use
JOURNAL Patent: WO 0063365-A 8 26-OCT-2000;
Pangene Corporation (US)
FEATURES
source Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Z-DNA"
Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGCGT 2336
Db 1 TGTGTGTGTGTGTGTGTGT 19
RESULT 248
AX132174
LOCUS AX132174 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3392 from Patent WO0130362.
ACCESSION AX132174
VERSION AX132174.1 GI:14138479
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases

JOURNAL Patent: WO 0130362-A 3392 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin B1 ribozyme binding site"

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2550 TCGGCTCTGCTTTCAC 2568
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DB 1 TCGGCTCTACCTTTCAC 19

RESULT 249
AR129716 AR129716 20 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 120 from patent US 6187545.
ACCESSION AR129716
VERSION AR129716.1 GI:14117613
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay, R., Butler, M.M., Wyatt, J. and Cowsett, L.M.
TITLE Antisense modulation of pepck-cytosolic expression
JOURNAL Patent: US 6187545-A 120 13-FEB-2001;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2325 GTGTGTGTGCTGTGTG 2343
|||||
DB 1 GTGTGTGTGCTGTGTG 19

RESULT 250
I33568 I33568 20 bp DNA linear PAT 06-FEB-1997
LOCUS
DEFINITION Sequence 7 from patent US 5593834.
ACCESSION I33568
VERSION I33568.1 GI:1824359
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lane, M.J., Benight, A.S. and Faldasz, B.D.
TITLE Method of preparing DNA sequences with known ligand binding characteristics
JOURNAL Patent: US 5593834-A 7 14-JAN-1997;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3463 TATATATCTATATATAT 3481
|||||
DB 2 TATATATAGCTATATATAT 20

RESULT 251
I33568/c I33568 20 bp DNA linear PAT 06-FEB-1997
LOCUS
DEFINITION Sequence 7 from patent US 5593834.
ACCESSION I33568
VERSION I33568.1 GI:1824359
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lane, M.J., Benight, A.S. and Faldasz, B.D.
TITLE Method of preparing DNA sequences with known ligand binding characteristics
JOURNAL Patent: US 5593834-A 7 14-JAN-1997;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3463 TATATATCTATATATAT 3481
|||||
DB 19 TATATATAGCTATATATAT 1

RESULT 252
AX462693 AX462693 20 bp DNA linear PAT 15-JUL-2002
LOCUS
DEFINITION Sequence 437 from Patent EP1217079.
ACCESSION AX462693
VERSION AX462693.1 GI:21885906
KEYWORDS Aegilops tauschii
SOURCE Aegilops tauschii
ORGANISM Aegilops tauschii
REFERENCE 1
AUTHORS Bernard, M., Sourdis, P. and Guyomarch, H.
TITLE Microsatellite markers from Triticum tauschii
JOURNAL Patent: EP 1217079-A 437 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES Location/Qualifiers
source
1. .20
/organism="Aegilops tauschii"
/mol_type="unassigned DNA"
/db_xref="taxon:37682"

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2330 TGTGCGTGTGTGTGTGT 2348
|||||
DB 1 TGTGCGTGTGTGTGTGT 19

RESULT 253
AR126570 AR126570 21 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 1 from patent US 6180349.
ACCESSION AR126570
VERSION AR126570.1 GI:14113163
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.


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REFERENCE 1 (bases 1 to 21)
AUTHORS  Ginzinger,D.G., Godfrey,T.E., Jensen,R.H. and Gray,J.W.
TITLE    Quantitative PCR method to enumerate DNA copy number
JOURNAL  Patent: US 6180349-A 1 30-JAN-2001;
FEATURES  Location/Qualifiers
source    1..21
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTCTGTGTGTGTGTGTGTG 2333
Db 2 GTGTGTGTGTGTGTGTGTG 20

RESULT 254
AR126571
LOCUS    AR126571
DEFINITION Sequence 2 from patent US 6180349.
ACCESSION AR126571
VERSION   AR126571.1 GI:14113164
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS  Ginzinger,D.G., Godfrey,T.E., Jensen,R.H. and Gray,J.W.
TITLE    Quantitative PCR method to enumerate DNA copy number
JOURNAL  Patent: US 6180349-A 2 30-JAN-2001;
FEATURES  Location/Qualifiers
source    1..21
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTCTGTGTGTGTGTGTGTG 2333
Db 2 GTGTGTGTGTGTGTGTGTG 20

RESULT 255
AX203572/c
LOCUS    AX203572
DEFINITION Sequence 202 from Patent WO0153520.
ACCESSION AX203572
VERSION   AX203572.1 GI:15392997
KEYWORDS  .
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS  Cullen,P. and Seedorf,U.
TITLE    Gene chip for neonate screening
JOURNAL  Patent: WO 0153520-A 202 26-JUL-2001;
          Cullen, Paul (DE) ; Seedorf, Udo (DE)
FEATURES  Location/Qualifiers
source    1..21
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3667 GCCATGGCTCAGGGTGGTC 3685
Db 2 GTGTGTGTGTGTGTGTGTG 20

RESULT 256
AX613777/c
LOCUS    AX613777
DEFINITION Sequence 4802 from Patent WO02072882.
ACCESSION AX613777
VERSION   AX613777.1 GI:28409206
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS  Cullen,P. and Seedorf,U.
TITLE    Coronary chip
JOURNAL  Patent: WO 02072882-A 4802 19-SEP-2002;
          OGHAM GmbH (DE)
FEATURES  Location/Qualifiers
source    1..21
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3667 GCCATGGCTCAGGGTGGTC 3685
Db 21 GCCATTGTCTCAGGGTGGTC 3

RESULT 257
AR264920
LOCUS    AR264920
DEFINITION Sequence 4 from patent US 6492121.
ACCESSION AR264920
VERSION   AR264920.1 GI:29693307
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS  Kurane,R., Kanagawa,T., Kanagata,Y., Kurata,S., Yamada,K.,
          Yokomaki,T., Koyama,O. and Furusho,K.
TITLE    Method for determining a concentration of target nucleic acid
          molecules, nucleic acid probes for the method, and method for
          analyzing data obtained by the method
          Patent: US 6492121-A 4 10-DEC-2002;
FEATURES  Location/Qualifiers
source    1..30
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTGCTTCTTCCTCTTTT 3285
Db 3 ATATATTTTTTTTGTGTTTTTTTTTTT 29

RESULT 258
AR264926
LOCUS    AR264926
DEFINITION Sequence 10 from patent US 6492121.
ACCESSION AR264926
VERSION   AR264926.1 GI:29693313
KEYWORDS  .

QY 3667 GCCATGGCTCAGGGTGGTC 3685
Db 21 GCCATTGTCTCAGGGTGGTC 3
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and method for analyzing data obtained by that method.
BD072871
VERSION BD072871.1 GI:22618474
KEYWORDS JP 2001286300-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
        and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 9 16-OCT-2001;
        JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
        NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
        AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
        PN JP 2001286300-A/9
        PD 16-OCT-2001
        PF 20-APR-2000 JP 2000120097
        PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
        KURATA,
        PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
        PC C12N15/00,C12M1/00,C12N15/09,G01N33/53,G01N33/542, PC
        G01N33/566,
        PC C12N15/00
        CC The base sequence was prepared synthetically on the aim of CC
        examining the
        CC decrease in fluorescence emission of a nucleic acid probe CC
        labeled with
        CC BODIBY FL/C6 upon the hybridization of the
        probe with a target
        CC nucleic
        CC acid.
        FH Key Location/Qualifiers
        FT source 1..30
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
FEATURES
        source
        1..30
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match 0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3285
Db | | | | | | | | | | | | | | | | | | | |
3 ATATATTTTTCCTTTTCTTTTCTTTTCTTTT 29

RESULT 264
BD107498
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION BD107498
ACCESSION BD107498
VERSION BD107498.1 GI:23202316
KEYWORDS JP 2002000275-A/7.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
        Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 7 08-JAN-2002;
        JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
        & TECHNOL
COMMENT OS Artificial Sequence
        PN JP 2002000275-A/7
        PD 08-JAN-2002
        PF 27-JUN-2000 JP 2000193133
        PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
        KURATA,
        PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
        PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base
        sequence was prepared synthetically on the aim of CC
        examining the
        CC decrease in fluorescence emission of a nucleic acid probe CC
        labeled with
        CC BODIBY FL/C6 upon the hybridization of the
        probe with a target
        CC nucleic
        CC acid.
        FH Key Location/Qualifiers
        FT source 1..30
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
FEATURES
        source
        1..30
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match 0.5%; Score 17.4; DB 1; Length 30;

OY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3285
Db | | | | | | | | | | | | | | | | | | | |
3 ATATATTTTTCCTTTTCTTTTCTTTTCTTTT 29

RESULT 263
BD107492
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION BD107492
ACCESSION BD107492
VERSION BD107492.1 GI:23202310
KEYWORDS JP 2002000275-A/1.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
        Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 1 08-JAN-2002;
        JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
        & TECHNOL
COMMENT OS Artificial Sequence
        PN JP 2002000275-A/1
        PD 08-JAN-2002
        PF 27-JUN-2000 JP 2000193133

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Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3285
DB 3 ATATATTTTCTTTTCTTTTCTTTT 29

RESULT 265
BD145024 30 bp DNA linear PAT 17-JAN-2003
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145024
VERSION BD145024.1 GI:27850782
KEYWORDS JP 2002119291-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
JOURNAL and method for analyzing data obtained by that method
PATENT: JP 2002119291-A 5 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/11
PD 23-APR-2002 JP 2001133529
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..30
/organism='Artificial Sequence'.

FEATURES
source
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3285
DB 3 ATATATTTTCTTTTCTTTTCTTTT 29

RESULT 267
BD166025 30 bp DNA linear PAT 17-JAN-2003
LOCUS Novel nucleic acid probes, method for determining concentrations of
DEFINITION nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166025
VERSION BD166025.1 GI:27871837
KEYWORDS JP 2002191372-A/5.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
TITLE Novel nucleic acid probes, method for determining concentrations of
JOURNAL nucleic acid by using the probes, and method for analyzing data
PATENT: JP 2002191372-A 5 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/5
PD 09-JUL-2002 JP 2001295145
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC

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C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
CC labeled with
CC BODIBY FL/C6 upon the hybridization of the
CC probe with a target
CC nucleic
CC acid.
CC FH key Location/Qualifiers
CC source 1..30
CC /organism='Artificial Sequence'.
CC /organism='unidentified'
CC /mol_type='genomic DNA'
CC /db_xref='taxon:32644'

FEATURES
source
    Location/Qualifiers
    1..30
    /organism='unidentified'
    /mol_type='genomic DNA'
    /db_xref='taxon:32644'

Query Match
Best Local Similarity 0.5%; Score 17.4; DB 1; Length 30;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTCCTTTT 3285
Db 3 ATATATTTTATTTGCTTTCCTTTT 29

RESULT 268
BD166030 30 bp DNA linear PAT 17-JAN-2003
LOCUS Novel nucleic acid probes, method for determining concentrations of
DEFINITION nucleic acid by using the probes, and method for analyzing data
ACCESSION BD166030
VERSION JP 2002191372-A/10.
KEYWORDS unidentified
SOURCE unclassified.
ORGANISM 1 (bases 1 to 30)
REFERENCE Kurane,K., Kanagawa,T., Kanagata,Y., Torimura,M., Kurata,S.,
AUTHORS Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
JOURNAL Patent: JP 2002191372-A 10 09-JUL-2002;
NATIONAL INSTITUTE FOR ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
COMMENT OS Artificial Sequence
PN JP 2002191372-A/10
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,VOICHI KAMAGATA,MASAKI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
CC labeled with
CC BODIBY FL/C6 upon the hybridization of the
CC probe with a target
CC nucleic
CC acid.
CC FH key Location/Qualifiers
CC source 1..30
CC /organism='unidentified'
CC /mol_type='genomic DNA'

FEATURES
source
    Location/Qualifiers
    1..30
    /organism='unidentified'
    /mol_type='genomic DNA'

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/db_xref='taxon:32644'

Query Match
Best Local Similarity 0.5%; Score 17.4; DB 1; Length 30;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTCCTTTT 3285
Db 3 ATATATTTTATTTGCTTTCCTTTT 29

RESULT 269
AX248881/C 31 bp DNA linear PAT 28-SEP-2001
LOCUS AX248881
DEFINITION Sequence 960 from Patent WO0166800.
ACCESSION AX248881
VERSION AX248881.1 GI:15863504
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 960 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source
    Location/Qualifiers
    1..31
    /organism='Homo sapiens'
    /mol_type='unassigned DNA'
    /db_xref='taxon:9606'

Query Match
Best Local Similarity 0.5%; Score 17.4; DB 1; Length 31;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3414 AGGGGCGCGCCCTGTGTGCAG 3434
Db 21 AGGGGCGCGCCCTGTGTGCAG 1

RESULT 270
A38159 22 bp DNA linear PAT 05-MAR-1997
LOCUS A38159
DEFINITION Sequence 3 from Patent WO9408008.
ACCESSION A38159
VERSION A38159.1 GI:2294765
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hawkins,R.E., Russell,S.J., Stevenson,F.K. and Winter,G.P.
TITLE IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
JOURNAL Patent: WO 9408008-A 3 14-APR-1994;
MEDICAL RES COUNCIL (GB)
COMMENT Other publication CA 2145064 940414
Other publication AU 4832493 940426
Other publication JP 8501699T 960227.
FEATURES
source
    Location/Qualifiers
    1..22
    /organism='unidentified'
    /mol_type='unassigned DNA'
    /db_xref='taxon:32644'

Query Match
Best Local Similarity 0.5%; Score 17.2; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGGTGGAGGCTG 874
Db 1 GAGGTGACAGCTGGTGGAGTCTG 22

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JOURNAL Patent: WO 9201047-A 62 23-JAN-1992;
 FEATURES Location/Qualifiers
 1..23
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

Query Match 0.5%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 5.8e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGGTGGAGGCTG 874
 |||||
 DB 1 GAGGTGCAGCTGGTGGAGTCTG 22
 |||||

RESULT 274
 A33834
 LOCUS 23 bp DNA linear PAT 02-SEP-2002
 DEFINITION Synthetic primer HuVh3aBACK.
 ACCESSION A33834
 VERSION A33834.1 GI:23956831
 SOURCE
 ORGANISM
 synthetic construct
 synthetic construct
 artificial sequences.
 1 (bases 1 to 23)
 JESPERSEN, S.A., Winter, G.P., Baier, M. and Hoogenboom, H.R.J.
 Production of chimeric antibodies - a combinatorial approach
 Patent: WO 9306213-A 32 01-APR-1993;
 CAMBRIDGE ANTIBODY TECH (GB); MEDICAL RES COUNCIL (GB)

FEATURES
 source
 1..23
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

Query Match 0.5%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 5.8e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGGTGGAGGCTG 874
 |||||
 DB 1 GAGGTGCAGCTGGTGGAGTCTG 22
 |||||

RESULT 275
 AR077343
 LOCUS 23 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 58 from patent US 5962255.
 ACCESSION AR077343
 VERSION AR077343.1 GI:10004089
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 1 (bases 1 to 23)
 Griffiths, A. David., Williams, S. Cameron., Waterhouse, P. Michael.,
 Nissim, A., Winter, G. Paul., Johnson, K. Stuart. and
 Smith, A. John. Hammond.
 Methods for producing recombinant vectors
 Patent: US 5962255-A 58 05-OCT-1999;
 Location/Qualifiers
 1..23
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.5%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 5.8e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGGTGGAGGCTG 874
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Db      1 GAGGTGCAGCTGCTGGAGTCTG 22
        23 bp DNA linear PAT 16-MAY-2001
RESULT 276
AR117963
LOCUS      AR117963
DEFINITION Sequence 12 from patent US 6140471.
ACCESSION AR117963
VERSION    AR117963.1 GI:14098869
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 23)
AUTHORS    Johnson,K.Stuart., Winter,G.Paul., Griffiths,A.David.,
           Smith,A.John.Hammond, and Waterhouse,P.Michael.
TITLE      Methods for producing members of specific binding pairs
JOURNAL    Patent: US 6140471-A 12 31-OCT-2000;
FEATURES   Location/Qualifiers
           1..23
           /organism="unknown"
           /mol_type="unassigned DNA"
Query Match      0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      853 GAGGAGGAGCTGCTGGAGGCTG 874
        23 bp DNA linear PAT 05-MAY-2004
        ||||| ||||| ||||| ||||| |||||
Db      1 GAGGTGCAGCTGCTGGAGTCTG 22

RESULT 278
CQ802102
LOCUS      CQ802102
DEFINITION Sequence 87 from Patent WO2004007717.
ACCESSION  CQ802102
VERSION     CQ802102.1 GI:47058632
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Unger,C.M., Beste,G., Jensen,K.H., Zehetmeier,C., Knaauer,R.,
           Quelbenzu,B.L., Torella,C. and Ilag,L.L.
TITLE      Proteomic screen to identify disease-related biological
           molecules and inhibitors thereof
JOURNAL    Patent: WO 2004007717-A 87 22-JAN-2004;
           Xerion Pharmaceuticals AG (DE)
FEATURES   Location/Qualifiers
           1..23
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="Description of Artificial Sequence: primer"
Query Match      0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      853 GAGGAGGAGCTGCTGGAGGCTG 874
        23 bp DNA linear PAT 02-AUG-2004
        ||||| ||||| ||||| ||||| |||||
Db      1 GAGGTGCAGCTGCTGGAGTCTG 22

RESULT 279
CQ846562
LOCUS      CQ846562
DEFINITION Sequence 83 from Patent EP1433846.
ACCESSION  CQ846562
VERSION     CQ846562.1 GI:50895792
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    McCafferty,J., Pope,A.R., Johnson,K.S., Hoogenboom,H.R.,
           Griffiths,A.D., Jackson,R.H., Holliger,K.P., Marks,J.D.,
           Clackson,T.P., Chiswell,D.J., Winter,G.P. and Bonnett,T.P.
TITLE      Phagemid-based method of producing filamentous bacteriophage
           particles displaying antibody molecules and the corresponding
           bacteriophage particles
JOURNAL    Patent: EP 1433846-A 83 30-JUN-2004;
           Cambridge Antibody Technology LTD (GB); Medical Research Council
           (GB)
FEATURES   Location/Qualifiers
           1..23
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="PCR Primer"
Query Match      0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      853 GAGGAGGAGCTGCTGGAGGCTG 874
        23 bp DNA linear PAT 17-JUL-2003
        ||||| ||||| ||||| ||||| |||||
Db      1 GAGGTGCAGCTGCTGGAGTCTG 22

METHODS for diagnosis and treatment of hemophilia A patients with
an inhibitor.
BD231857
LOCUS      BD231857
DEFINITION Methods for diagnosis and treatment of hemophilia A patients with
           an inhibitor.
ACCESSION  BD231857
VERSION     BD231857.1 GI:33041627
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 23)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Voorberg,J.J., Brink,E.N.V.D. and Turenhout,E.A.M.
           Methods for diagnosis and treatment of hemophilia A patients with
           an inhibitor
JOURNAL    Patent: JP 2002514422-A 5 21-MAY-2002;
           STICHTING SANQUIN BLOEDVOORZIENING
COMMENT    OS Homo sapiens (human)
           PN JP 2002514422-A/5
           PD 21-MAY-2002 JP 2000548471
           PF 07-MAY-1999 JP 2000548471
           PR 08-MAY-1998 EP 98201543.0
           PI JOHANNES JACOBUS VOORBERG, EDWARD NORBERT VAN DEN BRINK, PI
           ELLEN ANNE MARIA TURENHOUT
           PC C12N15/09,A61K38/36,A61K39/395,A61K39/395,A61P7/04,A61P43/00,
           PC C07K16/36
           CC C07K16/42,C12Q1/68,C12N15/00,A61K37/46
           Note = 'primer huV3aback'
           Key Location/Qualifiers
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Query Match      0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 280
E09110 LOCUS linear PAT 29-SEP-1997
DEFINITION 23 bp DNA
ACCESSION Synthetic oligonucleotides for primer.
VERSION E09110.1 GI:22025736
KEYWORDS JP 1995115978-A/5.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Katou,T., Yamamoto,K., Nishioka,K. and Mizushima,Y.
TITLE METHOD FOR DETECTING AND CLONING ANTIBODY GENE
JOURNAL Patent: JP 1995115978-A 5 09-MAY-1995;
L T T KENKYUSHO:KK
COMMENT OS None
OC Artificial sequences.
PN JP 1995115978-A/5
PD 09-MAY-1995
PF 22-OCT-1993 JP 1993287628
PI KATOU TOMOHIRO, YAMAMOTO KAZUHIKO, NISHIOKA KUZUKI, PI
PC C12N15/09.C12Q1/68.G01N33/53;
CC strandedness: Single;
CC topology: Linear; Location/Qualifiers
FH Key 1..23
FT source
FT misc_feature 1..23 /organism='Artificial sequences' FT
FT /note='Synthetic oligonucleotide for primer of
5'-side'.
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 853 GAGGAGGAGCTGGTGGAGCTG 874
Db 1 GAGGTGCAGCTGGTGGAGCTG 22
RESULT 281
127518 LOCUS linear PAT 06-FEB-1997
DEFINITION 23 bp DNA
ACCESSION Sequence 32 from patent US 5565332.
VERSION 127518.1 GI:1818294
KEYWORDS JP 1995115978-A/5.
SOURCE Unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hoogenboom,H.R.J.M., Baier,M., Jespers,L.S.A.T. and Winter,G.P.
TITLE Production of chimeric antibodies - a combinatorial approach
JOURNAL Patent: US 5565332-A 32 15-OCT-1996;
L T T KENKYUSHO:KK
COMMENT OS None
OC Artificial sequences.
PN JP 1995115978-A/5
PD 09-MAY-1995
PF 22-OCT-1993 JP 1993287628
PI KATOU TOMOHIRO, YAMAMOTO KAZUHIKO, NISHIOKA KUZUKI, PI
PC C12N15/09.C12Q1/68.G01N33/53;
CC strandedness: Single;
CC topology: Linear; Location/Qualifiers
FH Key 1..23
FT source
FT misc_feature 1..23 /organism='Artificial sequences' FT
FT /note='Synthetic oligonucleotide for primer of
5'-side'.
FEATURES
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Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 853 GAGGAGGAGCTGGTGGAGCTG 874
Db 1 GAGGTGCAGCTGGTGGAGCTG 22
RESULT 282
144506 LOCUS linear PAT 07-OCT-1997
DEFINITION 23 bp DNA
ACCESSION Sequence 2 from patent US 5635177.
VERSION 144506.1 GI:2469219
KEYWORDS JP 1995115978-A/5.
SOURCE Unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 2 03-JUN-1997;
L T T KENKYUSHO:KK
COMMENT OS None
OC Artificial sequences.
PN JP 1995115978-A/5
PD 09-MAY-1995
PF 22-OCT-1993 JP 1993287628
PI KATOU TOMOHIRO, YAMAMOTO KAZUHIKO, NISHIOKA KUZUKI, PI
PC C12N15/09.C12Q1/68.G01N33/53;
CC strandedness: Single;
CC topology: Linear; Location/Qualifiers
FH Key 1..23
FT source
FT misc_feature 1..23 /organism='Artificial sequences' FT
FT /note='Synthetic oligonucleotide for primer of
5'-side'.
FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 853 GAGGAGGAGCTGGTGGAGCTG 874
Db 1 GAGGTGCAGCTGGTGGAGCTG 22
RESULT 283
195684 LOCUS linear PAT 01-DEC-1998
DEFINITION 23 bp DNA
ACCESSION Sequence 12 from patent US 5733743.
VERSION 195684.1 GI:3940154
KEYWORDS JP 1995115978-A/5.
SOURCE Unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Johnson,K.Stuart., Winter,G.Paul., Griffiths,A.David.,
Smith,A.John.Hammond. and Waterhouse,P.Michael.
TITLE Methods for producing members of specific binding pairs
JOURNAL Patent: US 5733743-A 12 31-MAR-1998;
L T T KENKYUSHO:KK
COMMENT OS None
OC Artificial sequences.
PN JP 1995115978-A/5
PD 09-MAY-1995
PF 22-OCT-1993 JP 1993287628
PI KATOU TOMOHIRO, YAMAMOTO KAZUHIKO, NISHIOKA KUZUKI, PI
PC C12N15/09.C12Q1/68.G01N33/53;
CC strandedness: Single;
CC topology: Linear; Location/Qualifiers
FH Key 1..23
FT source
FT misc_feature 1..23 /organism='Artificial sequences' FT
FT /note='Synthetic oligonucleotide for primer of
5'-side'.
FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
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Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 853 GAGGAGGAGCTGGTGGAGCTG 874
Db 1 GAGGTGCAGCTGGTGGAGCTG 22
RESULT 284
AR262782 LOCUS linear PAT 29-JAN-2003
DEFINITION 23 bp DNA
ACCESSION Sequence 2 from patent US 6331302.
VERSION AR262782.1 GI:28074466
KEYWORDS JP 1995115978-A/5.
SOURCE Unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett,B.D., Goeddel,D., Lee,J.M., Matthews,W., Tsai,S.P. and
Wood,W.I.
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<p>TITLE Protein tyrosine kinase agonist antibodies</p> <p>JOURNAL Patent: US 6331302-A 2 18-DEC-2001;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1. .23</p> <p>/organism="unknown"</p> <p>/mol_type="genomic DNA"</p> <p>Query Match 0.5%; Score 17.2; DB 1; Length 23;</p> <p>Best Local Similarity 86.4%; Pred. No. 5.8e+02;</p> <p>Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p> <p>QY 1801 GACGCTGTCCTTGGGCTCC 1822</p> <p>DB 23 GACGCTGTCCTTGGGAATTC 2</p> <p>RESULT 285</p> <p>AR265406 AR265406 23 bp DNA linear PAT 10-APR-2003</p> <p>LOCUS</p> <p>DEFINITION Sequence 58 from patent US 6492160.</p> <p>ACCESSION AR265406</p> <p>VERSION AR265406.1 GI:29693938</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 23)</p> <p>AUTHORS Griffiths,A.D., Williams,S.C., Waterhouse,P.M., Nissim,A., Winter,G.P., Johnson,K.S. and Smith,A.J.H.</p> <p>TITLE Methods for producing members of specific binding pairs</p> <p>JOURNAL Patent: US 6492160-A 58 10-DEC-2002;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1. .23</p> <p>/organism="unknown"</p> <p>/mol_type="genomic DNA"</p> <p>Query Match 0.5%; Score 17.2; DB 1; Length 23;</p> <p>Best Local Similarity 86.4%; Pred. No. 5.8e+02;</p> <p>Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p> <p>QY 853 GAGGAGGAGCTGGTGAGGCTG 874</p> <p>DB 1 GAGGTGCAGCTGGTGAGGCTG 22</p>	<p>RESULT 287</p> <p>AR428817 AR428817 23 bp DNA linear PAT 18-DEC-2003</p> <p>LOCUS</p> <p>DEFINITION Sequence 35 from patent US 6642041.</p> <p>ACCESSION AR428817</p> <p>VERSION AR428817.1 GI:40188603</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 23)</p> <p>AUTHORS Chen,J., Feder,J.N., Nelson,T.C., Krystek,S.R. and Duclos,F.</p> <p>TITLE Polynucleotides encoding a novel metalloprotease, MP-1</p> <p>JOURNAL Patent: US 6642041-A 35 04-NOV-2003;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1. .23</p> <p>/organism="unknown"</p> <p>/mol_type="genomic DNA"</p> <p>Query Match 0.5%; Score 17.2; DB 1; Length 23;</p> <p>Best Local Similarity 86.4%; Pred. No. 5.8e+02;</p> <p>Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p> <p>QY 853 GAGGAGGAGCTGGTGAGGCTG 874</p> <p>DB 1 GAGGTGCAGCTGGTGAGGCTG 22</p> <p>RESULT 288</p> <p>AR438219 AR438219 23 bp DNA linear PAT 20-FEB-2004</p> <p>LOCUS</p> <p>DEFINITION Sequence 35 from patent US 6663485.</p> <p>ACCESSION AR438219</p> <p>VERSION AR438219.1 GI:42662835</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 23)</p> <p>AUTHORS Niermann,M.</p> <p>TITLE Combine having a feeding device for transferring and an outlet zone for discharging materials</p> <p>JOURNAL Patent: US 6663485-A 35 16-DEC-2003;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1. .23</p> <p>/organism="unknown"</p> <p>/mol_type="genomic DNA"</p> <p>Query Match 0.5%; Score 17.2; DB 1; Length 23;</p> <p>Best Local Similarity 86.4%; Pred. No. 5.8e+02;</p> <p>Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p> <p>QY 853 GAGGAGGAGCTGGTGAGGCTG 874</p> <p>DB 1 GAGGTGCAGCTGGTGAGGCTG 22</p> <p>RESULT 289</p> <p>AR447097 AR447097 23 bp DNA linear PAT 20-FEB-2004</p> <p>LOCUS</p> <p>DEFINITION Sequence 2 from patent US 6673343.</p> <p>ACCESSION AR447097</p> <p>VERSION AR447097.1 GI:42674995</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 23)</p> <p>AUTHORS Bennett,B.D., Goeddel,D.V., Lee,J.M., Matthews,W., Tsai,S.P. and Wood,W.I.</p> <p>TITLE SAL-S1 receptor protein tyrosine kinase agonist antibodies</p> <p>JOURNAL Patent: US 6673343-A 2 06-JAN-2004;</p>
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Query Match
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QY 1801 GAGCTGTGTCCTTTGGGTCC 1822
Db 23 GAGTCTGTGTCCTTTGGAATTC 2

RESULT 290
AX010545
LOCUS AX010545 23 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 5 from Patent WO958680.
ACCESSION AX010545
VERSION AX010545.1 GI:9997375
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1
  AUTHORS Voorberg,J.J., Turenhout,E.A. and Van Den Brink,E.N.
  TITLE Method for diagnosis and treatment of haemophilia a patients with
    an inhibitor
  JOURNAL Patent: WO 958680-A 5 18-NOV-1999;
    VOORBERG JOHANNES JACOBUS (NL); DEN BRINK EDWARD NORBERT VAN (NL);
    STICHTING SANQUIN BLOEDVOORZIE (NL); TURENHOUT ELLEN ANNE MARIA
    (NL)

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        /db_xref="taxon:9606"
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        /note="primer huVH3aback"

Query Match
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  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGTGGAGTCTG 22

RESULT 291
AX203707
LOCUS AX203707 23 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 42 from Patent WO0152904.
ACCESSION AX203707
VERSION AX203707.1 GI:15393156
KEYWORDS synthetic construct
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
  REFERENCE 1
  AUTHORS Gill,P.S. and Masood,R.
  TITLE Methods and compositions for antisense vegf oligonucleotides
  JOURNAL Patent: WO 0152904-A 42 26-JUL-2001;
    Gill, Parkash, S. (US)

FEATURES
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    Location/Qualifiers
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        /organism="synthetic construct"
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        /db_xref="taxon:32630"
        /note="VEGFR-1 gene specific primers for RT-PCR"

Query Match
  Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1573 CAGGTGGCCCGGGCATGGAGT 1594
Db 1 CAAGTGGCCAGAGGCATGGAGT 22

RESULT 293
AX357138
LOCUS AX357138 23 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 14 from Patent WO020834.
ACCESSION AX357138
VERSION AX357138.1 GI:18674311
KEYWORDS synthetic construct
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
  REFERENCE 1
  AUTHORS Ault-Riche,D. and Kassner,P.D.
  TITLE Collections of binding proteins and tags and uses thereof for
    nested sorting and high throughput screening
  JOURNAL Patent: WO 0206834-A 14 24-JAN-2002;
    Pointilliste, Inc. (US)

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    Location/Qualifiers
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  Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGTGGAGTCTG 22

RESULT 294
AR058875
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Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1573 CAGGTGGCCCGGGCATGGAGT 1594
Db 1 CAAGTGGCCAGAGGCATGGAGT 22

RESULT 292
AX203708
LOCUS AX203708 23 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 43 from Patent WO0152904.
ACCESSION AX203708
VERSION AX203708.1 GI:15393157
KEYWORDS synthetic construct
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
  REFERENCE 1
  AUTHORS Gill,P.S. and Masood,R.
  TITLE Methods and compositions for antisense vegf oligonucleotides
  JOURNAL Patent: WO 0152904-A 43 26-JUL-2001;
    Gill, Parkash, S. (US)

FEATURES
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    Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="VEGFR-1 gene specific primers for RT-PCR"

Query Match
  Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1573 CAGGTGGCCCGGGCATGGAGT 1594
Db 1 CAAGTGGCCAGAGGCATGGAGT 22

RESULT 293
AX357138
LOCUS AX357138 23 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 14 from Patent WO020834.
ACCESSION AX357138
VERSION AX357138.1 GI:18674311
KEYWORDS synthetic construct
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
  REFERENCE 1
  AUTHORS Ault-Riche,D. and Kassner,P.D.
  TITLE Collections of binding proteins and tags and uses thereof for
    nested sorting and high throughput screening
  JOURNAL Patent: WO 0206834-A 14 24-JAN-2002;
    Pointilliste, Inc. (US)

FEATURES
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        /note="Primer:HuVH3aBACK"

Query Match
  Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGTGGAGTCTG 22

RESULT 294
AR058875
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LOCUS AR058875 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5837835.
ACCESSION AR058875
VERSION AR058875.1 GI:5984452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 7 17-NOV-1998;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 295
LOCUS AR058877 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5837835.
ACCESSION AR058877
VERSION AR058877.1 GI:5984454
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 9 17-NOV-1998;
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source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 296
LOCUS AR079580 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 7 from patent US 5965720.
ACCESSION AR079580
VERSION AR079580.1 GI:10006324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates
JOURNAL Patent: US 5965720-A 7 12-OCT-1999;
FEATURES
source Location/Qualifiers
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/organism="unknown"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 297
LOCUS AR079582 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 9 from patent US 5965720.
ACCESSION AR079582
VERSION AR079582.1 GI:10006326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates
JOURNAL Patent: US 5965720-A 9 12-OCT-1999;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 298
LOCUS AR123289 24 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6169170.
ACCESSION AR123289
VERSION AR123289.1 GI:14108255
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 7 02-JAN-2001;
FEATURES
source Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 299
LOCUS AR123291 24 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6169170.
ACCESSION AR123291
VERSION AR123291.1 GI:14108257

LOCUS AR058875 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5837835.
ACCESSION AR058875
VERSION AR058875.1 GI:5984452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 7 17-NOV-1998;
FEATURES
source Location/Qualifiers
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Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 295
LOCUS AR058877 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5837835.
ACCESSION AR058877
VERSION AR058877.1 GI:5984454
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 9 17-NOV-1998;
FEATURES
source Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 296
LOCUS AR079580 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 7 from patent US 5965720.
ACCESSION AR079580
VERSION AR079580.1 GI:10006324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates
JOURNAL Patent: US 5965720-A 7 12-OCT-1999;
FEATURES
source Location/Qualifiers
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/organism="unknown"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 297
LOCUS AR079582 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 9 from patent US 5965720.
ACCESSION AR079582
VERSION AR079582.1 GI:10006326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates
JOURNAL Patent: US 5965720-A 9 12-OCT-1999;
FEATURES
source Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 298
LOCUS AR123289 24 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6169170.
ACCESSION AR123289
VERSION AR123289.1 GI:14108255
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 7 02-JAN-2001;
FEATURES
source Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db TATATATATTTTATATATATA 24

RESULT 299
LOCUS AR123291 24 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6169170.
ACCESSION AR123291
VERSION AR123291.1 GI:14108257

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3' to P5' phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 9 02-JAN-2001;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2844
|||||
Db 3 TATATATATTTTATATATATA 24

RESULT 300
BD188891
LOCUS 24 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound;
hybridization and nuclease tolerant characteristics.

ACCESSION BD188891
VERSION BD188891.1 GI:32998630
KEYWORDS JP 2003012688-A/7.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
JOURNAL Patent: JP 2003012688-A 7 15-JAN-2003;
COMMENT LYNX THERAPEUTICS INC

PN JP 2003012688-A/7
PD 15-JAN-2003
PF 12-JUN-2002 JP 2002171743
PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI
SERGEI M GRVYZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02,C12Q1/68
CC Strandedness: Both;
CC Topology: Linear;
CC hybridization and nuclease tolerant characteristics FH Key
CC Oligonucleotide N3' to P5' phosphoramidate: synthesis and CC
compound;
CC Location/Qualifiers
FT source 1..24
FT /organism="Unidentified".
FEATURES Location/Qualifiers
source 1..24
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2844
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Db 3 TATATATATTTTATATATATA 24

RESULT 301
BD188893
LOCUS 24 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound;

hybridization and nuclease tolerant characteristics.
BD188893
VERSION BD188893.1 GI:32998632
KEYWORDS JP 2003012688-A/9.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
JOURNAL Patent: JP 2003012688-A 9 15-JAN-2003;
COMMENT LYNX THERAPEUTICS INC

PN JP 2003012688-A/9
PD 15-JAN-2003
PF 12-JUN-2002 JP 2002171743
PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI
SERGEI M GRVYZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02,C12Q1/68
CC Strandedness: Both;
CC Topology: Linear;
CC hybridization and nuclease tolerant characteristics FH Key
CC Oligonucleotide N3' to P5' phosphoramidate: synthesis and CC
compound;
CC Location/Qualifiers
FT source 1..24
FT /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2844
|||||
Db 3 TATATATATTTTATATATATA 24

RESULT 302
BD188893
LOCUS 24 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 7 from patent US 5591607.
ACCESSION I33252
VERSION I33252.1 GI:1824043
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3.fwdarw.p5' phosphoramidates: triplex DNA
JOURNAL Patent: US 5591607-A 7 07-JAN-1997;

RESULT 305

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source
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.5%; Score 17.2; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 308
LOCUS 192005 24 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 7 from patent US 5726297.
ACCESSION 192005
VERSION 192005.1 GI:3936475
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligodeoxyribonucleotide N3, P5' phosphoramidates
JOURNAL Patent: US 5726297-A 7 10-MAR-1998;
FEATURES
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.5%; Score 17.2; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 309
LOCUS 192007 24 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 9 from patent US 5726297.
ACCESSION 192007
VERSION 192007.1 GI:3936477
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligodeoxyribonucleotide N3, P5' phosphoramidates
JOURNAL Patent: US 5726297-A 9 10-MAR-1998;
FEATURES
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.5%; Score 17.2; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 310
LOCUS 192007 17 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for gaining probe which is for screening human Tie gene.

ACCESSION E11484
VERSION 1
KEYWORDS JP 1996143598-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Yasunaga,K., Suda,T., Iwama,A., Kurozumi,K., Shimizu,Y., Nakada,S.
TITLE ANTI-TIE MONOCLONAL ANTIBODY AND HYBRIDOMA
JOURNAL Patent: JP 1996143598-A 2 04-JUN-1996;
FEATURES
COMMENT OS None
OC Artificial sequences.
PN JP 1996143598-A/2
PD 04-JUN-1996
PF 17-NOV-1994 JP 1994308249
PI YASUNAGA KUNIO, SUDA TOSHIO, IWAMA ATSUSHI, KUROZUMI KOICHI,
PT SHIMIZU YASUAKI, NAKADA SUSUMU, MASUYASU YASUHIKO PC
C07K16/28, C12N5/10, C12P21/08, G01N33/53, G01N33/53, PC
G01N33/577//C12N15/02,
PC (C12P21/08.C12R1:91);
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH Key
FH Location/Qualifiers
FT source 1..17
FT /organism='Artificial sequences'.
FEATURES
source 1..17
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1765 GAGGCGTTGTTTGACCG 1781
Db 17 GAGGCGTTGTTTGACCG 1

RESULT 311
LOCUS AR455908 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 18 from patent US 6686160.
ACCESSION AR455908
VERSION AR455908.1 GI:42690802
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 18 03-FEB-2004;
FEATURES
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTG 2333
Db 1 CTGTGTGTGTGTGTGTG 17
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RESULT 312
AR455910/c
LOCUS          AR455910          17 bp      DNA          linear          PAT 20-FEB-2004
DEFINITION     Sequence 20 from patent US 686160.
ACCESSION      AR455910
VERSION        AR455910.1  GI:42690804
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       van Haeringen,W.A. and van Haeringen,H.
TITLE         Universal variable fragments
JOURNAL       Patent: US 686160-A 20 03-FEB-2004;
FEATURES      Location/Qualifiers
                source
                1..17
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTC 2334
Db 17 TGTGTGTGTGTGTGTC 1

RESULT 313
AX239678
LOCUS          AX239678          17 bp      DNA          linear          PAT 26-SEP-2001
DEFINITION     Sequence 18 from Patent WO0164948.
ACCESSION      AX239678
VERSION        AX239678.1  GI:15797343
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      1
AUTHORS       van Haeringen,W.A. and van Haeringen,H.
TITLE         Universal variable fragments
JOURNAL       Patent: WO 0164948-A 18 07-SEP-2001;
FEATURES      Dr. van Haeringen Laboratorium B.V. (NL)
                Location/Qualifiers
                source
                1..17
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="primer"

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTG 2333
Db 1 CTGTGTGTGTGTGTG 17

RESULT 314
AX239680/c
LOCUS          AX239680          17 bp      DNA          linear          PAT 26-SEP-2001
DEFINITION     Sequence 20 from Patent WO0164948.
ACCESSION      AX239680
VERSION        AX239680.1  GI:15797345
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      1
AUTHORS       van Haeringen,W.A. and van Haeringen,H.
TITLE         Universal variable fragments
JOURNAL       Patent: WO 0164948-A 20 07-SEP-2001;
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FEATURES      Dr. van Haeringen Laboratorium B.V. (NL)
                Location/Qualifiers
                1..17
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="primer"

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTC 2334
Db 17 TGTGTGTGTGTGTGTC 1

RESULT 315
AR071773/c
LOCUS          AR071773          18 bp      DNA          linear          PAT 18-FEB-2000
DEFINITION     Sequence 2 from patent US 5912147.
ACCESSION      AR071773
VERSION        AR071773.1  GI:7222661
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS       Stoler,D., Basik,M. and Anderson,G.
TITLE         Rapid means of quantitating genomic instability
JOURNAL       Patent: US 5912147-A 2 15-JUN-1999;
FEATURES      Location/Qualifiers
                source
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                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 316
AR071777/c
LOCUS          AR071777          18 bp      DNA          linear          PAT 18-FEB-2000
DEFINITION     Sequence 6 from patent US 5912147.
ACCESSION      AR071777
VERSION        AR071777.1  GI:7222665
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS       Stoler,D., Basik,M. and Anderson,G.
TITLE         Rapid means of quantitating genomic instability
JOURNAL       Patent: US 5912147-A 6 15-JUN-1999;
FEATURES      Location/Qualifiers
                source
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                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 317
AR071777/c
LOCUS          AR071777          18 bp      DNA          linear          PAT 18-FEB-2000
DEFINITION     Sequence 6 from patent US 5912147.
ACCESSION      AR071777
VERSION        AR071777.1  GI:7222665
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS       Stoler,D., Basik,M. and Anderson,G.
TITLE         Rapid means of quantitating genomic instability
JOURNAL       Patent: US 5912147-A 6 15-JUN-1999;
FEATURES      Location/Qualifiers
                source
                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1
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RESULT 317
AR071778/c
LOCUS       AR071778                18 bp      DNA             linear      PAT 18-FEB-2000
DEFINITION   Sequence 7 from patent US 5912147.
ACCESSION   AR071778
VERSION     AR071778.1  GI:72226666
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclonated.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 7 15-JUN-1999;
FEATURES    Location/Qualifiers
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 318
AR071779/c
LOCUS       AR071779                18 bp      DNA             linear      PAT 18-FEB-2000
DEFINITION   Sequence 8 from patent US 5912147.
ACCESSION   AR071779
VERSION     AR071779.1  GI:7222667
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclonated.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 8 15-JUN-1999;
FEATURES    Location/Qualifiers
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 319
AR071801/c
LOCUS       AR071801                18 bp      DNA             linear      PAT 18-FEB-2000
DEFINITION   Sequence 30 from patent US 5912147.
ACCESSION   AR071801
VERSION     AR071801.1  GI:7222689
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclonated.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 30 15-JUN-1999;
FEATURES    Location/Qualifiers
             1..18
             /organism="unknown"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 320
AR071802/c
LOCUS       AR071802                18 bp      DNA             linear      PAT 18-FEB-2000
DEFINITION   Sequence 31 from patent US 5912147.
ACCESSION   AR071802
VERSION     AR071802.1  GI:7222690
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclonated.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 31 15-JUN-1999;
FEATURES    Location/Qualifiers
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTG 1

RESULT 321
AR071803/c
LOCUS       AR071803                18 bp      DNA             linear      PAT 18-FEB-2000
DEFINITION   Sequence 32 from patent US 5912147.
ACCESSION   AR071803
VERSION     AR071803.1  GI:7222691
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclonated.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 32 15-JUN-1999;
FEATURES    Location/Qualifiers
             1..18
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTG 1

RESULT 322
AR178165/c
LOCUS       AR178165                18 bp      DNA             linear      PAT 18-DEC-2001
DEFINITION   Sequence 1 from patent US 6316186.
ACCESSION   AR178165
VERSION     AR178165.1  GI:17921058
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclonated.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 6316186
FEATURES    Location/Qualifiers
             1..18
             /organism="unknown"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTG 1
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KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 18)
AUTHORS       Ekins,R.Philip.
TITLE        Binding assay using binding agents with tail groups
JOURNAL      Patent: US 6316186-A 1 13-NOV-2001;
FEATURES     Location/Qualifiers
              1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTGTG 1

RESULT 323
AR178166
LOCUS      AR178166      18 bp      DNA      linear      PAT 18-DEC-2001
DEFINITION Sequence 2 from patent US 6316186.
ACCESSION  AR178166
VERSION     AR178166.1 GI:17921059
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Ekins,R.Philip.
TITLE       Binding assay using binding agents with tail groups
JOURNAL     Patent: US 6316186-A 2 13-NOV-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTGTG 1

RESULT 324
AR182079
LOCUS      AR182079      18 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 28 from patent US 6337188.
ACCESSION  AR182079
VERSION     AR182079.1 GI:20224995
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Head,S.R., Golet,P., Karn,J. and Boyce-Jacino,M.
TITLE       De novo or 'universal' sequencing array
JOURNAL     Patent: US 6337188-A 28 08-JAN-2002;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 1 GTGTGTGTGTGTGTGTG 17

RESULT 325
AR175253
LOCUS      AR175253      18 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION Sequence 17 from Patent WO0144465.
ACCESSION  AR175253
VERSION     AR175253.1 GI:14598621
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGCG 2335
Db 1 GTGTGTGTGTGTGTGCG 17

RESULT 327
AX175253
LOCUS      AX175253      18 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION Sequence 17 from Patent WO0144465.
ACCESSION  AX175253
VERSION     AX175253.1 GI:14598621
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct

KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 18)
AUTHORS       Ekins,R.Philip.
TITLE        Binding assay using binding agents with tail groups
JOURNAL      Patent: US 6316186-A 1 13-NOV-2001;
FEATURES     Location/Qualifiers
              1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTGTG 1

RESULT 323
AR178166
LOCUS      AR178166      18 bp      DNA      linear      PAT 18-DEC-2001
DEFINITION Sequence 2 from patent US 6316186.
ACCESSION  AR178166
VERSION     AR178166.1 GI:17921059
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Ekins,R.Philip.
TITLE       Binding assay using binding agents with tail groups
JOURNAL     Patent: US 6316186-A 2 13-NOV-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTGTG 1

RESULT 324
AR182079
LOCUS      AR182079      18 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 28 from patent US 6337188.
ACCESSION  AR182079
VERSION     AR182079.1 GI:20224995
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Head,S.R., Golet,P., Karn,J. and Boyce-Jacino,M.
TITLE       De novo or 'universal' sequencing array
JOURNAL     Patent: US 6337188-A 28 08-JAN-2002;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 1 GTGTGTGTGTGTGTGTG 17

RESULT 325
AR261503
LOCUS      AR261503      18 bp      DNA      linear      PAT 29-JAN-2003
DEFINITION Sequence 28 from patent US 6322968.
ACCESSION  AR261503
VERSION     AR261503.1 GI:28072570
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Head,S.R., Golet,P., Karn,J. and Boyce-Jacino,M.
TITLE       De novo or 'universal' sequencing array
JOURNAL     Patent: US 6322968-A 28 27-NOV-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 2 GTGTGTGTGTGTGTGTG 18

RESULT 326
AX115187
LOCUS      AX115187      18 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 310 from Patent WO0129262.
ACCESSION  AX115187
VERSION     AX115187.1 GI:14032129
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Picoult-Newburg,L. and Pohl,M.
TITLE       Genotyping reagents, kits and methods of use thereof
JOURNAL     Patent: WO 0129262-A 310 26-APR-2001;
            Orchid Biosciences, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGCG 2335
Db 1 GTGTGTGTGTGTGTGCG 17

RESULT 327
AX175253
LOCUS      AX175253      18 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION Sequence 17 from Patent WO0144465.
ACCESSION  AX175253
VERSION     AX175253.1 GI:14598621
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
```

```

C12N15/00
CC Synthetic primer Location/Qualifiers
FH Key 1..18
FT source /organism='Artificial Sequence'
FEATURES
    source Location/Qualifiers
        1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GTGTGTGTGTGTGTGTG 2351
    |||||
DB 2 GTGTGTGTGTGTGTGTG 18

RESULT 330
CQ818365/c
LOCUS CQ818365 20 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 7 from Patent WO2004044581.
ACCESSION CQ818365
VERSION CQ818365.1 GI:48427038
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mackenzie, I., Rees, C.M., Nikitenko, L.L., Bicknell, R. and Smith, D.M.
TITLE Transcriptional regulation of crlr and uses thereof
JOURNAL Patent: WO 2004044581-A 7 27-MAY-2004;
ISIS INNOVATION LIMITED (GB)
FEATURES
    source Location/Qualifiers
        1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2333 GCGTGTGTGTGTGTGTG 2349
    |||||
DB 17 GCGTGTGTGTGTGTGTG 1

RESULT 331
CQ818387/c
LOCUS CQ818387 20 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 29 from Patent WO2004044581.
ACCESSION CQ818387
VERSION CQ818387.1 GI:48427060
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Mackenzie, I., Rees, C.M., Nikitenko, L.L., Bicknell, R. and Smith, D.M.
TITLE Transcriptional regulation of crlr and uses thereof
JOURNAL Patent: WO 2004044581-A 29 27-MAY-2004;
ISIS INNOVATION LIMITED (GB)
FEATURES
    source Location/Qualifiers
        1..20
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match 0.4%; Score 17; DB 1; Length 20;

```

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artificial sequences.
REFERENCE 1
AUTHORS Phillips, N.C. and Filion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 17 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
    source Location/Qualifiers
        1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GTGTGTGTGTGTGTGTG 2351
    |||||
DB 2 GTGTGTGTGTGTGTGTG 18

RESULT 328
AX175254
LOCUS AX175254 18 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 18 from Patent WO0144465.
ACCESSION AX175254
VERSION AX175254.1 GI:14598622
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips, N.C. and Filion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 18 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
    source Location/Qualifiers
        1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GTGTGTGTGTGTGTGTG 2351
    |||||
DB 1 GTGTGTGTGTGTGTGTG 17

RESULT 329
BD087486
LOCUS BD087486 18 bp DNA linear PAT 27-AUG-2002
DEFINITION De novo or universal sequencing array.
ACCESSION BD087486
VERSION BD087486.1 GI:22633096
KEYWORDS JP 2001524319-A/28
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Head, S.R., Golet, P., Karn, J. and Jacino, M.B.
TITLE De novo or universal sequencing array
JOURNAL Patent: JP 2001524319-A 28 04-DEC-2001;
ORCHID BIOSCIENCES INC
COMMENT OS Artificial Sequence
PN JP 2001524319-A/28
PD 04-DEC-2001
PF 20-NOV-1998 JP 2000522278
PR 21-NOV-1997 US 08/976427
PI STEVEN R HEAD, PHILIP GOLETT, JONATHAN KARN, MICHAEL BOYCE JACINO
PC C12N15/09, C12N15/03, C12M1/00, C12Q1/68, G01N33/50, C12N15/00, PC

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Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2333 GCGTGTGTGTGTGTGTG 2349
Db 17 GCGTGTGTGTGTGTGTG 1

RESULT 332
AR010007/c
LOCUS AR010007 20 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 19 from patent US 5756684.
ACCESSION AR010007
VERSION AR010007.1 GI:3968812
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Cloning and expression of PUR protein
JOURNAL Patent: US 5756684-A 19 26-MAY-1998;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2329 GTGTGCGTGTGTGTGTGTGT 2348
Db 20 GTATGCATGTGTGTGTGTGT 1

RESULT 333
AR034742/c
LOCUS AR034742 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5869622.
ACCESSION AR034742
VERSION AR034742.1 GI:5950347
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Monoclonal antibodies to the pur protein
JOURNAL Patent: US 5869622-A 19 09-FEB-1999;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2329 GTGTGCGTGTGTGTGTGTGT 2348
Db 20 GTATGCATGTGTGTGTGTGT 1

RESULT 334
AR058876
LOCUS AR058876 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5837835.
ACCESSION AR058876
VERSION AR058876.1 GI:5984453
KEYWORDS
SOURCE
ORGANISM Unknown.

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2329 GTGTGCGTGTGTGTGTGTGT 2348
Db 20 GTATGCATGTGTGTGTGTGT 1

RESULT 335
AR058876/c
LOCUS AR058876 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5837835.
ACCESSION AR058876
VERSION AR058876.1 GI:5984453
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 8 17-NOV-1998;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3463 TATATATATCTATATATATA 3482
Db 1 TATATATATTTTATATATA 20

RESULT 336
AR079581
LOCUS AR079581 20 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 8 from patent US 5965720.
ACCESSION AR079581
VERSION AR079581.1 GI:10006325
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates
JOURNAL Patent: US 5965720-A 12-OCT-1999;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3463 TATATATATCTATATATATA 3482
Db 1 TATATATATTTTATATATA 20
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Journal Patent: US 6169170-A 8 02-JAN-2001;
Location/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2842
|||||
Db 20 TATATATAAAATATATATA 1

RESULT 340
AR130163/c
LOCUS AR130163 20 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 66 from patent US 6187587.
ACCESSION AR130163
VERSION AR130163.1 GI:14118060
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Popoff, I., Brown-Driver, V.L. and Cowsert, L.M.
TITLE Antisense inhibition of e2f transcription factor 1 expression
JOURNAL Patent: US 6187587-A 66 13-FEB-2001;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2325 GTGTGTGTGCGTGTGTGTGT 2344
|||||
Db 20 GTGTGTGAGCATGTGTGTGT 1

RESULT 341
AR177700/c
LOCUS AR177700 20 bp DNA PAT 17-DEC-2001
DEFINITION Sequence 40 from patent US 6312949.
ACCESSION AR177700
VERSION AR177700.1 GI:17920055
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Sakurada, K., Palmer, T. and Gage, F.H.
TITLE Regulation of tyrosine hydroxylase expression
JOURNAL Patent: US 6312949-A 40 06-NOV-2001;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1666 ATGAAGATCGCAGACTTCGG 1685
|||||
Db 20 ATGAAGATGCGDCACTTGG 1

RESULT 342
BD188892

Journal Patent: US 6169170-A 8 02-JAN-2001;
Location/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2842
|||||
Db 20 TATATATAAAATATATATA 1

RESULT 338
AR123290
LOCUS AR123290 20 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6169170.
ACCESSION AR123290
VERSION AR123290.1 GI:14108256
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gryaznov, S.M., Schultz, R.G. and Chen, J.-k.
TITLE Oligonucleotide N3'. fddarw.N5' Phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 8 02-JAN-2001;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3463 TATATATATCTATATATATA 3482
|||||
Db 1 TATATATATTTTATATATA 20

RESULT 339
AR123290/c
LOCUS AR123290 20 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6169170.
ACCESSION AR123290
VERSION AR123290.1 GI:14108256
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gryaznov, S.M., Schultz, R.G. and Chen, J.-k.
TITLE Oligonucleotide N3'. fddarw.N5' Phosphoramidate Duplexes

Query Match 0.4%; Score 16.8; DB 1; Length 20;

AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.

TITLE Polymorphic repeats in human genes

JOURNAL Patent: US 6472154-A 337 29-OCT-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 5.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2313 TGGTCTGTGTGTGTGTGT 2332

Db 20 TGGGGTGTGTGTGTGTGT 1

RESULT 356

AX956707/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Rosa sp.

Eukaryota;

Spermatophyta;

Rosids; eucotyls 1;

Rosaceae; Rosa.

REFERENCE

AUTHORS

TITLE

JOURNAL

Con/Cipio GmbH (DE)

Patent: WO 03097869-A 257 27-NOV-2003;

Microsatellite markers for genetic analyses and the differentiation

of roses

FEATURES

source 1..20

/organism="Rosa sp."

/mol_type="unassigned DNA"

/db_xref="taxon:36598"

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 5.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2337 GTGTGTGTGTGTGTGTGT 2356

Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 357

DOGKIT1A

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

Canis familiaris

Eukaryota; Metazoa;

Mammalia; Eutheria;

Carnivora; Fissipedia;

Canidae; Canis.

REFERENCE

AUTHORS

TITLE

JOURNAL

Unpublished (1996)

Gene-specific universal mammalian sequence-tagged sites:

application to the canine genome

Original source text: Canis familiaris DNA.

Gene-specific universal mammalian sequence-tagged site for KIT1.

Primer for the 5' end is in exon 18. Human product is 650 bp.

Canine product is 650 bp. PCR conditions: 1 min, 94 C, 2 min, 57 C,

3 min, 72 C, 35 cycles.

FEATURES Location/Qualifiers

source 1..20

/organism="Canis familiaris"

/mol_type="genomic DNA"

/db_xref="taxon:9615"

STS 1..20

primer_bind complement(1..20)

/note="PCR primer binding site"

/evidence=experimental

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 5.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1744 CCCGTGAAGTGGATGGGCC 1763

Db 1 CCTGTGAAGTGGATGGCACC 20

RESULT 358

AR074234

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Unclassified.

REFERENCE

AUTHORS

Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,

Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and

Imbach,J.Louis.

Oligonucleotides having a conserved G4 core sequence

Patent: US 5952490-A 42 14-SEP-1999;

FEATURES

source 1..21

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 6e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2920 GGGCGGGCGGTGGGGGCG 2939

Db 2 GGGCGGGCGGGCGGGCGCG 21

RESULT 359

AR098876/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Unclassified.

REFERENCE

AUTHORS

Trofatter,J.A., MacCollin,M.M. and Guseella,J.F.

Tumor suppressor merlin and antibodies thereof

Patent: US 6077685-A 11 20-JUN-2000;

FEATURES

source 1..21

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 6e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1614 CATCCACAGGGACCTGGCTG 1633


```
Db      21 CATCCATGGAGCTGGCTG 2
||||| ||||| ||||| ||||| |||||
RESULT 360
I79716/c
LOCUS      I79716          21 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 11 from patent US 5707863.
ACCESSION  I79716
VERSION     I79716.1 GI:3208006
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE     Tumor suppressor gene merlin
JOURNAL   Patent: US 5707863-A 11 13-JAN-1998;
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1614 CATCCACGGGACCTGGCTG 1633
||||| ||||| ||||| ||||| |||||
Db      21 CATCCATGGAGCTGGCTG 2

RESULT 361
AR301331
LOCUS      AR301331          21 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 22 from patent US 6538126.
ACCESSION  AR301331
VERSION     AR301331.1 GI:31689115
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Cho,J.M., Lee,Y.B., Park,Y.W., Lim,K.J., Choi,D.Y., So,H.S.,
            Kim,C.H., Kim,S.T. and Yang,J.Y.
TITLE     Hepatitis C diagnostics and vaccines
JOURNAL   Patent: US 6538126-A 22 25-MAR-2003;
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2006 TGGTGGAGGACCTGGACCGT 2025
||||| ||||| ||||| ||||| |||||
Db      1 TGGTGGTGAACCTGGACCGT 20

RESULT 362
AX020545/c
LOCUS      AX020545          21 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 45 from Patent WO9934016.
ACCESSION  AX020545
VERSION     AX020545.1 GI:10044235
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1

AUTHORS   Vider,B.Z.
TITLE     A method for identifying and characterizing cells and tissues
JOURNAL   Patent: WO 9934016-A 45 08-JUL-1999;
GENENA LTD (IL); VIDER BEN ZION (IL)
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1798 AGTGACGTCTGCTCTTTGG 1817
||||| ||||| ||||| ||||| |||||
Db      21 AGTGACGTGTGGCCTTTGG 2

RESULT 363
AX032596
LOCUS      AX032596          21 bp      DNA      linear      PAT 20-SEP-2000
DEFINITION Sequence 42 from Patent EP1016715.
ACCESSION  AX032596
VERSION     AX032596.1 GI:10279534
KEYWORDS   .
SOURCE     unidentified
            unidentified
            unclassified.
REFERENCE  1
AUTHORS   Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
            Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
            Wyatt,J.R.
TITLE     Oligonucleotides having a conserved g4 core sequence
JOURNAL   Patent: EP 1016715-A 42 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2920 GGGCGGGGGCTGGGGGGCG 2939
||||| ||||| ||||| ||||| |||||
Db      2 GGGCGGGGGCGGGGGCGGCG 21

RESULT 364
AR171534/c
LOCUS      AR171534          22 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 60 from patent US 6297048.
ACCESSION  AR171534
VERSION     AR171534.1 GI:17910484
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 22)
AUTHORS   Jolly,D.J., Chang,S.M.W., Lee,W.T.L., Townsend,K. and O'Dea,J.
TITLE     Hepatitis therapeutics
JOURNAL   Patent: US 6297048-A 60 02-OCT-2001;
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Thu Oct 28 12:48:19 2004

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QY 1820 TCCTGCTCGGAGATCTTC 1839
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Db 20 TCTTGCTCTGGAGATCTGC 1

RESULT 365
BD005554/c
LOCUS 22 bp DNA linear PAT 31-JAN-2002
DEFINITION Compositions and methods for treating intracellular diseases.
ACCESSION BD005554
VERSION BD005554.1 GI:18633925
KEYWORDS JP 2001500738-A/60.
SOURCE unidentified
ORGANISM unidentified

REFERENCE
1 (bases 1 to 22)
Salberg,M., Millich,D.R. and Lee,W.T.L.
Compositions and methods for treating intracellular diseases
Patent: JP 2001500738-A 60 23-JAN-2001;
CHIRON CORP.,THE SCRIPPS RESEARCH INSTITUTE
OS Unidentified
PN JP 2001500738-A/60
PD 23-JAN-2001
PF 16-SEP-1997 JP 1998514832
PR MATTI SALLBERG,DAVID R MILICH,WILLIAM T L LEE PC
C12N15/36,C12N15/19,A61K48/00,A61K39/12,A61K39/29 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..22 /organism='Unidentified'.

FEATURES
source
1..22 Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1820 TCCTGCTCGGAGATCTTC 1839
    |||||||
Db 20 TCTTGCTCTGGAGATCTGC 1

RESULT 366
BD107557/c
LOCUS 22 bp DNA linear PAT 18-SEP-2002
DEFINITION Nucleic acid probe for detecting pectinatus, and method for
detecting nucleic acid derived from the bacterium.
ACCESSION BD107557
VERSION BD107557.1 GI:23202375
KEYWORDS JP 2002017356-A/17.
SOURCE Pectinatus frisingensis
ORGANISM Bacteria; Firmicutes; Clostridia; Clostridiales;
Acidaminococaceae; Pectinatus.
1 (bases 1 to 22)
Motoyama,Y., Yasuhara,T. and Takahashi,K.
Nucleic acid probe for detecting pectinatus, and method for
detecting nucleic acid derived from the bacterium
Patent: JP 2002017356-A 17 22-JAN-2002;
ASAHI BREWERIES LTD
OS Pectinatus frisingensis
PN JP 2002017356-A/17
PD 22-JAN-2002
PF 03-JUL-2000 JP 2000201258
FT YASUO MOTOYAMA,TAKAOMI YASUHARA,KYOKO TAKAHASHI PC
C12N15/09,C12Q1/04,C12Q1/06,C12Q1/68,C12Q1/68,C12M1/00,C12M1/40,
40,

PC (C12N15/09,C12R1:01),(C12Q1/06,C12R1:01),(C12Q1/68,C12R1:01),
C12N15/00.
PC (C12N15/00,C12R1:01)
CC Nucleic acid probe for detecting pectinatus, and method for
detecting
CC nucleic acid derived from the bacterium
CC Location/Qualifiers
FH Key 1..22
FT source 1..22 /organism='Pectinatus frisingensis'.

FEATURES
source
1..22 Location/Qualifiers
/organism='Pectinatus frisingensis'
/mol_type='genomic DNA'
/db_xref='taxon:865'

Query Match 0.4%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1140 CGAGCTCGAGCTGCTGCCG 1159
    |||||||
Db 22 CGCGCTCGAGCTGCTGCTG 3

RESULT 367
BD271420
LOCUS 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Fab fragment libraries and method of using the same.
ACCESSION BD271420
VERSION BD271420.1 GI:33081188
KEYWORDS JP 2002543830-A/12.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 23)
Hoogenboom,H.R.J.M.
Novel Fab fragment libraries and method of using the same
Patent: JP 2002543830-A 12 24-DEC-2002;
DYAX CORP
OS Artificial Sequence
PN JP 2002543830-A/12
PD 24-DEC-2002
PF 18-MAY-2000 JP 2000618429
PR 18-MAY-1999 EP 99201558.6
PI HENDRICUS RENERUS JACOBUS MATTHEUS HOOGENBOOM PC
C12N15/09,C07K16/34,G01N33/53,C12N15/00
CC Description of Artificial Sequence: Primer
FH Key Location/Qualifiers
FT source 1..23 /organism='Artificial Sequence'.

FEATURES
source
1..23 Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGGTGAGGCTG 874
    |||||||
Db 1 SAGGTGACAGCTGGTGAGGCTG 22

RESULT 368
BD271421
LOCUS 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Fab fragment libraries and method of using the same.
ACCESSION BD271421
VERSION BD271421.1 GI:33081189
KEYWORDS JP 2002543830-A/13.
SOURCE synthetic construct

```

ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hoogenboom,H.R.J.M.
TITLE Novel Rab fragment libraries and method of using the same
JOURNAL Patent: JP 2002543830-A 13 24-DEC-2002;
DIAX CORP
COMMENT OS Artificial Sequence
PN JP 2002543830-A/13
PD 24-DEC-2002
PF 18-MAY-2000 JP 2000618429
PR 18-MAY-1999 EP 9201558.6
PI HENDRICUS RENERUS JACOBUS MATTHEUS HOOGENBOOM PC
C12N15/09,C07K16/34,G01N33/53,C12N15/00
CC Description of Artificial Sequence: Primer
FH Key Location/Qualifiers
FT source 1..23
FT /organism='Artificial Sequence'.
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGGTGAGGCTG 874
Db 1 GAGGTGAGCTGGTGAGGCTG 22
RESULT 369
AX074547
LOCUS AX074547 23 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 5 from Patent WO0104159.
ACCESSION AX074547
VERSION AX074547.1 GI:12710650
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Arepally,G., Kisiel,W., Kamei,K. and Kamei,S.
TITLE Compositions and methods useful for the diagnosis and treatment of
heparin induced thrombocytopenia/thrombosis
JOURNAL Patent: WO 0104159-A 5 18-JAN-2001;
Science & Technology Corporation UNM (US)
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"
Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGGTGAGGCTG 874
Db 1 GAGGTGAGCTGGTGAGGCTG 22
RESULT 370
AX455018
LOCUS AX455018 23 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 85 from Patent WO0208453.
ACCESSION AX455018
VERSION AX455018.1 GI:21714203
KEYWORDS
SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1
AUTHORS Farr,S.B., Pickett,G.G., Neft,R.E. and Dunn,R.T.
TITLE Canine toxicity genes
JOURNAL Patent: WO 0208453-A 85 31-JAN-2002;
Phase-1 Molecular Toxicology (US)
FEATURES
source
1..23
/organism="Canis familiaris"
/mol_type="unassigned DNA"
/db_xref="taxon:9615"
Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1040 AGGTGTCCCTGGAGTCCAC 1059
Db 1 AGGTGTCCCTGGAGTCCAC 20
RESULT 371
AX785090
LOCUS AX785090 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 3 from Patent WO03050531.
ACCESSION AX785090
VERSION AX785090.1 GI:32952919
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Lasters,I., Pletinckx,J., Boutonnet,N., Lauwereys,M. and
Beirnaert,E.
TITLE Method for displaying loops from immunoglobulin domains in
different contexts
JOURNAL Patent: WO 03050531-A 3 19-JUN-2003;
AlgoNomics N.V. (BE); Ablynx N.V. (BE)
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="VH3B-Back primer"
Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGGTGAGGCTG 874
Db 1 SAGGTGCAGCTGGTGAGTCTG 22
RESULT 372
AX799210
LOCUS AX799210 23 bp DNA linear PAT 10-OCT-2003
DEFINITION Sequence 17 from Patent WO03054016.
ACCESSION AX799210
VERSION AX799210.1 GI:37605153
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Muyldermans,S.
TITLE Method for cloning of variable domain sequences
JOURNAL Patent: WO 03054016-A 17 03-JUL-2003;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="VH3B-Back primer"

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="set 2 primer 1 in table 2"

Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGCTGGAGGCTG 874
||||| ||||| ||||| ||||| |||||
Db 1 SAGGTCAGCTGGTGGAGTCTG 22

RESULT 373
A57513/c 24 bp DNA linear PAT 03-MAR-1998
LOCUS
DEFINITION Sequence 5 from Patent WO9632483.
ACCESSION A57513
VERSION A57513.1 GI:3713371
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Masucci,M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 5 17-OCT-1996;
COMMENT MASUCCI MARIA GRAZIA (SE)
Other publication AU 5284296 961030.
FEATURES
source Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2104 ACCCGCAGCTCCAGCTCCTC 2123
||||| ||||| ||||| ||||| |||||
Db 24 ACCCGCAGCTCCAGCTCCTC 5

RESULT 374
A57516 24 bp DNA linear PAT 03-MAR-1998
LOCUS
DEFINITION Sequence 8 from Patent WO9632483.
ACCESSION A57516
VERSION A57516.1 GI:3713374
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Masucci,M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 8 17-OCT-1996;
COMMENT MASUCCI MARIA GRAZIA (SE)
Other publication AU 5284296 961030.
FEATURES
source Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2103 CACCCCGAGCTCCAGCTCCT 2122
||||| ||||| ||||| ||||| |||||

Db 4 CACCCGACCTCCAGCTCCT 23

RESULT 375
AR052979/c 24 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 8 from patent US 5833991.
ACCESSION AR052979
VERSION AR052979.1 GI:5977841
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Masucci,M.G.
TITLE Glycine-containing sequences conferring invisibility to the immune system
JOURNAL Patent: US 5833991-A 8 10-NOV-1998;
FEATURES Location/Qualifiers
1..24
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2104 ACCCGCAGCTCCAGCTCCTC 2123
||||| ||||| ||||| ||||| |||||
Db 24 ACCCGCAGCTCCAGCTCCTC 5

RESULT 376
AR052982 24 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 13 from patent US 5833991.
ACCESSION AR052982
VERSION AR052982.1 GI:5977844
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Masucci,M.G.
TITLE Glycine-containing sequences conferring invisibility to the immune system
JOURNAL Patent: US 5833991-A 13 10-NOV-1998;
FEATURES Location/Qualifiers
1..24
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2103 CACCCCGAGCTCCAGCTCCT 2122
||||| ||||| ||||| ||||| |||||
Db 4 CACCCGACCTCCAGCTCCT 23

RESULT 377
CQ828722/c 24 bp DNA linear PAT 05-JUL-2004
LOCUS
DEFINITION Sequence 440 from Patent WO2004053120.
ACCESSION CQ828722
VERSION CQ828722.1 GI:49732205
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1

```
AUTHORS Weihe, E., Bieller, A. and Schaefer, M.K.
TITLE Regulatory elements in the 5' region of the vrl gene
JOURNAL Patent: WO 2004053120-A 440 24-JUN-2004;
Gruenthal GmbH (DE)
FEATURES
    source
        1..24
            /organism="Mus musculus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:10090"
            /note="V$GF11 01"
Query Match 0.4%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3299 TTCTATAGGATTTTCTTT 3318
|||||
Db 21 TTCTCTAGATTTTGTTT 2

RESULT 378
LOCUS E31758 24 bp DNA linear PAT 18-JUN-2001
DEFINITION DNA encoding protein regulating the expression of fibronectin gene.
ACCESSION E31758
VERSION E31758.1 GI:13018607
KEYWORDS JP 2000014385-A/4.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Takeshi, N. and Koichiro, O.
TITLE DNA encoding protein regulating the expression of fibronectin gene
JOURNAL Patent: JP 2000014385-A 4 18-JAN-2000;
SUMITOMO ELECTRIC IND LTD
COMMENT OS Unidentified
PN JP 2000014385-A/4
PD 18-JAN-2000
PF 06-JUL-1998 JP 1998190001
PR TAKESHI NAKAMURA, KOICHIRO ODA
PC C12N15/09, C07K14/47, C07K16/18, C12P21/08, C12N5/10, C12P21/02,
PC C12Q1/68,
PC C12N15/00, C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..24
/organism="Unidentified".
FEATURES
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        1..24
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
Query Match 0.4%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2928 CTTGGGGGGCGTGGAGGGA 2947
|||||
Db 3 CGTGGGGGGCGGGAAGGA 22

RESULT 379
A48768/c
LOCUS A48768 23 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 106 from Patent WO9604385.
ACCESSION A48768
VERSION A48768.1 GI:2302438
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
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unclassified.
1 (bases 1 to 23)
Maertens, G., Bosman, F., De M.G. and Buyse, M.
PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND
THERAPEUTIC USE
Patent: WO 9604385-A 106 15-FEB-1996;
INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
    source
        1..23
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2164 GCCCACCACGAGTGGGGGCTC 2186
|||||
Db 23 GCGCTACCCAGCAGCGGGAGCTC 1

RESULT 380
ARI57364/c
LOCUS ARI57364 23 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 106 from patent US 6245503.
ACCESSION ARI57364
VERSION ARI57364.1 GI:16218298
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
TITLE Purified hepatitis C virus envelope proteins for diagnostic and
therapeutic use
JOURNAL Patent: US 6245503-A 106 12-JUN-2001;
Location/Qualifiers
    source
        1..23
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2164 GCCCACCACGAGTGGGGGCTC 2186
|||||
Db 23 GCGCTACCCAGCAGCGGGAGCTC 1

RESULT 381
BD195029/c
LOCUS BD195029 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Utilization of inhibitor for treating RTK hyperfunction-induced
disorder, in particular, cancer.
ACCESSION BD195029
VERSION BD195029.1 GI:33004785
KEYWORDS JP 2002518292-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Ullrich, A., Bange, J. and Kuyazev, P.
TITLE Utilization of inhibitor for treating RTK hyperfunction-induced
disorder, in particular, cancer
JOURNAL Patent: JP 2002518292-A 4 25-JUN-2002;
MAX PLANCK GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN EV
COMMENT OS Artificial Sequence
PN JP 2002518292-A/4
PD 25-JUN-2002
```

PF 22-JAN-1999 JP 2000528281
PR 22-JAN-1998 DE 198 02 377.4
PI AXEL ULLRICH, JOHANNES BANGE, PJOTR KNYAZEY
PC A61K45/00, A61P43/00, A61P43/71, C07K16/28, C12N15/09,
PC C12Q1/68,
PC GOIN33/15, GOIN33/50, GOIN33/566, C12N15/00
CC PCR primer for the amplification of the transmembrane domain
CC of FGFR-4
CC (wild-type and mutant)
PH Key Location/Qualifiers
FT source 1..23
FT Location/Qualifiers
FT 1..23 /organism="Artificial Sequence".
FEATURES
source
1..23 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1009 CACAGATCTCCCGCTTCCCGCT 1031
Db |||||
23 CAGAGCTTCCCTCTCCCTCT 1
RESULT 382
LOCUS 23 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 207 from Patent WO2004031413.
ACCESSION CQ799557
VERSION CQ799557.1 GI:46848504
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Nakamura, Y., Daigo, Y. and Nakateury, S.
TITLE Method for diagnosing non-small cell lung cancers
JOURNAL Patent: WO 2004031413-A 207 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
FEATURES
source
1..23 Location/Qualifiers
1..23 /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially synthesized primer sequence for
RT-PCR"
Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2972 AGCAGAGACACGAGCGCTTTTCT 2994
Db |||||
1 AGCAGAGACACGAGCTTTCTTT 23
RESULT 383
LOCUS 23 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 34 from Patent WO2004061105.
ACCESSION CQ841335
VERSION CQ841335.1 GI:50893127
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ciliberto, G.I., Lahm, A.I., la Monica, N.I., Monaci, P.I. and
Nuzzo, M.I.

TITLE Rhesus her2/neu, nucleotides encoding same, and uses thereof
JOURNAL Patent: WO 2004061105-A 34 22-JUL-2004;
(IT) ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.
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/db_xref="taxon:32630"
/note="PCR Primer"
Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2144 CCCAGACCTGCTGCCCGCCG 2166
Db |||||
23 CCCCTGACCTGCAGCCCCCAGCC 1
RESULT 384
LOCUS 23 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 39 from Patent WO2004061105.
ACCESSION CQ841340
VERSION CQ841340.1 GI:50893132
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ciliberto, G.I., Lahm, A.I., la Monica, N.I., Monaci, P.I. and
Nuzzo, M.I.
TITLE Rhesus her2/neu, nucleotides encoding same, and uses thereof
JOURNAL Patent: WO 2004061105-A 39 22-JUL-2004;
(IT) ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.
FEATURES
source
1..23 Location/Qualifiers
1..23 /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"
Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2144 CCCAGACCTGCTGCCCGCCG 2166
Db |||||
1 CCCCTGACCTGCAGCCCCCAGCC 23
RESULT 385
LOCUS 23 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent WO9937299.
ACCESSION AX020199
VERSION AX020199.1 GI:10043988
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Knyazev, P., Bange, J. and Ullrich, A.
TITLE Use of inhibitors for the treatment of disorders related to rtk
hyperfunction, especially cancer
JOURNAL Patent: WO 9937299-A 6 29-JUL-1999;
(DE); ULLRICH AXEL (DE); KNYAZEY PJOTR (DE); BANGE JOHANNES
FEATURES
source
1..23 Location/Qualifiers
1..23 /organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer zur Amplifizierung der Transmembranomane
von FGFR-4 (Wildtyp und Mutante). Antisinn-Richtung."

Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1009 CACAGATCTCCCGCTCCCGCT 1031
Db 23 CAGAGCTCTCCCTCTTCCCTCT 1

RESULT 386
AX452855/c
LOCUS 23 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 106 from Patent EP1211315.
ACCESSION AX452855
VERSION AX452855.1 GI:21712497
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1
AUTHORS Maertens, G., Bosman, F., de Martynoff, G. and Buyse, M.A.
TITLE Recombinant vectors for producing hcv envelope proteins
JOURNAL Patent: EP 1211315-A 106 05-JUN-2002;
Innogenetics N.V. (BE)
FEATURES
source
1..23
/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"

Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2164 GCCCACCACGAGTGGGGCTC 2186
Db 23 GCCTACCCAGCAGCGGGAGCTC 1

RESULT 397
AX685107/c
LOCUS 23 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 106 from Patent WO2055548.
ACCESSION AX685107
VERSION AX685107.1 GI:29371469
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1
AUTHORS Maertens, G., Bosman, F. and Buyse, M.A.
TITLE Purified Hepatitis C virus envelope proteins for diagnostic and
therapeutic use
JOURNAL Patent: WO 02055548-A 106 18-JUL-2002;
Innogenetics N.V. (BE)
FEATURES
source
1..23
/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"

Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2164 GCCCACCACGAGTGGGGCTC 2186

Db 23 GCGCTACCCAGCAGCGGGAGCTC 1

RESULT 388
AX794949/c
LOCUS 23 bp DNA linear PAT 04-OCT-2003
DEFINITION Sequence 106 from Patent WO03051912.
ACCESSION AX794949
VERSION AX794949.1 GI:37515795
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1
AUTHORS Maertens, G., Depla, E. and Bosman, F.
TITLE Purified Hepatitis C virus envelope proteins for diagnostic and
therapeutic use
JOURNAL Patent: WO 03051912-A 106 26-JUN-2003;
Innogenetics N.V. (BE)
FEATURES
source
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/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"

Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2164 GCCCACCACGAGTGGGGCTC 2186
Db 23 GCGCTACCCAGCAGCGGGAGCTC 1

RESULT 389
AX926751/c
LOCUS 23 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 34 from Patent WO03085133.
ACCESSION AX926751
VERSION AX926751.1 GI:40247107
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Nagaraju, J.G.
TITLE Novel fissr-pcr primers and method of identifying genotyping
diverse genomes of plant and animal systems including rice
varieties, a kit thereof
JOURNAL Patent: WO 03085133-A 34 16-OCT-2003;
Centre for DNA Fingerprinting and Diagnostics, Centre for; the
Department of Biotechnology, Ministry of Science & Technology (IN)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="A novel FISRR-PCR primer for genotyping eukaryotes"

Query Match 0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2309 GCTTGGTCTGTGTGTGTGTG 2331
Db 23 GCTGTGCTATTGTGTGTGTGTG 1

RESULT 390
AR071772/c
LOCUS 18 bp DNA linear PAT 18-FEB-2000

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DEFINITION Sequence 1 from patent US 5912147.
ACCESSION AR071772
VERSION AR071772.1 GI:7222660
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 1 15-JUN-1999;
FEATURES
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Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2334 CGTGTGTGTGTGTGTG 2351
Db 18 CTTGTGTGTGTGTGTG 1

RESULT 391
LOCUS AR071799/c 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 28 from patent US 5912147.
ACCESSION AR071799
VERSION AR071799.1 GI:7222687
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 28 15-JUN-1999;
FEATURES
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Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTG 2333
Db 18 TTTGTGTGTGTGTGTG 1

RESULT 392
LOCUS E28534 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28534
VERSION E28534.1 GI:13025386
KEYWORDS JP 1999075880-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 199075880-A 1 23-MAR-1999;
COMMENT OS Unidentified
PN JP 1999075880-A/1
PD 23-MAR-1999
PP 10-JUL-1998 JP 1998195719
PR

FEATURES
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Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTG 2333
Db 18 TTTGTGTGTGTGTGTG 1

RESULT 393
LOCUS E28534/c 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28534
VERSION E28534.1 GI:13025386
KEYWORDS JP 1999075880-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 199075880-A 1 23-MAR-1999;
COMMENT OS Unidentified
PN JP 1999075880-A/1
PD 23-MAR-1999
PP 10-JUL-1998 JP 1998195719
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FEATURES
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Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATA 2840
Db 18 TATATATATATATATATA 1

RESULT 394
LOCUS AR241816 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 104 from patent US 6472154.
ACCESSION AR241816
VERSION AR241816.1 GI:27287628
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Unidentified'.

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Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2823 TATATATACATATATATA 2840
Db 1 TATATATATATATATATA 18

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RESULT 393
LOCUS E28534/c 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28534
VERSION E28534.1 GI:13025386
KEYWORDS JP 1999075880-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 199075880-A 1 23-MAR-1999;
COMMENT OS Unidentified
PN JP 1999075880-A/1
PD 23-MAR-1999
PP 10-JUL-1998 JP 1998195719
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FEATURES
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Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2823 TATATATACATATATATA 2840
Db 18 TATATATATATATATATA 1

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RESULT 394
LOCUS AR241816 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 104 from patent US 6472154.
ACCESSION AR241816
VERSION AR241816.1 GI:27287628
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2823 TATATATACATATATATA 2840
Db 18 TATATATATATATATATA 1

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RESULT 394
LOCUS AR241816 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 104 from patent US 6472154.
ACCESSION AR241816
VERSION AR241816.1 GI:27287628
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 104 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2822 GTATATACATATATAT 2839
Db 1 GTATATATATATATAT 18

RESULT 395
AX355057 18 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 85 from Patent WO0197843.
DEFINITION AX355057
ACCESSION AX355057
VERSION AX355057.1 GI:18619724
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 85 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATAT 2841
Db 1 ATATATATATATATAT 18

RESULT 396
AX355057/c 18 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 85 from Patent WO0197843.
DEFINITION AX355057
ACCESSION AX355057
VERSION AX355057.1 GI:18619724
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 85 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATAT 2841
Db 1 ATATATATATATATAT 18

RESULT 397
AX338196 20 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 17 from patent US 6569618.
DEFINITION AR338196
ACCESSION AR338196
VERSION AR338196.1 GI:33724947
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Yasue,H. and Yoshimura,M.
TITLE Diagnosis of diseases associated with coronary twitching
JOURNAL Patent: US 6569618-A 17 27-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3064 TGTTCACACACCCCAACA 3081
Db 3 TGTTCACACACCCCAACA 20

RESULT 398
AX393666 21 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 205 from patent US 6617122.
DEFINITION AR393666
ACCESSION AR393666
VERSION AR393666.1 GI:40120447
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hayden,M.R., Brooks-Wilson,A.R. and Pimstone,S.N.
TITLE Process for identifying modulators of ABC1 activity
JOURNAL Patent: US 6617122-A 205 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 497 ACACGCTGGACGTGCTGG 514
Db 1 ACACGCTGGGCGTGCTGG 18

RESULT 399
AX020767/c 21 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 267 from Patent WO9934016.
DEFINITION AX020767
ACCESSION AX020767
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FEATURES	source	Location/Qualifiers	Query Match	Best Local Similarity	Mismatches	Indels	Gaps
VERSION	AX020767.1	GI:10044466					
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE							
AUTHORS	Vider, B.Z.						
TITLE	A method for identifying and characterizing cells and tissues						
JOURNAL	GENA LTD (IL); VIDER BEN ZION (IL)						
FEATURES							
source							
LOCUS	AX092707	21 bp DNA					
DEFINITION	Sequence 119 from Patent WO0115676.						
ACCESSION	AX092707						
VERSION	AX092707.1	GI:13444764					
KEYWORDS	Homo sapiens (human)						
SOURCE	Homo sapiens						
ORGANISM	Homo sapiens						
REFERENCE							
AUTHORS	Nemeth, E.F. and Brown, E.M.						
TITLE	CALCIUM RECEPTOR-ACTIVE MOLECULES						
JOURNAL	Patent: WO 9418959-A 2 01-SEP-1994;						
FEATURES							
source							
LOCUS	AX092707	23 bp DNA					
DEFINITION	Sequence 2 from Patent EP1366764.						
ACCESSION	AX092707						
VERSION	AX092707.1	GI:40733337					
KEYWORDS	unidentified						
SOURCE	unidentified						
ORGANISM	unclassified.						
REFERENCE							
AUTHORS	Brown, E.M., Balandrin, M.F., Hebert, S.C., Fuller, F.H., del Mar, E.G., Nemeth, E.F. and van Wageningen, B.C.						
TITLE	Method of screening for calcium receptor-active molecules						
JOURNAL	Patent: EP 1366764-A 2 03-DEC-2003;						
FEATURES							
source							
LOCUS	AX092707	21 bp DNA					
DEFINITION	Sequence 119 from Patent WO0115676.						
ACCESSION	AX092707						
VERSION	AX092707.1	GI:13444764					
KEYWORDS	Homo sapiens (human)						
SOURCE	Homo sapiens						
ORGANISM	Homo sapiens						
REFERENCE							
AUTHORS	Nemeth, E.F. and Brown, E.M.						
TITLE	CALCIUM RECEPTOR-ACTIVE MOLECULES						
JOURNAL	Patent: WO 9418959-A 2 01-SEP-1994;						
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source							
LOCUS	AX092707	23 bp DNA					
DEFINITION	Sequence 2 from Patent EP1366764.						
ACCESSION	AX092707						
VERSION	AX092707.1	GI:40733337					
KEYWORDS	unidentified						
SOURCE	unidentified						
ORGANISM	unclassified.						
REFERENCE							
AUTHORS	Brown, E.M., Balandrin, M.F., Hebert, S.C., Fuller, F.H., del Mar, E.G., Nemeth, E.F. and van Wageningen, B.C.						
TITLE	Method of screening for calcium receptor-active molecules						
JOURNAL	Patent: EP 1366764-A 2 03-DEC-2003;						
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LOCUS	AX092707	23 bp DNA					
DEFINITION	Sequence 2 from Patent EP1366764.						
ACCESSION	AX092707						
VERSION	AX092707.1	GI:40733337					
KEYWORDS	unidentified						
SOURCE	unidentified						
ORGANISM	unclassified.						
REFERENCE							
AUTHORS	Brown, E.M., Balandrin, M.F., Hebert, S.C., Fuller, F.H., del Mar, E.G., Nemeth, E.F. and van Wageningen, B.C.						
TITLE	Method of screening for calcium receptor-active molecules						
JOURNAL	Patent: EP 1366764-A 2 03-DEC-2003;						
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source							
LOCUS	AX092707	23 bp DNA					
DEFINITION	Sequence 2 from Patent EP1366764.						
ACCESSION	AX092707						
VERSION	AX092707.1	GI:40733337					

AR121232/c
 LOCUS AR121232 21 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 12 from patent US 6159710.
 ACCESSION AR121232
 VERSION AR121232.1 GI:14104808
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Fraser, N.W., Zabolotny, J.M. and Krummenacher, C.F.
 TITLE Method and compositions for stabilizing unstable gene transcripts
 JOURNAL Patent: US 6159710-A 12 DEC-2000;
 FEATURES
 source
 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 183 CGGGAGGACGAGGCTGAGGA 203
 Db 21 CGAGGAGGAGGAGGAGGAGGA 1
 RESULT 410
 LOCUS 132944 21 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 5 from patent US 5589451.
 ACCESSION 132944
 VERSION 132944.1 GI:1823735
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Wilson, S.E.
 TITLE Methods and treatments for corneal healing with hepatocyte and
 keratinocyte growth factors
 JOURNAL Patent: US 5589451-A 5 31-DEC-1996;
 FEATURES
 source
 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1807 TGGTCCTTTGGGGTCTGCTC 1827
 Db 1 TGGTCCTTTGGGGTCTGCTC 21
 RESULT 411
 LOCUS 187090 21 bp DNA linear PAT 10-JUN-1998
 DEFINITION Sequence 4 from patent US 5703047.
 ACCESSION 187090
 VERSION 187090.1 GI:3206808
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Wilson, S.E.
 TITLE Methods and treatments for corneal healing with growth factors
 JOURNAL Patent: US 5703047-A 4 30-DEC-1997;
 FEATURES
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 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1807 TGGTCCTTTGGGGTCTGCTC 1827
 Db 1 TGGTCCTTTGGGGTCTGCTC 21

/mol_type="unassigned DNA"
 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1807 TGGTCCTTTGGGGTCTGCTC 1827
 Db 1 TGGTCCTTTGGGGTCTGCTC 21
 RESULT 412
 LOCUS BD132045 21 bp DNA linear PAT 18-SEP-2002
 DEFINITION Gene associated with neoplastic disease or malignancy associated
 gene.
 ACCESSION BD132045
 VERSION BD132045.1 GI:23226990
 KEYWORDS JP 2002503450-A/2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Black, K., Ljubimova, J.Y. and Demetriou, A.A.
 TITLE Gene associated with neoplastic disease or malignancy associated
 JOURNAL Patent: JP 2002503450-A 2 05-FEB-2002;
 COMMENT CEDARS SINAI MEDICAL CENTER
 OS Homo sapiens (human)
 PN JP 2002503450-A/2
 PD 05-FEB-2002 JP 2000524431
 PF 11-DEC-1998 JP 08/989750
 PR 12-DEC-1997 US 08/989750
 PI KEITH BLACK, JULIA Y LJUBIMOVA, ACHILLES A DEMETRIOU PC
 C12N15/09, A61K38/00, C07K14/47, C07K16/18, C12Q1/68, G01N33/53, PC
 G01N33/566
 PC G01N33/574, C12N15/00, A61K37/02
 CC Gene associated with neoplastic disease or malignancy CC
 associated gene
 FH Key Location/Qualifiers
 FT source 1..21 /organism='Homo sapiens (human)'.
 Location/Qualifiers
 1..21 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'
 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1807 TGGTCCTTTGGGGTCTGCTC 1827
 Db 1 TGGTCCTTTGGGGTCTGCTC 21
 RESULT 413
 LOCUS BD140705 21 bp DNA linear PAT 18-SEP-2002
 DEFINITION Methods for the simultaneous identification of novel biological
 targets and lead structures for drug development.
 ACCESSION BD140705
 VERSION BD140705.1 GI:23235650
 KEYWORDS JP 2002508507-A/7.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Heekner, D.L., Zepp, C.M., Gao, Y. and Jones, S.W.
 TITLE Methods for the simultaneous identification of novel biological
 targets and lead structures for drug development
 JOURNAL Patent: JP 2002508507-A 7 19-MAR-2002;

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SEPRACOR INC
OS Artificial Sequence
PN JP 2002508507-A/7
PD 19-MAR-2002
PF 18-DEC-1998 JP 2000539165
PR 18-DEC-1997 US 60/068035
PI DONALD L. HEEFER, CHARLES W. ZEPPE, YUN GAO, STEVEN W. JONES, PC
G01N33/542, C12Q1/04, C12Q1/69, C12Q1/70, G01N21/00, G01N21/76, PC
G01N33/53,
PC G01N33/566//C12N15/09, C12N15/00
CC Description of Artificial Sequence: construct FH Key
FT Location/Qualifiers
FT source
FT 1..21
FT /organism='Artificial Sequence'.

FEATURES
source
LOCUS AR074772 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 69 from patent US 5955276.
ACCESSION AR074772
VERSION AR074772.1 GI:10001525
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 69 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3463 TATATATATCTATATATATAA 3483
Db 21 TATATATACCTAGGTATATAA 1

RESULT 414
AR074772/c
LOCUS AR074772 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 69 from patent US 5955276.
ACCESSION AR074772
VERSION AR074772.1 GI:10001525
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 69 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATA 2844
Db 21 ACACACATATATATATA 1

RESULT 415
AR074786/c
LOCUS AR074786 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 83 from patent US 5955276.
ACCESSION AR074786
VERSION AR074786.1 GI:10001539
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 83 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATA 2844
Db 21 ACACACATATATATATA 1

RESULT 416
AR074787
LOCUS AR074787 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 84 from patent US 5955276.
ACCESSION AR074787
VERSION AR074787.1 GI:10001540
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 84 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATAT 2843
Db 1 TATATATATATATATATGTGT 21

RESULT 417
AR074787/c
LOCUS AR074787 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 84 from patent US 5955276.
ACCESSION AR074787
VERSION AR074787.1 GI:10001540
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 84 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATA 2844
Db 21 ACACACATATATATATA 1

RESULT 418
AR074787/c
LOCUS AR074787 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 84 from patent US 5955276.
ACCESSION AR074787
VERSION AR074787.1 GI:10001540
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 84 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATA 2844
Db 21 ACACACATATATATATA 1

RESULT 418
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CQ754864/c
LOCUS CQ754864 22 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 11 from Patent EP1375510.
ACCESSION CQ754864
VERSION CQ754864.1 GI:44845992
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS te Koppelaar, J.M. and Bank, R.A.
TITLE Modification of collagenous materials and medical treatment,
diagnosis and monitoring of fibrotic conditions
JOURNAL Patent: EP 1375510-A 11 02-JAN-2004;
Nederlandse Organisatie voor Toegepast-Natuurwetenschappelijk
Onderzoek TNO (NL)
FEATURES
source Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: forward primer
exon 7"
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2325 GTGTGTGTGCTGTGTGTGTG 2345
Db 21 GTGTGTGTGTGTGTGTGTG 1
RESULT 419
AX184223/c
LOCUS AX184223 22 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1976 from Patent WO0142511.
ACCESSION AX184223
VERSION AX184223.1 GI:15135567
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1976 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES
source Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3469 TATCTATATATATATATTTTATG 3490
Db 22 TATATATATATATANGTTGTG 1
RESULT 420
BD140700/c
LOCUS BD140700 22 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods for the simultaneous identification of novel biological
targets and lead structures for drug development.
ACCESSION BD140700
VERSION BD140700.1 GI:23235645
KEYWORDS JP 2002508507-A/2.

synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Heefner, D.L., Zepp, C.M., Gao, Y. and Jones, S.W.
TITLE Methods for the simultaneous identification of novel biological
targets and lead structures for drug development
JOURNAL Patent: JP 2002508507-A 2 19-MAR-2002;
SEPRACOR INC
COMMENT OS Artificial Sequence
PN JP 2002508507-A/2
PD 19-MAR-2002
PF 18-DEC-1998 JP 2000539165
PI 18-DEC-1997 US 60/068035
PR DONALD L. HEFFNER, CHARLES M. ZEPP, YUN GAO, STEVEN W. JONES PC
GOIN33/542, CI2Q1/04, CI2Q1/68, CI2Q1/70, G01N21/00, G01N21/76, PC
GOIN33/53,
PC G01N33/566//CI2N15/09, CI2N15/00
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FT source Location/Qualifiers
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3463 TATATATATCTATATATATAA 3483
Db 21 TATATATACCTAGGTATATAA 1
RESULT 421
AR233986/c
LOCUS AR233986 23 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 4 from patent US 6458551.
ACCESSION AR233986
VERSION AR233986.1 GI:27276620
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Wilkinson, H.
TITLE Estrogen receptor
JOURNAL Patent: US 6458551-A 4 01-OCT-2002;
FEATURES
source Location/Qualifiers
1..23
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 666 GGTGGGCGCGGACGCGACACC 686
Db 23 GGTGGGCGCTGCTCGGACACC 3
RESULT 422
AR316862/c
LOCUS AR316862 23 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6562592.
ACCESSION AR316862
VERSION AR316862.1 GI:33695952
KEYWORDS Unknown.
SOURCE

Query Match	0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity	85.7%; Pred. No. 7.6e+02;
Matches	18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1950 GATCATGGGGAGTGTGGCA 1970
Db	
	21 GACATGCTGGACTGTGGCA 1
RESULT 425	
AX376782	
LOCUS	AX376782 23 bp DNA linear PAT 18-MAR-2002
DEFINITION	Sequence 12 from Patent WO0212513.
ACCESSION	AX376782
VERSION	AX376782.1 GI:19573167
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Burnie, J.P., Matthews, R.C. and Rigg, G.
TITLE	Combinatorial Chemistry method
JOURNAL	Patent: WO 0212513-A 12 14-FEB-2002;
FEATURES	Neutec Pharma PLC (GB)
source	Location/Qualifiers
	1. .23
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="PCR primer"
Query Match	0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity	85.7%; Pred. No. 7.6e+02;
Matches	18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	854 AGGAGGAGCTGTGGAGGCTG 874
Db	
	2 AGGTGCAGCTGTGTGGAGTCTG 22
RESULT 426	
AX795214	
LOCUS	AX795214 23 bp DNA linear PAT 04-OCT-2003
DEFINITION	Sequence 9 from Patent WO03052416.
ACCESSION	AX795214
VERSION	AX795214.1 GI:37515974
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Burnie, J.P., Matthews, R.C., Rigg, G.P. and Williamson, P.
TITLE	Focused antibody technology
JOURNAL	Patent: WO 03052416-A 9 26-JUN-2003;
FEATURES	Neutec Pharma PLC (GB)
source	Location/Qualifiers
	1. .23
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="PCR Primer"
Query Match	0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity	85.7%; Pred. No. 7.6e+02;
Matches	18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	854 AGGAGGAGCTGTGGAGGCTG 874
Db	
	2 AGGTGCAGCTGTGTGGAGTCTG 22
RESULT 427	
AX804134	

LOCUS AX804134 23 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 302 from Patent WO03060160.
ACCESSION AX804134
VERSION AX804134.1 GI:38521269
KEYWORDS Oreochromis niloticus (Nile tilapia)
SOURCE Oreochromis niloticus
ORGANISM Oreochromis niloticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidae; Cichlidae; Oreochromis.
1
REFERENCE Lie Y., Slettan, A., Hoeyum, M. and Lingaas, F.
AUTHORS Verification of food origin based on nucleic acid pattern
TITLE recognition
JOURNAL Patent: WO 03060160-A 302 24-JUL-2003;
Genomar ASA (NO)
FEATURES Location/Qualifiers
source
1. .23
/organism="Oreochromis niloticus"
/mol_type="unassigned DNA"
/db_xref="taxon:8128"
Query Match 0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 730 AAGGAGCTAGAGTTCTCTCC 750
||||| ||||| ||||| |||||
Db 2 AAGGAGATAGAGATGCTCTCC 22
RESULT 428
LOCUS BD091393/c 23 bp DNA linear PAT 27-AUG-2002
DEFINITION Estrogen receptor.
ACCESSION BD091393
VERSION BD091393.1 GI:22637004
KEYWORDS JP 2001525319-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Wilkenson, H.
AUTHORS Estrogen receptor
TITLE Patent: JP 2001525319-A 3 11-DEC-2001;
JOURNAL MERCK AND CO INC
COMMENT OS Homo sapiens (human)
PN JP 2001525319-A/3
PD 11-DEC-2001
PF 04-SEP-1998 JP 2000510766
PR 08-SEP-1997 US 60/058271, 30-SEP-1997 US 60/060520 PR
30-OCT-1997 GB 9722884.5, 20-MAR-1998 GB 9806032.0 PI HILARY
WILKINSON
PC C07K14/72, A61K45/00, A61P3/10, A61P3/14, A61P5/32, A61P19/10, PC
A61P25/28.
PC A61P35/00, C12N15/09, G01N33/53, G01N33/566, C12N15/00 CC
Estrogen receptor
FH Key Location/Qualifiers
FT source
1. .23
/organism="Homo sapiens (human)"
FEATURES Location/Qualifiers
source
1. .23
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 666 GGTGGGCCCCGACGCACACC 686

LOCUS S61964 23 bp DNA linear PRI 07-MAY-1993
DEFINITION (beta C)-beta-globin [5'region] [human, Genomic Mutant, 23 nt].
ACCESSION S61964
VERSION S61964.1 GI:236198
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 23)
REFERENCE Trabuchet, G., Elion, J., Dunda, O., Lapoumeroulie, C., Ducrocq, R.,
AUTHORS Nadifi, S., Zohoun, I., Chaventre, A., Carnevale, P., Nagel, R.L., et, al.
TITLE Nucleotide sequence evidence of the uniceentric origin of the beta C
mutation in Africa
JOURNAL Hum. Genet. 87 (5), 597-601 (1991)
MEDLINE 92009838
PubMed 1680789
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 61964] from the original journal article.
FEATURES Location/Qualifiers
source
1. .23
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1. .23
/gene="beta-globin"
/allele="beta C"
Query Match 0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3469 TATCTATATATATATATTTATT 3489
||||| ||||| ||||| |||||
Db 1 TATATATATATATATTTT 21
RESULT 430
LOCUS A12053 16 bp DNA linear PAT 09-DEC-1993
DEFINITION Oligonucleotide.
ACCESSION A12053
VERSION A12053.1 GI:491255
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Epplen, J.T.
TITLE Process for the detection of restriction fragment length
polymorphisms in eukaryotic genomes
JOURNAL Patent: EP 0266787-A 13 11-MAY-1988;
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften
FEATURES Location/Qualifiers
source
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GTGTGTGTGTGTGTGT 2350
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Db 1 GTGTGTGTGTGTGTGT 16


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RESULT 431
A12054/c
LOCUS       A12054               16 bp    DNA    linear    PAT 09-DEC-1993
DEFINITION  Oligonucleotide.
ACCESSION   A12054
VERSION     A12054.1  GI:489449
KEYWORDS    .
SOURCE      synthetic construct
            artificial sequences.
ORGANISM    1 (bases 1 to 16)
REFERENCE   Eppleten,J.T.
AUTHORS     Process for the detection of restriction fragment length
TITLE       polymorphisms in eukaryotic genomes
JOURNAL     Patent: EP 0266787-A 14 11-MAY-1988;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften
FEATURES    Location/Qualifiers
             source
               1..16
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGT 2350
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Db 16 GTGTGTGTGTGTGTGT 1

RESULT 432
E32224/c
LOCUS       E32224               16 bp    DNA    linear    PAT 18-JUN-2001
DEFINITION  Method for isolating satellite sequence.
ACCESSION   E32224
VERSION     E32224.1  GI:13021854
KEYWORDS    JP 2000060559-A/26.
SOURCE      Hallotis discus discus
            Hallotis discus discus
            Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
            Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE    Hideaki.T. and Masashi.S.
AUTHORS      Method for isolating satellite sequence
TITLE        Patent: JP 2000060559-A 26 29-FEB-2000;
JOURNAL      NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT      OS Hallotis discus discus
             PN JP 2000060559-A/26
             PD 29-FEB-2000
             PF 18-AUG-1998 JP 1998232153
             PR HIDEAKI TAKAHASHI,MASASHI SEKINO
             PC C12N15/09,C12Q1/68,C12N15/00
             CC CC
             FH Key
             FT source
             Location/Qualifiers
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               /mol_type="genomic DNA"
               /sub_species="discus"
               /db_xref="taxon:91233"
Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||||
Db 16 TGTGTGTGTGTGTGTG 1

RESULT 433
I31527/c
LOCUS       I31527               16 bp    DNA    linear    PAT 06-FEB-1997
DEFINITION  Sequence 439 from patent US 5582979.
ACCESSION   I31527
VERSION     I31527.1  GI:1822318
KEYWORDS    .
SOURCE      Unknown.
            Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 16)
REFERENCE   Weber,J.L.
AUTHORS     Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
TITLE       method of using the same
JOURNAL     Patent: US 5582979-A 439 10-DEC-1996;
            Location/Qualifiers
FEATURES    source
               1..16
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||||
Db 16 TGTGTGTGTGTGTGTG 1

RESULT 434
AR328666
LOCUS       AR328666             16 bp    RNA    linear    PAT 17-AUG-2003
DEFINITION  Sequence 6068 from patent US 6566127.
ACCESSION   AR328666
VERSION     AR328666.1  GI:33714474
KEYWORDS    .
SOURCE      Unknown.
            Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 16)
REFERENCE   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
AUTHORS     Method and reagent for the treatment of diseases or conditions
TITLE       related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 6068 20-MAY-2003;
            Location/Qualifiers
FEATURES    source
               1..16
               /organism="unknown"
               /mol_type="unassigned RNA"
Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGT 2332
      |||||
Db 1 CTGTGTGTGTGTGTGT 16

RESULT 435
AR328667
LOCUS       AR328667             16 bp    RNA    linear    PAT 17-AUG-2003
DEFINITION  Sequence 6069 from patent US 6566127.
ACCESSION   AR328667
VERSION     AR328667.1  GI:33714475
KEYWORDS    .
SOURCE      Unknown.
            Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 16)
REFERENCE   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
AUTHORS     Method and reagent for the treatment of diseases or conditions
TITLE
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related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 609 20-MAY-2003;
Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2335 GTGTGTGTGTGTGTG 2350
|||||
Db 1 GTGTGTGTGTGTGTG 16

RESULT 436
LOCUS I31536 17 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 448 from patent US 5582979.
ACCESSION I31536
VERSION I31536.1 GI:1822327
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dc-da).sub.n. (dg-dt).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 448 10-DEC-1996;
FEATURES
Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 437
LOCUS AR455906 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 16 from patent US 6686160.
ACCESSION AR455906
VERSION AR455906.1 GI:42690800
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 16 03-FEB-2004;
FEATURES
Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 438
LOCUS AR455907 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 17 from patent US 6686160.
ACCESSION AR455907
VERSION AR455907.1 GI:42690801
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 17 03-FEB-2004;
FEATURES
Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||
Db 2 TGTGTGTGTGTGTGTG 17

RESULT 439
LOCUS AR455909/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 19 from patent US 6686160.
ACCESSION AR455909
VERSION AR455909.1 GI:42690803
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 19 03-FEB-2004;
FEATURES
Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 440
LOCUS AR455911/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 21 from patent US 6686160.
ACCESSION AR455911
VERSION AR455911.1 GI:42690805
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 21 03-FEB-2004;
FEATURES
Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="genomic DNA"
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/mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 441
AX239676
LOCUS AX239676 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 16 from Patent WO0164948.
ACCESSION AX239676
VERSION AX239676.1 GI:15797341
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 16 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 442
AX239677
LOCUS AX239677 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 17 from Patent WO0164948.
ACCESSION AX239677
VERSION AX239677.1 GI:15797342
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 17 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 2 TGTGTGTGTGTGTGTG 17

RESULT 443
AX239679/c
LOCUS AX239679 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 19 from Patent WO0164948.
ACCESSION AX239679
VERSION AX239679.1 GI:15797344
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 19 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 444
AX239681/c
LOCUS AX239681 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 21 from Patent WO0164948.
ACCESSION AX239681
VERSION AX239681.1 GI:15797346
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 21 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 445
AR071774/c
LOCUS AR071774 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 3 from patent US 5912147.
ACCESSION AR071774
VERSION AR071774.1 GI:7222662
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
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AUTHORS      Stoler,D., Basik,M. and Anderson,G.
TITLE        Rapid means of quantitating genomic instability
JOURNAL      Patent: US 5912147-A 3 15-JUN-1999;
FEATURES     Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 446
AR071775/c
LOCUS      AR071775      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 4 from patent US 5912147.
ACCESSION  AR071775
VERSION     AR071775.1 GI:7222663
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 4 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 447
AR071776/c
LOCUS      AR071776      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 5 from patent US 5912147.
ACCESSION  AR071776
VERSION     AR071776.1 GI:7222664
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 5 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 448
AR071804/c
LOCUS      AR071804      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 33 from patent US 5912147.
ACCESSION  AR071804
VERSION     AR071804.1 GI:7222692
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 33 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 449
AR071805/c
LOCUS      AR071805      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 34 from patent US 5912147.
ACCESSION  AR071805
VERSION     AR071805.1 GI:7222693
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 34 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 450
AR071806/c
LOCUS      AR071806      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 35 from patent US 5912147.
ACCESSION  AR071806
VERSION     AR071806.1 GI:7222694
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 35 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 451
AR071807/c
LOCUS      AR071807      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 36 from patent US 5912147.
ACCESSION  AR071807
VERSION     AR071807.1 GI:7222695
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 36 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1
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/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTG 2333
Db 16 TGTGTGTGTGTGTG 1

RESULT 451
AR071807/c
LOCUS AR071807 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 36 from patent US 5912147.
ACCESSION AR071807
VERSION AR071807.1 GI:7222695
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 36 15-JUN-1999;
FEATURES Location/Qualifiers
1..18
source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTG 2333
Db 16 TGTGTGTGTGTGTG 1

RESULT 452
AR071808/c
LOCUS AR071808 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 37 from patent US 5912147.
ACCESSION AR071808
VERSION AR071808.1 GI:7222696
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 37 15-JUN-1999;
FEATURES Location/Qualifiers
1..18
source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTG 2333
Db 16 TGTGTGTGTGTGTG 1

RESULT 453
AR071809/c
LOCUS AR071809 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 38 from patent US 5912147.
ACCESSION AR071809
VERSION AR071809.1 GI:7222697

/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTG 2333
Db 16 TGTGTGTGTGTGTG 1

RESULT 454
AR071807/c
LOCUS AR071807 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Reagents and methods useful for detecting diseases of the prostate.
ACCESSION BD082088
VERSION BD082088.1 GI:22627698
KEYWORDS JP 2001523948-A/15.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,M., Friedman,P.N., Gordon,J., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
TITLE Reagents and methods useful for detecting diseases of the prostate
JOURNAL Patent: JP 2001523948-A 15 27-NOV-2001;
COMMENT ABBOTT LABORATORIES
PN JP 2001523948-A/15
PD 27-NOV-2001
PF 08-OCT-1997 JP 1998517758
PR 08-OCT-1996 US 08/727688
PI MAURICE COHEN,PAULA N FRIEDMAN,JULIAN GORDON,STEVEN C HODGES,PI MICHAEL R KLASS,JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C PI RUSSELL,STEVEN D STROUPE
PC C12Q1/68,C07K14/47//C07K16/30,G01N33/574
CC Strandedness: Single;
CC Topology: Linear;
PH Key Location/Qualifiers.
1..18
source
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 832 TGGCTGGTGGTGTGC 847
Db 3 TGGCTGGTGGTGTGC 18

RESULT 455
AR181773
LOCUS AR181773 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 235 from patent US 6335194.
ACCESSION AR181773
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VERSION      AR181773.1  GI:20223987
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Bennett,C.Frank., Ackermann,E.J., Swayze,E.E. and Cowseert,L.M.
TITLE        Antisense modulation of survivin expression
JOURNAL      Patent: US 6335194-A 235 01-JAN-2002;
FEATURES     Location/Qualifiers
             source
             1..20
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2830 ACATATATATATATAA 2845
Db      1 ACATATATATATATAA 16

RESULT 456
LOCUS      AR373540/c
DEFINITION Sequence 110 from patent US 6602713.
ACCESSION  AR373540
VERSION     AR373540.1  GI:40075669
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Wyatt,J.
TITLE        Antisense modulation of protein phosphatase 2 catalytic subunit
JOURNAL      Patent: US 6602713-A 110 05-AUG-2003;
FEATURES     Location/Qualifiers
             source
             1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2823 TATATATACATATATA 2838
Db      16 TATATATACATATATA 1

RESULT 457
LOCUS      AX926743
DEFINITION Sequence 26 from Patent WO03085133.
ACCESSION  AX926743
VERSION     AX926743.1  GI:40247078
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1
AUTHORS      Nagaraju,J.G.
TITLE        Novel fiber-pcr primers and method of identifying genotyping
JOURNAL      diverse genomes of plant and animal systems including rice
              varieties, a kit thereof
              Patent: WO 03085133-A 26 16-OCT-2003;
              Centre for DNA Fingerprinting and Diagnostics, Centre for; the
              Department of Biotechnology, Ministry of Science & Technology (IN)
FEATURES     Location/Qualifiers
             source
             1..20
             /organism="synthetic construct"

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      832 TGCGTGGTGGTCTGTC 847
Db      16 TGCGTGGTGGTCTGTC 1

RESULT 459
LOCUS      A33318
DEFINITION Synthetic APP gene exon 17 sequencing primer.
ACCESSION  A33318
VERSION     A33318.1  GI:1567858
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 22)
AUTHORS
TITLE        TEST AND MODEL FOR ALZHEIMER'S DISEASE
JOURNAL      Patent: WO 9213069-A 30 06-AUG-1992;

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2335 GTGTGTGTGTGTGTGT 2350
Db      1 GTGTGTGTGTGTGTGT 16

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="A novel FISSR-PCR primer for genotyping eukaryotes"

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2335 GTGTGTGTGTGTGTGT 2350
Db      1 GTGTGTGTGTGTGTGT 16

RESULT 458
LOCUS      BD082093/c
DEFINITION Reagents and methods useful for detecting diseases of the prostate.
ACCESSION  BD082093
VERSION     BD082093.1  GI:22627703
KEYWORDS    JP 2001523948-A/20.
SOURCE      Zea mays
ORGANISM    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 20)
Cohen,M., Friedman,P.N., Gordon,J., Hodges,S.C., Klass,M.R.,
Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
Reagents and methods useful for detecting diseases of the prostate
Patent: JP 2001523948-A 20 27-NOV-2001;
ABBOTT LABORATORIES
PN JP 2001523948-A/20
PD 27-NOV-2001
PF 08-OCT-1997 JP 1998517758
PR 08-OCT-1996 US 08/727688
PI MAURICE COHEN,PAULA N FRIEDMAN,JULIAN GORDON,STEVEN C HODGES,
PI MICHAEL R KLASS,JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C PI
RUSSELL,
PI STEVEN D STROUPE
PC C1201/68, C07K14/47//C07K16/30, G01N33/574
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
   source
   1..20
   /organism="Zea mays"
   /mol_type="genomic DNA"
   /db_xref="taxon:4577"

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      832 TGCGTGGTGGTCTGTC 847
Db      16 TGCGTGGTGGTCTGTC 1

RESULT 459
LOCUS      A33318
DEFINITION Synthetic APP gene exon 17 sequencing primer.
ACCESSION  A33318
VERSION     A33318.1  GI:1567858
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 22)
AUTHORS
TITLE        TEST AND MODEL FOR ALZHEIMER'S DISEASE
JOURNAL      Patent: WO 9213069-A 30 06-AUG-1992;

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Best Local Similarity 79.2%; Pred. No. 9.7e+02; Mismatches 5; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 3474 ATATATATAATTTATTGAGTTTTT 3497
Db 1 ATATATATTTTGTGTTTTT 24

RESULT 464
LOCUS AR478202
DEFINITION AR478202 30 bp DNA linear PAT 14-MAY-2004
ACCESSION Sequence 5 from patent US 6699661.
VERSION AR478202
KEYWORDS AR478202.1 GI:47236850
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanegawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 5 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..30
/mol_type="genomic DNA"

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATAATTTATTGAGTTTTT 3497
Db 1 ATATATATTTTGTGTTTTT 24

RESULT 465
LOCUS AR478205
DEFINITION AR478205 30 bp DNA linear PAT 14-MAY-2004
ACCESSION Sequence 8 from patent US 6699661.
VERSION AR478205
KEYWORDS AR478205.1 GI:47236853
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 8 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..30
/mol_type="genomic DNA"

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATAATTTATTGAGTTTTT 3497
Db 1 ATATATATTTTGTGTTTTT 24

RESULT 466
LOCUS BD072866
DEFINITION BD072866 30 bp DNA linear PAT 27-AUG-2002
ACCESSION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
VERSION BD072866
KEYWORDS BD072866.1 GI:22618471
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 6 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
OS Artificial Sequence
PN JP 2001286300-A/4
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKEHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA
PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FI/CS upon the hybridization of the
probe with a target
nucleic.
CC acid.
PH Key Location/Qualifiers
FT source 1..30
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATAATTTATTGAGTTTTT 3497
Db 1 ATATATATTTTGTGTTTTT 24

RESULT 467
LOCUS BD072868
DEFINITION BD072868 30 bp DNA linear PAT 27-AUG-2002
ACCESSION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
VERSION BD072868
KEYWORDS BD072868.1 GI:22618471
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 6 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY

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COMMENT
OS Artificial Sequence
PN JP 2001286300-A/6
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
/organism="synthetic construct"
/locus="genomic DNA"
/db_xref="taxon:32630"
FEATURES
source
1..30
Location/Qualifiers
/organism="synthetic construct"
/locus="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

43474 ATATATATAATTTATTGAGTTTTT 3497
||||| ||||| ||||| |||||
1 ATATATATTTTGTGTTTTT 24

RESULT 468
BD107493
LOCUS Novel quantitative polymorphism analysis method
DEFINITION
ACCESSION BD107493
VERSION BD107493.1 GI:23202311
KEYWORDS JP 2002000275-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 2 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOLOGY
COMMENT
OS Artificial Sequence
PN JP 2002000275-A/2
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12Q1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
/organism="synthetic construct"
/locus="genomic DNA"
/db_xref="taxon:32630"
FEATURES
source
1..30
Location/Qualifiers
/organism="synthetic construct"
/locus="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

43474 ATATATATAATTTATTGAGTTTTT 3497
||||| ||||| ||||| |||||
1 ATATATATTTTGTGTTTTT 24

RESULT 470
BD145025
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145025
VERSION BD145025.1 GI:27850783
KEYWORDS JP 2002119291-A/6.

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source 1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

3474 ATATATATAATTTATTGAGTTTTT 3497
||||| ||||| ||||| |||||
1 ATATATATTTTGTGTTTTT 24

RESULT 469
BD107495
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION
ACCESSION BD107495
VERSION BD107495.1 GI:23202313
KEYWORDS JP 2002000275-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 4 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOLOGY
COMMENT
OS Artificial Sequence
PN JP 2002000275-A/4
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12Q1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
/organism="synthetic construct"
/locus="genomic DNA"
/db_xref="taxon:32630"
FEATURES
source
1..30
Location/Qualifiers
/organism="synthetic construct"
/locus="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

3474 ATATATATAATTTATTGAGTTTTT 3497
||||| ||||| ||||| |||||
1 ATATATATTTTGTGTTTTT 24

RESULT 470
BD145025
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145025
VERSION BD145025.1 GI:27850783
KEYWORDS JP 2002119291-A/6.

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 30)
AUTHORS     Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
TITLE       Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
JOURNAL     Patent: JP 2002119291-A 6 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS Artificial Sequence
            PN JP 2002119291-A/6
            PD 23-APR-2002
            PF 27-APR-2001 JP 2001133529
            PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, VOICHI KAMAGATA, MASAKI
            TORIMURA,
            SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
            C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/58, G01N33/
            53, G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
            PC G01N1/28,
            PC G01N1/28
            CC The base sequence was prepared synthetically on the aim of CC
            decrease in fluorescence emission of
            a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
            hybridization of
            the probe with a target nucleic acid.
            FH Key Location/Qualifiers
            FT source 1..30
            FT /organism='Artificial Sequence'.

FEATURES
source
1..30
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATAATTTATTGAGTTTTT 3497
Db 1 ATATATATTTTGTGTTTTT 24

RESULT 472
BD145027
LOCUS
DEFINITION
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION
BD145027.1 GI:27850785
VERSION
JP 2002119291-A/8.
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
Patent: JP 2002119291-A 8 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002119291-A/8
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, VOICHI KAMAGATA, MASAKI
TORIMURA,
SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 30)
AUTHORS     Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
TITLE       Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
JOURNAL     Patent: JP 2002119291-A 6 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS Artificial Sequence
            PN JP 2002119291-A/6
            PD 23-APR-2002
            PF 27-APR-2001 JP 2001133529
            PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, VOICHI KAMAGATA, MASAKI
            TORIMURA,
            SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
            C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N1/28, G01N33/
            53, G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
            PC G01N1/28,
            PC G01N1/28
            CC The base sequence was prepared synthetically on the aim of CC
            decrease in fluorescence emission of
            a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
            hybridization of
            the probe with a target nucleic acid.
            FH Key Location/Qualifiers
            FT source 1..30
            FT /organism='Artificial Sequence'.

FEATURES
source
1..30
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATAATTTATTGAGTTTTT 3497
Db 1 ATATATATTTTGTGTTTTT 24

RESULT 472
BD166026
LOCUS
DEFINITION
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166026
VERSION
BD166026.1 GI:27871838
KEYWORDS
JP 2002191372-A/6.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL
Patent: JP 2002191372-A 6 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002191372-A/6
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, VOICHI KAMAGATA, MASAKI
TORIMURA,
SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
            C12N15/09, C12N15/00, C12Q1/68, G01N33/58, G01N33/53, G01N33/566, PC
            C12N15/00
            CC The base sequence was prepared synthetically on the aim of CC
            decrease in fluorescence emission of a nucleic acid probe CC
            labeled with
            BODIBY FL/C6 upon the hybridization of the
            probe with a target
            nucleic
            CC acid.
            CC Location/Qualifiers
            FH Key 1..30
            FT source /organism='Artificial Sequence'.
            FT Location/Qualifiers
            FT 1..30
            FT /organism='unidentified'

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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATATTTTATTGAGTTT 3497
||||| ||||| ||||| |||||
Db 1 ATATATATTTTGTGTTTGT 24

RESULT 473
BD166028
LOCUS
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166028
VERSION 30 bp DNA linear PAT 17-JAN-2003
KEYWORDS Novel nucleic acid probes, method for determining concentrations of
SOURCE JP 2002191372-A/8.
ORGANISM unidentified
unidentified
unclassified.
1 (bases 1 to 30)
REFERENCE Kuran, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,
AUTHORS Yamada, K. and Yokomaku, T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL PATENT: JP 2002191372-A 8 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
COMMENT KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002191372-A/8
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12M1/00, C12Q1/68, G01N33/58//G01N33/53, G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
CC acid. Location/Qualifiers
FH Key 1..30
FT source /organism='Artificial Sequence'.
FEATURES
source
1..30
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATATTTTATTGAGTTT 3497
||||| ||||| ||||| |||||
Db 1 ATATATATTTTGTGTTTGT 24

RESULT 474
AR074777
LOCUS
DEFINITION Sequence 74 from patent US 5955276.
ACCESSION AR074777
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VERSION AR074777.1 GI:10001530
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
TITLE Morgante, M. and Vogel, J. Marie.
JOURNAL Compound microsatellite primers for the detection of genetic
FEATURES polymorphisms
Patent: US 5955276-A 74 21-SEP-1999;
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2338 TGTGTGTGTGTGTGCACAT 2356
||||| ||||| ||||| |||||
Db 1 TGTGTGTGTGTGTATAT 19

RESULT 475
BD192775/c
LOCUS
DEFINITION Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor.
ACCESSION BD192775
VERSION 19 bp DNA linear PAT 17-JUL-2003
KEYWORDS Generation, characterization and isolation of neuroepithelial stem
SOURCE JP 2002513291-A/2.
ORGANISM Staphylococcus aureus
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Rao, M. S., Proschel, M. M. and Mujtaba, T.
TITLE Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor
JOURNAL Patent: JP 2002513291-A 2 08-MAY-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION
COMMENT PN JP 2002513291-A/2
PF 08-MAY-2002
PF 07-MAY-1998 JP 1998548581
PR 07-MAY-1997 US 08/852744, 06-MAY-1998 US 09/073881 PI
MAHENDRA S RAO, MARGOT MAYER PROSCHEL, TAHMINA MUJTABA PC
C12N5/06, C12N5/08
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source
1..19
/organism="Staphylococcus aureus"
/mol_type="genomic DNA"
/db_xref="taxon:1280"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1210 GGGGAGGGGCTGCTCGGCC 1228
||||| ||||| ||||| |||||
Db 19 GCGGAGGGGCTGCTCGGCC 1

RESULT 476
AX132173
LOCUS
DEFINITION Sequence 3391 from Patent WO0130362.
ACCESSION AX132173
VERSION AX132173.1 GI:14138478
KEYWORDS Homo sapiens (human)
SOURCE
```

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 3391 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin B1 ribozyme binding site"
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2548 GCTCGGCTCTGCTTTC 2566
Db 1 GGTGGCTCTACCTTTC 19
RESULT 477
A80994
LOCUS A80994 20 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 46 from Patent EP0918091.
ACCESSION A80994
VERSION A80994.1 GI:6731567
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kahn,A. and Chelly,J.
TITLE A gene called XLIS and the XLIS gene product, called doublecortin
and their applications
JOURNAL Patent: EP 0918091-A 46 26-MAY-1999;
INST NAT SANTE RECH MED (FR)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2973 GCAGAGACACAGGCTTTT 2991
Db 1 GCATGAGACACAGGCTCTT 19
RESULT 478
A88143
LOCUS A88143 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 291 from Patent WO9833904.
ACCESSION A88143
VERSION A88143.1 GI:6736713
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
1 (bases 1 to 20)
Brysch,W. and Schlingensiepen,K.
AUTHORS AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
TITLE
JOURNAL Patent: WO 9833904-A 291 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
Location/Qualifiers
source
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2973 GCAGAGACACAGGCTTTT 2991
Db 1 GCATGAGACACAGGCTCTT 19
RESULT 479
A90110
LOCUS A90110 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 291 from Patent EP0856579.
ACCESSION A90110
VERSION A90110.1 GI:6738624
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
1 (bases 1 to 20)
Brysch,W.D. and Schlingensiepen,K.D.
AUTHORS An antisense oligonucleotide preparation method
TITLE
JOURNAL Patent: EP 0856579-A 291 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
Location/Qualifiers
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1478 GGGCGCGCGCGCGCGG 1496
Db 1 GGGCGCGCGCGCGCGG 19
RESULT 480
A95373
LOCUS A95373 20 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 46 from Patent WO9927089.
ACCESSION A95373
VERSION A95373.1 GI:6779417
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Francis,F. and Kahn,A.
TITLE A GENE CALLED XLIS AND THE XLIS GENE PRODUCT, CALLED DOUBLECORTIN
AND THEIR PREPARATIONS
JOURNAL Patent: WO 9927089-A 46 03-JUN-1999;
INST NAT SANTE RECH MED (FR); FRANCIS FIONA (FR)
FEATURES
Location/Qualifiers
source
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2973 GCAGAGACACAGGCTTTT 2991
Db 1 GCATGAGACACAGGCTCTT 19
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source
1. .20
/organism="Rattus"
/mol_type="genomic DNA"
/db_xref="taxon:10114"

Query Match
Best Local Similarity 0.4%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3685 CTCTTCTTGGGCCAGTG 3703
Db 19 CTCTTCTTGGGCTACTG 1

RESULT 486
BD250309/c
LOCUS BD250309 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of p38 mitogen activated protein kinase
expression.
ACCESSION BD250309
VERSION BD250309.1 GI:33060079
KEYWORDS JP 2002540781-A/61.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Gaarde,W.A., Nero,P.S., McKay,R. and Popoff,I.
TITLE Antisense modulation of p38 mitogen activated protein kinase
JOURNAL Patent: JP 2002540781-A 61 03-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002540781-A/61
PD 03-DEC-2002
PF 04-APR-2000 JP 2000609429
PR 06-APR-1999 US 09/286904
PI BRETT P MONIA, WILLIAM A GAARDE, PAMELA S NERO, ROBERT MCKAY, IAN
POPOFF
PC C12N15/09, A61K31/711, A61P19/02, A61P29/00, A61P37/06,
A61P43/00
PC C12N5/10, C12N9/99, C12N15/00, C12N5/00
CC Antisense modulation of p38 mitogen activated protein kinase
expression
CQ Antisense modulation of p38 mitogen activated protein kinase
expression
FH Key location/Qualifiers
FT source 1. .20
/organism="Artificial Sequence".
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 43 GGGCCCCAGCGGCTGCAGG 61
Db 20 GTGCCGCGAGCGGCTGCAGG 2

RESULT 487
E32215/c
LOCUS E32215 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION E32215
VERSION E32215.1 GI:13021826
KEYWORDS JP 2000060559-A/17.
SOURCE Haliotis discus discus
ORGANISM Haliotis discus discus
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hideaki,T. and Masashi,S.

TITLE Method for isolating satellite sequence
PATENT: JP 2000060559-A 17 29-FEB-2000;
NATL INST OF AGROBIOLOGICAL RESOURCES
OS Haliotis discus discus
PN JP 2000060559-A/17
PD 29-FEB-2000
PR 18-AUG-1998 JP 1998232153
PC HIDAKI TAKAHASHI, MASASHI SEKINO
CC C12N15/09, C12Q1/68, C12N15/00
FH Key location/Qualifiers
FT source 1. .20
/organism="Haliotis discus discus".
FEATURES
source
1. .20
/organism="Haliotis discus discus"
/mol_type="genomic DNA"
/sub_species="discus"
/db_xref="taxon:91233"

Query Match
Best Local Similarity 0.4%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2329 GTGTGCGTGTGTGTGTGTG 2347
Db 19 GCGCGCGTGTGTGTGTGTG 1

RESULT 488
AR228858/c
LOCUS AR228858 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 65 from patent US 6448079.
ACCESSION AR228858
VERSION AR228858.1 GI:27267997
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Gaarde,W.A., Nero,P. and McKay,R.
TITLE Antisense modulation of p38 mitogen activated protein kinase
expression
JOURNAL Patent: US 6448079-A 65 10-SEP-2002;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 43 GGGCCCCAGCGGCTGCAGG 61
Db 20 GTGCCGCGAGCGGCTGCAGG 2

RESULT 489
AR271190/c
LOCUS AR271190 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 133 from patent US 6503152.
ACCESSION AR271190
VERSION AR271190.1 GI:29702493
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pelz,D.T.
TITLE Putting trainer
JOURNAL Patent: US 6503152-A 133 07-JAN-2003;

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Query Match	0.4%	Score 15.8	DB 1	Length 20
Best Local Similarity	89.5%	Pred. No. 7.6e+02		
Matches	17	Conservative	0	Mismatches 2; Indels 0; Gaps 0
QY	843	GCTGCCAGCGGAGGAGGAG 861		
DB	2	GCTGCCAGCGGAGGAGGAG 20		
RESULT 492				
AX224884/c				
LOCUS	AX224884	20 bp	DNA	linear
DEFINITION	Sequence 38 from Patent WO0161030.			
ACCESSION	AX224884			
VERSION	AX224884.1	GI:15524957		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1			
TITLE	Gray, D.M. and Bollon, A.P.			
JOURNAL	Libraries of optimum subsequence regions of mrna and genomic dna for control of gene expression			
FEATURES	Patent: WO 0161030-A 38 23-AUG-2001; Cytoclonal Pharmaceuticals, Inc. (US); University of Texas at Dallas, Dept. of Molecular and Cell Biology (US); Lab. of Experimental Carcinogenesis, National Cancer Institute/NIH (US) Location/Qualifiers			
source	1..20			
	/organism="Homo sapiens"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:9606"			
Query Match	0.4%	Score 15.8	DB 1	Length 20
Best Local Similarity	89.5%	Pred. No. 7.6e+02		
Matches	17	Conservative	0	Mismatches 2; Indels 0; Gaps 0
QY	843	GCTGCCAGCGGAGGAGGAG 861		
DB	19	GCTGCCAGCGGAGGAGGAG 1		
RESULT 493				
AX250713				
LOCUS	AX250713	20 bp	DNA	linear
DEFINITION	Sequence 5 from Patent WO0168670.			
ACCESSION	AX250713			
VERSION	AX250713.1	GI:15984451		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1			
TITLE	Lazdunski, M., Lesage, P. and Maingret, P.			
JOURNAL	Novel family of mechanically sensitive human potassium channels activated by polyunsaturated fatty acids and use thereof			
FEATURES	Patent: WO 0168670-A 5 20-SEP-2001; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR) Location/Qualifiers			
source	1..20			
	/organism="Homo sapiens"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:9606"			
misc_feature	1..20			
	/notes="Amorce deduite partir de l'intron 5 de hTAAK, amorce sens"			
Query Match	0.4%	Score 15.8	DB 1	Length 20
Best Local Similarity	89.5%	Pred. No. 7.6e+02		
Matches	17	Conservative	0	Mismatches 2; Indels 0; Gaps 0


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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 323 CTCCTCCATCTCTGGCT 341
DB 2 CTCCTCCATCTCTGGCT 20

RESULT 498
BD065656
LOCUS      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Oligonucleotide modulation of protein kinase C-eta.
ACCESSION  BD065656
VERSION     BD065656.1 GI:22611259
KEYWORDS   JP 2001511000-A/291.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Schlengensiepen,K.H. and Brysch,W.
TITLE      An antisenase oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 291 07-AUG-2001;
           BIOGHOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS Unknown

FEATURES
source
1..20
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 323 CTCCTCCATCTCTGGCT 341
DB 2 CTCCTCCATCTCTGGCT 20

RESULT 499
BD065656
LOCUS      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisenase oligonucleotide preparation method.
ACCESSION  BD065656
VERSION     BD065656.1 GI:22611259
KEYWORDS   JP 2001511000-A/291.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Schlengensiepen,K.H. and Brysch,W.
TITLE      An antisenase oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 291 07-AUG-2001;
           BIOGHOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS Unknown

PN JP 2001511000-A/291
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisenase oligonucleotide preparation method FH Key
FT Location/Qualifiers
   source 1..20
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   /organism="unidentified"
   /mol_type="genomic DNA"
   /db_xref="taxon:32644"

Query Match      0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1478 GGGCGCGCGCGCGCGG 1496
DB 1 GGGCGCGCGCGCGCGG 19

RESULT 500
BD174235/c
LOCUS      20 bp      DNA      linear      PAT 18-FEB-2003
DEFINITION Transgenic animal having drug-metabolizing enzyme and
           utilization thereof.
ACCESSION  BD174235
VERSION     BD174235.1 GI:28415574
KEYWORDS   WO 02066635-A/5.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Katsuki,M., Kamataki,T., Teranishi,Y., Ishida,M. and Kato,M.
TITLE      Transgenic animal having drug-metabolizing enzyme gene and
           utilization thereof
JOURNAL    Patent: WO 02066635-A 5 29-AUG-2002;
           GENCOM CORP,MOTOYA KATSUKI,TETSUYA KAWATAKI,YUTAKA TERANISHI,
           MITSUYOSHI ISHIDA,MINORU KATO
COMMENT     OS Artificial Sequence
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"

Query Match      0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 842 TGCTGCCAGCCGAGGAGGA 860
DB 20 TGCTGCCAGCCGAGGAGGA 2
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C12N5/10,
PC C12P21/02.C12Q1/68.G01N33/53.C12N15/00.C12N5/00 CC Primer
for analysis of human TSC gene
FH Key Location/Qualifiers
FEATURES
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    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
Query Match      0.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3404 GTTTCAGGAGGAGGCGCG 3422
    |||||
DB 21 GTTCCAGGAGGAGGCGCCAG 3

RESULT 503
AR264925
LOCUS AR264925 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 9 from patent US 6492121.
ACCESSION AR264925
VERSION AR264925.1 GI:29693312
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
        molecules, nucleic acid probes for the method, and method for
        analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 9 10-DEC-2002;
FEATURES
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    /organism="unknown"
    /mol_type="genomic DNA"
Query Match      0.4%; Score 15.8; DB 1; Length 30;
Best Local Similarity 74.1%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 ACATATTTTATTTGCTTGTCTCTTTT 3285
    |||||
DB 3 ATATATTTTCTTTTCTTTTCTTTT 29

RESULT 504
AR478206
LOCUS AR478206 30 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 9 from patent US 6699661.
ACCESSION AR478206
VERSION AR478206.1 GI:47236854
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
        molecules, nucleic acid probes for the method, and method for
        analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 9 02-MAR-2004;
FEATURES
    source
    1..30
    /organism="unknown"
    /mol_type="genomic DNA"
Query Match      0.4%; Score 15.8; DB 1; Length 30;

C12N5/10,
PC C12P21/02.C12Q1/68.G01N33/53.C12N15/00.C12N5/00 CC Primer
for analysis of human TSC gene
FH Key Location/Qualifiers
FEATURES
    source
    1..21
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
Query Match      0.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3404 GTTTCAGGAGGAGGCGCG 3422
    |||||
DB 21 GTTCCAGGAGGAGGCGCCAG 3

RESULT 503
AR264925
LOCUS AR264925 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 9 from patent US 6492121.
ACCESSION AR264925
VERSION AR264925.1 GI:29693312
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
        molecules, nucleic acid probes for the method, and method for
        analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 9 10-DEC-2002;
FEATURES
    source
    1..30
    /organism="unknown"
    /mol_type="genomic DNA"
Query Match      0.4%; Score 15.8; DB 1; Length 30;
Best Local Similarity 74.1%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 ACATATTTTATTTGCTTGTCTCTTTT 3285
    |||||
DB 3 ATATATTTTCTTTTCTTTTCTTTT 29

RESULT 504
AR478206
LOCUS AR478206 30 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 9 from patent US 6699661.
ACCESSION AR478206
VERSION AR478206.1 GI:47236854
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
        molecules, nucleic acid probes for the method, and method for
        analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 9 02-MAR-2004;
FEATURES
    source
    1..30
    /organism="unknown"
    /mol_type="genomic DNA"
Query Match      0.4%; Score 15.8; DB 1; Length 30;

E14785
LOCUS E14785 21 bp DNA linear PAT 28-JUL-1999
DEFINITION PCR primer.
ACCESSION E14785
VERSION E14785.1 GI:5709468
KEYWORDS JP 1998014570-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 21)
AUTHORS Matsuda,M. and Kamei,M.
TITLE ANTIBODY DNA
JOURNAL PATENT: JP 1998014570-A 16 20-JAN-1998;
        MATSUDA MORIHIRO, MORINAGA & CO LTD
COMMENT
    OS None
    OC Artificial sequences.
    PN JP 1998014570-A/16
    PD 20-JAN-1998
    PF 05-JUL-1996 JP 1996194095
    PI MATSUDA MORIHIRO, KAMEI MASANORI
    PC C12N15/02.C07H21/04.C07K16/12.G01N33/53.G01N33/569, PC
    GOIN33/577//A61K39/395,
    PC A61K39/395.C12N1/21.C12P21/08.C12Q1/68.(C12N15/02.C12R1:91),
    PC (C12N1/21,
    PC C12R1:19);
    CC strandedness: Single;
    CC topology: Linear;
    FH Key Location/Qualifiers
    FH
    FT source 1..21
    FT /organism="Artificial sequences".
    FT Location/Qualifiers
    1..21
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
Query Match      0.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 7.9e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGTGCAGCTGCTGGAGCT 873
    |||||
DB 1 GAGGTGCAGCTGCTGGAGTCT 21

RESULT 502
BD056548/C
LOCUS BD056548 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Method to diagnose and treat pathological conditions resulting from
        deficient ion transport.
ACCESSION BD056548
VERSION BD056548.1 GI:22602154
KEYWORDS JP 2001508291-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lifton,R.P. and Simon,D.B.
TITLE Method to diagnose and treat pathological conditions resulting from
        deficient ion transport
JOURNAL Patent: JP 2001508291-A 5 26-JUN-2001;
        YALE UNIVERSITY
COMMENT
    OS Artificial Sequence
    PN JP 2001508291-A/5
    PD 26-JUN-2001
    PF 19-DEC-1997 JP 1998530123
    PR 31-DEC-1996 US 08/778052
    PI RICHARD P LIFTON, DAVID B SIMON
    PC C12N15/09.C07K14/435.C07K16/00.C12N1/15.C12N1/19.C12N1/21, PC

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Best Local Similarity 74.1%; Pred. No. 1e+03; Mismatches 7; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 3259 AGATATTTTATTTGCTTTCCTTTT 3285
Db 3 ATATATTTTTCCTTTTTCCTTTT 29

RESULT 505
BD072870
LOCUS 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072870
VERSION 1 GI:22618473
KEYWORDS JP 2001286300-A/8.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 8 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
FEATURES
source
OS Artificial Sequence
PN JP 2001286300-A/8
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC acid.
FH Key Location/Qualifiers
FT source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"

QY 3259 AGATATTTTATTTGCTTTCCTTTT 3285
Db 3 ATATATTTTTCCTTTTTCCTTTT 29

RESULT 507
BD145029
LOCUS 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145029
VERSION 1 GI:27850787
KEYWORDS JP 2002119291-A/10.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K., and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 10 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002119291-A/10
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28

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CC The base sequence was prepared synthetically on the aim of CC
 CC decrease in fluorescence emission of
 CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
 CC hybridization of
 CC the probe with a target nucleic acid.
 FH Key Location/Qualifiers
 FT source 1..30
 FT Location/Qualifiers
 FT /organism='Artificial Sequence'.
 FT 1..30
 FT /organism="synthetic construct"
 FT /mol_type="genomic DNA"
 FT /db_xref="taxon:32630"

Query Match 0.4%; Score 15.8; DB 1; Length 30;
 Best Local Similarity 74.1%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATGCTTCTGCTTTT 3285
 Db 3 ATATATTTTCTTTCTTTT 29

RESULT 508
 BD166029 30 bp DNA linear PAT 17-JAN-2003
 LOCUS Novel nucleic acid probes, method for determining concentrations of
 DEFINITION nucleic acid by using the probes, and method for analyzing data
 obtained by the method.
 ACCESSION BD166029
 VERSION BD166029.1 GI:27871841
 KEYWORDS JP 2002191372-A/9.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Kurane, R., Kanagawa, T., Torimura, Y., Kurata, S.,
 Yamada, K., and Yokomaki, T.
 TITLE Novel nucleic acid probes, method for determining concentrations of
 nucleic acid by using the probes, and method for analyzing data
 obtained by the method
 JOURNAL Patent: JP 2002191372-A 9 09-JUL-2002;
 NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
 KANKYO ENGINEERING CO LTD
 COMMENT OS Artificial Sequence
 PN JP 2002191372-A/9
 PD 09-JUL-2002
 PF 26-SEP-2001 JP 2001295145
 PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KANAGATA, MASAKI PI
 TORIMURA,
 PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
 C12N15/09, C12M1/00, C12Q1/68, G01N33/58//G01N33/53, G01N33/566, PC
 C12N15/00
 CC The base sequence was prepared synthetically on the aim of CC
 CC decrease in fluorescence emission of a nucleic acid probe
 CC labeled with
 CC BODIBY FL/C6 upon the hybridization of the
 CC probe with a target
 CC nucleic
 CC acid.
 FH Key Location/Qualifiers
 FT source 1..30
 FT Location/Qualifiers
 FT /organism='Artificial Sequence'.
 FT 1..30
 FT /organism="unidentified"
 FT /mol_type="genomic DNA"
 FT /db_xref="taxon:32644"

Query Match 0.4%; Score 15.8; DB 1; Length 30;
 Best Local Similarity 74.1%; Pred. No. 1e+03;

Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATGCTTCTGCTTTT 3285
 Db 3 ATATATTTTCTTTCTTTT 29

RESULT 509
 AR309630 41 bp DNA linear PAT 12-JUN-2003
 LOCUS Sequence 9 from patent US 6555657.
 DEFINITION AR309630
 ACCESSION AR309630
 VERSION AR309630.1 GI:31701680
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 41)
 AUTHORS Christensen, T.
 TITLE Isolated transcription factor for an alpha-amylase promoter in
 filamentous fungi
 JOURNAL Patent: US 6555657-A 9 29-APR-2003;
 FEATURES Location/Qualifiers
 source 1..41
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 15.8; DB 1; Length 41;
 Best Local Similarity 65.7%; Pred. No. 1.2e+03;
 Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3300 TTCTATAGATTTTCTTTAGGAGATTTATTTT 3334
 Db 1 TTTTGAAGCTTTTCTTTTCTTTTCTTTT 35

RESULT 510
 BD238391 42 bp RNA linear PAT 17-JUL-2003
 LOCUS Sorting of proteins using RNA-protein fused body.
 DEFINITION BD238391
 ACCESSION BD238391.1 GI:33048161
 VERSION JP 2002536025-A/9.
 KEYWORDS synthetic construct
 SOURCE artificial sequences.
 ORGANISM 1 (bases 1 to 42)
 REFERENCE Szostak, J.W., Roberts, R.W. and Liu, R.
 AUTHORS Sorting of proteins using RNA-protein fused body
 TITLE Patent: JP 2002536025-A 9 29-OCT-2002;
 JOURNAL THE GENERAL HOSPITAL CORP
 COMMENT OS Artificial Sequence
 PN JP 2002536025-A/9
 PD 29-OCT-2002
 PF 01-FEB-2000 JP 2000598669
 PR 09-FEB-1999 US 09/247190
 PI JACK W SZOSTAK, RICHARD W ROBERTS, RIHE LIU
 PC C12N15/09, C07K7/00, C07K14/00, C12Q1/68, C12N15/00 CC
 Translation template
 FH Key Location/Qualifiers
 FT source 1..42
 /organism='Artificial Sequence'.
 /mol_type="genomic RNA"
 /db_xref="taxon:32630"

Query Match 0.4%; Score 15.8; DB 1; Length 42;
 Best Local Similarity 74.1%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3262 TATTTATTTGCTTCTTTTCTTTTCTTTT 3288

Db 37 TTTTTCATTTTTTTTTTTTTTTTTTTTCAG 11

RESULT 511
AR279817/c LOCUS linear PAT 10-APR-2003
DEFINITION Sequence 12 from patent US 6518018.
ACCESSION AR279817
VERSION AR279817.1 GI:29714962
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 42)
AUTHORS Szostak,J.W. and Roberts,R.W.
TITLE RNA-antibody fusions and their selection
JOURNAL Patent: US 6518018-A 12 11-FEB-2003;
FEATURES Location/Qualifiers
source 1..42
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.8; DB 1; Length 42;
Best Local Similarity 74.1%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3262 TATTTCATTTGCTGTCCCTTTTCAG 3288
| | | | | | | | | | | | | | | | | | | |
Db 37 TTTTTCATTTTTTTTTTTTTTTTTTTTCAG 11

RESULT 512
AR138717 LOCUS linear PAT 16-JUN-2001
DEFINITION Sequence 15 from patent US 6200754.
ACCESSION AR138717
VERSION AR138717.1 GI:14481062
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Housman,D.E., Ledley,F.D. and Stanton,V.P. Jr.
TITLE Inhibitors of alternative alleles of genes encoding products that mediate cell response to environmental changes
JOURNAL Patent: US 6200754-A 15 13-MAR-2001;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.6; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 8.3e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1294 GTCAAGATGCTGAAG 1309
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Db 6 GTGAASATGCTGAAG 21

RESULT 513
AX094910 LOCUS linear PAT 30-MAR-2001
DEFINITION Sequence 88 from Patent WO0118250.
ACCESSION AX094910
VERSION AX094910.1 GI:13511113
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Lander,B.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 88 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.6; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 8.3e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1294 GTGAAGATGCTGAAG 1309
| | | | | | | | | | | | | | | | | | | |
Db 6 GTGAASATGCTGAAG 21

RESULT 514
A39908 LOCUS linear PAT 05-MAR-1997
DEFINITION Sequence 6 from Patent EP0619372.
ACCESSION A39908
VERSION A39908.1 GI:2296126
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Banner,D., Lesslauer,W., Loetscher,H. and Stueber,D.
TITLE Tumor necrosis factor muteins
JOURNAL Patent: EP 0619372-A 6 12-OCT-1994;
HOFFMANN LA ROCHE (CH)
COMMENT Other publication CZ 9400676 950215
Other publication JP 8009976 960116
Other publication CA 2119089 940930
Other publication AU 590194 941006
Other publication CN 1099802 950308
Other publication HU 68218 950628
Other publication NZ 260146 951026
Other publication BR 9401321 941018
Other publication FI 941459 940930
Other publication NO 941142 940930.

FEATURES Location/Qualifiers
source 1..22
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3633 GAGTCTGGGCAGCTGTCCCTTG 3654
| | | | | | | | | | | | | | | | | | | |
Db 1 GAGTCTGGGCAGCTGTACTTTG 22

RESULT 515
AR036420/c LOCUS linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5872214.
ACCESSION AR036420
VERSION AR036420.1 GI:5953088
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclasiied.
REFERENCE 1 (bases 1 to 22)
AUTHORS Seizinger,B.R., Klev,N.A. and Bianchi,A.B.

<p>TITLE NF2 isoforms</p> <p>JOURNAL Patent: US 5872214-A 12 16-FEB-1999;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>Db</p> <p>1 CCCCACTCTCACCTATGTCCTCC 22</p> <p>RESULT 518</p> <p>LOCUS I29861/c</p> <p>DEFINITION Sequence 12 from patent US 5578462.</p> <p>ACCESSION I29861</p> <p>VERSION I29861.1 GI:1820652</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 22)</p> <p>AUTHORS Seizinger,B.R., Kley,N.A. and Bianchi,A.B.</p> <p>TITLE NF2 isoforms</p> <p>JOURNAL Patent: US 5578462-A 12 26-NOV-1996;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 850 GCCGAGGAGGAGCTGTGGAGG 871</p> <p>Db</p> <p>22 GCTGAAGAGGAGCTGTTCAGG 1</p> <p>RESULT 519</p> <p>LOCUS I34465</p> <p>DEFINITION Sequence 6 from patent US 5597899.</p> <p>ACCESSION I34465</p> <p>VERSION I34465.1 GI:1825256</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 22)</p> <p>AUTHORS Banner,D., Lesslauer,W., Lotscher,H. and Stuber,D.</p> <p>TITLE Tumor necrosis factor muteins</p> <p>JOURNAL Patent: US 5597899-A 6 28-JAN-1997;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 1803 CQCTGGTCTTTGGGTCCTG 1824</p> <p>Db</p> <p>22 CTTGAGTCTCTTTGGGACCTG 1</p> <p>RESULT 517</p> <p>LOCUS CQ812601</p> <p>DEFINITION Sequence 5 from Patent WO2004037281.</p> <p>ACCESSION CQ812601</p> <p>VERSION CQ812601.1 GI:47602071</p> <p>KEYWORDS</p> <p>SOURCE synthetic construct</p> <p>ORGANISM synthetic construct</p> <p>REFERENCE 1</p> <p>AUTHORS Ozog,M.A., Bechberger,J. and Naus,C.</p> <p>TITLE Methods for neuroprotection</p> <p>JOURNAL Patent: WO 2004037281-A 5 06-MAY-2004;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="synthetic construct"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:32630"</p> <p>/note="Primer"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 1119 CCCACGCTGGCCATGTCCTCC 1140</p> <p>Db</p> <p>22 GCTGAAGAGGAGCTGTTCAGG 1</p> <p>RESULT 520</p> <p>LOCUS AX252963</p> <p>DEFINITION Sequence 6 from Patent WO0168900.</p> <p>ACCESSION AX252963</p> <p>VERSION AX252963.1 GI:15986217</p> <p>KEYWORDS</p> <p>SOURCE synthetic construct</p> <p>ORGANISM synthetic construct</p> <p>REFERENCE 1</p> <p>AUTHORS Walcher,M., Wagner,M. and Snaidr,J.</p> <p>TITLE Method for specifically detecting microorganisms by polymerase chain reaction</p>
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JOURNAL Patent: WO 0168900-A 6 20-SEP-2001;
FEATURES Vermicon AG (DE)
source Location/Qualifiers
1. .22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen Sequenz:
Oligonukleotidprimer"

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2328 TGTGTCGTGTGTGTGTGTG 2349
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Db 1 TGTGTCGTGTGTGTATTGTG 22

RESULT 521
AX367061 22 bp DNA linear PAT 16-FEB-2002
LOCUS
DEFINITION Sequence 20 from Patent WO0147859.
ACCESSION AX367061
VERSION AX367061.1 GI:18855281
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and
TITLE Isolated nucleic acid molecules encoding cancer associated
antigens, the antigens per se, and uses thereof
JOURNAL Patent: WO 0147959-A 20 05-JUL-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; MEMORIAL
SLOAN-KETTERING CANCER CENTER (US) ; Cornell Research Foundation
(US)
FEATURES
source Location/Qualifiers
1. .22
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2608 CAAAGCTGAGCCTGCAGGGAAG 2629
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Db 1 CAAAGCAGAGCCTCCGAGAG 22

RESULT 522
AX740255 22 bp DNA linear PAT 10-MAY-2003
LOCUS
DEFINITION Sequence 11 from Patent EP1300146.
ACCESSION AX740255
VERSION AX740255.1 GI:30523429
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Hilberg,F., Brandstetter,I., van Meel,J., Bette,P. and Kleemann,R.
TITLE Pharmaceutical composition for the treatment of animal mammary
tumors
JOURNAL Patent: EP 1300146-A 11 09-APR-2003;
Boehringer Ingelheim International GmbH (DE)
FEATURES
source Location/Qualifiers
1. .22
/organism="synthetic construct"

JOURNAL Patent: WO 0168900-A 6 20-SEP-2001;
FEATURES Vermicon AG (DE)
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen Sequenz:
Oligonukleotidprimer"

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1748 TGAAGTGGATGGCGCTGAGGC 1769
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Db 1 TCAAGTGGATGGCGCTGGAGTC 22

RESULT 523
AX743831 22 bp DNA linear PAT 14-MAY-2003
LOCUS
DEFINITION Sequence 11 from Patent WO03030910.
ACCESSION AX743831
VERSION AX743831.1 GI:30722583
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Hilberg,F., Brandstetter,I., Bette,P., Kleemann,R. and van Meel,J.
TITLE Pharmaceutical composition for the treatment of disorders of
non-human mammals
JOURNAL Patent: WO 03030910-A 11 17-APR-2003;
Boehringer Ingelheim International GmbH (DE)
FEATURES
source Location/Qualifiers
1. .22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1748 TGAAGTGGATGGCGCTGAGGC 1769
||||| ||||| ||||| |||||
Db 1 TCAAGTGGATGGCGCTGGAGTC 22

RESULT 524
AX937575 22 bp DNA linear PAT 06-JAN-2004
LOCUS
DEFINITION Sequence 55 from Patent EP1361433.
ACCESSION AX937575
VERSION AX937575.1 GI:40713615
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Yanai,Y.C., Yamamoto,S.C., Yamamoto,K.C. and Ikegami,H.C.
TITLE Method for estimating therapeutic efficacy of tumor necrosis factor
(TNF)
JOURNAL Patent: EP 1361433-A 55 12-NOV-2003;
KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)
FEATURES
source Location/Qualifiers
1. .22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide used as primer for PCR detection of
ERK1 mRNA"

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 855 GGAGGAGCTGTGGAGGCTGAC 876
Db 1 GCAGGACCTGTGGAGGCTGAC 22

RESULT 525
A95626/c
LOCUS 17 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 28 from Patent WO9925815.
ACCESSION A95626
VERSION A95626.1 GI:6779563
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 17)
AUTHORS Herrmann, B. and Kispert, A.
TITLE NUCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATIONS
JOURNAL THEREOF
PATENT: WO 9925815-A 28 27-MAY-1999;
HERRMANN BERNHARD (DE); MAX PLANCK GESELLSCHAFT (DE)

FEATURES
source 1..17
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32844"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 GTGAAGTGGATGGGCC 1763
Db 17 GTGAAGTGGATGGCAC 1

RESULT 526
AR023742
LOCUS 17 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 24 from patent US 5795726.
ACCESSION AR023742
VERSION AR023742.1 GI:3977036
KEYWORDS diabetes
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Glucksmann, M. Alexandra.
TITLE Methods for identifying compounds useful in treating type II diabetes
JOURNAL Patent: US 5795726-A 24 18-AUG-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 54 GCTGCAGGTGCTGAATG 70
Db 1 GCTGCAGGTGCTGAATG 17

RESULT 527
AR036967
LOCUS 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 21 from patent US 5800998.
ACCESSION AR036967
VERSION AR036967.1 GI:5954823
KEYWORDS diabetes
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Glucksmann, M. Alexandra.
TITLE Assays for diagnosing type II diabetes in a subject
JOURNAL Patent: US 5800998-A 21 01-SEP-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 54 GCTGCAGGTGCTGAATG 70
Db 1 GCTGCAGGTGCTGAATG 17

RESULT 528
BD199067
LOCUS 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
ACCESSION BD199067
VERSION BD199067.1 GI:33008837
KEYWORDS JP 2002509721-A/2093.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P. A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J. A.
TITLE Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 2093 02-APR-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/2093
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions. CC
concerning molecule
CC participating in vasculogenic response
PH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FT Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 ACAGGACCTGGCTGCC 1635
Db 1 ACAGGACCTGGCTGCC 17

RESULT 529
BD226525/c


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LOCUS       BD226525               17 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION  Method and probes for the detection of chromosome aberrations.
ACCESSION   BD226525
VERSION     BD226525.1 GI:33036295
KEYWORDS    JP 2002513587-A/71.
SOURCE      synthetic construct
            artificial sequences.
ORGANISM    1 (bases 1 to 17)
REFERENCE   1 (bases 1 to 17)
AUTHORS     Dongen,J.J.M.V., Pluzek,K.J., Nielsen,K.V. and Adelhorst,K.
TITLE       Method and probes for the detection of chromosome aberrations
JOURNAL     Patent: JP 2002513587-A 71 14-MAY-2002;
            DAKO AS
COMMENT     OS Artificial Sequence
            PN JP 2002513587-A/71
            PD 14-MAY-2002
            PE 04-MAY-1999 JP 2000547260
            PR 04-MAY-1998 DK 0615/98
            PI JACOBUS JOHANNES MARIA VAN DONGEN,KARL JOHAN PLUZEK,KIRSTEN PI
               VANG NIELSEN,
            PI KIM ADELHORST
            PC C12N15/09,C07H21/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
            Description of Artificial Sequence:PNA probe, HER-2, position CC
            2776-2760
FH Key      Location/Qualifiers
FT source   1..17
FEATURES    Location/Qualifiers
            1..17
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 AGACTTCGGGCTGGCCCC 1693
Db 17 AGACTTCGGGCTGGCTC 1

RESULT 530
LOCUS       CQ623256               17 bp    DNA    linear    PAT 02-FEB-2004
DEFINITION  Sequence 7996 from Patent WO0192524.
ACCESSION   CQ623256
VERSION     CQ623256.1 GI:41673474
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE       Myosin-like gene expressed in human heart and muscle
JOURNAL     Patent: WO 0192524-A 7996 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1992 CACCTTCAGCAGCTGG 2008
Db 1 CACCATCAAGCAGCTGG 17

LOCUS       BD226525               17 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION  Method and probes for the detection of chromosome aberrations.
ACCESSION   BD226525
VERSION     BD226525.1 GI:33036295
KEYWORDS    JP 2002513587-A/71.
SOURCE      synthetic construct
            artificial sequences.
ORGANISM    1 (bases 1 to 17)
REFERENCE   1 (bases 1 to 17)
AUTHORS     Dongen,J.J.M.V., Pluzek,K.J., Nielsen,K.V. and Adelhorst,K.
TITLE       Method and probes for the detection of chromosome aberrations
JOURNAL     Patent: JP 2002513587-A 71 14-MAY-2002;
            DAKO AS
COMMENT     OS Artificial Sequence
            PN JP 2002513587-A/71
            PD 14-MAY-2002
            PE 04-MAY-1999 JP 2000547260
            PR 04-MAY-1998 DK 0615/98
            PI JACOBUS JOHANNES MARIA VAN DONGEN,KARL JOHAN PLUZEK,KIRSTEN PI
               VANG NIELSEN,
            PI KIM ADELHORST
            PC C12N15/09,C07H21/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
            Description of Artificial Sequence:PNA probe, HER-2, position CC
            2776-2760
FH Key      Location/Qualifiers
FT source   1..17
FEATURES    Location/Qualifiers
            1..17
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 AGACTTCGGGCTGGCCCC 1693
Db 17 AGACTTCGGGCTGGCTC 1

RESULT 530
LOCUS       CQ623256               17 bp    DNA    linear    PAT 02-FEB-2004
DEFINITION  Sequence 7996 from Patent WO0192524.
ACCESSION   CQ623256
VERSION     CQ623256.1 GI:41673474
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE       Myosin-like gene expressed in human heart and muscle
JOURNAL     Patent: WO 0192524-A 7996 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1992 CACCTTCAGCAGCTGG 2008
Db 1 CACCATCAAGCAGCTGG 17

LOCUS       AR188722               17 bp    DNA    linear    PAT 20-APR-2002
DEFINITION  Sequence 4210 from patent US 6346398.
ACCESSION   AR188722
VERSION     AR188722.1 GI:20234687
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 4210 12-FEB-2002;
            JOURNAL Location/Qualifiers
            FEATURES 1..17
            source /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1609 AAGTGCATCCACAGGGA 1625
Db 1 AAGTGTATCCACAGGGA 17

RESULT 532
LOCUS       AR188754               17 bp    DNA    linear    PAT 20-APR-2002
DEFINITION  Sequence 4242 from patent US 6346398.
ACCESSION   AR188754
VERSION     AR188754.1 GI:20234719
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 4242 12-FEB-2002;
            JOURNAL Location/Qualifiers
            FEATURES 1..17
            source /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1798 AGTGACGTCTGCTCCTT 1814
Db 1 AGTGACGTCTGCTCCTT 17

RESULT 533
LOCUS       AR190296               17 bp    DNA    linear    PAT 20-APR-2002
DEFINITION  Sequence 5784 from patent US 6346398.
ACCESSION   AR190296
VERSION     AR190296.1 GI:20236261
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 5784 12-FEB-2002;
            JOURNAL Location/Qualifiers
            FEATURES 1..17
            source /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1992 CACCTTCAGCAGCTGG 2008
Db 1 CACCATCAAGCAGCTGG 17

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JOURNAL Patent: US 6346398-A 5784 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1609 AAGTGCATCCACAGGGA 1625
Db 1 AAGTGTATCCACAGGGA 17
|||||
|

RESULT 534
AR286400 17 bp RNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 772 from patent US 6528640.
ACCESSION AR286400
VERSION AR286400.1 GI:29723996
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
TITLE Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
JOURNAL Synthetic ribonucleic acids with RNase activity
PATENT: US 6528640-A 772 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1678 GACTTCGGGCTGGCCG 1694
Db 1 GACTTCGGGCTGGCTCG 17
|||||
|

RESULT 535
AR324575 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 1977 from patent US 6566127.
ACCESSION AR324575
VERSION AR324575.1 GI:33710383
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1977 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1609 AAGTGCATCCACAGGGA 1625
Db 1 AAGTGTATCCACAGGGA 17
|||||
|

JOURNAL Patent: US 6346398-A 5784 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1798 AGTGACGTCGTCCTT 1814
Db 1 AGTGACGTCGTCCTTT 17
|||||
|

RESULT 536
AR324607 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 2009 from patent US 6566127.
ACCESSION AR324607
VERSION AR324607.1 GI:33710415
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2009 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1798 AGTGACGTCGTCCTT 1814
Db 1 AGTGACGTCGTCCTTT 17
|||||
|

RESULT 537
AR329327 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 6729 from patent US 6566127.
ACCESSION AR329327
VERSION AR329327.1 GI:33715135
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6729 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1610 AGTGATCCACAGGAC 1626
Db 1 AGTGATCCACAGGAC 17
|||||
|

RESULT 538
AR329328 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 6730 from patent US 6566127.
ACCESSION AR329328
VERSION AR329328.1 GI:33715136
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6730 20-MAY-2003;
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FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1611 GTGATCCACAGGAC 1627
Db 1 GTGATCCACAGGAC 17

RESULT 539
AR329329
LOCUS AR329329 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6731 from patent US 6566127.
ACCESSION AR329329
VERSION AR329329.1 GI:33715137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6731 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1613 GCATCCACAGGACCTG 1629
Db 1 GTATCCACAGGACCTG 17

RESULT 540
AR329360
LOCUS AR329360 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6762 from patent US 6566127.
ACCESSION AR329360
VERSION AR329360.1 GI:33715168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6762 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1799 GTGACGCTGGTCTTT 1815
Db 1 GTGACGCTGGTCTTT 17

RESULT 541

AR398390
LOCUS AR398390 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 771 from patent US 6617438.
ACCESSION AR398390
VERSION AR398390.1 GI:40136163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matelic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 771 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCG 1694
Db 1 GACTTCGGCTGGCTCG 17

RESULT 542
AR429225/c
LOCUS AR429225 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 28 from patent US 6642369.
ACCESSION AR429225
VERSION AR429225.1 GI:40189374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herrmann,B., Koschorz,B. and Kispert,A.
TITLE Nucleic acids involved in the responder phenotype and applications thereof
JOURNAL Patent: US 6642369-A 28 04-NOV-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 GTGAAGTGGATGCGCC 1763
Db 17 GTGAAGTGGATGCGACC 1

RESULT 543
AR464319
LOCUS AR464319 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7996 from patent US 6686188.
ACCESSION AR464319
VERSION AR464319.1 GI:42699376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7996 03-FEB-2004;

QY	2206	GGTCCCAACAATGTGA	2222
Db	1	GATCCCAACAATGTGA	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1992	CACCTTCAAGCAGCTGG	2008
Db	1	CACCATCAAGCAGCTGG	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	546	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	545	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	546	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	545	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	546	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	545	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	546	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	545	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	546	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	545	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	546	GGGGCTGCCGGCAACC	562
Db	1	GGGGCTGCCGGCAACC	17
FEATURES	Location/Qualifiers		
source	1..17		
Query Match	0.4%; Score 15.4; DB 1; Length 17;		
Best Local Similarity	94.1%; Pred. No. 7.4e+02;		
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	545	GGGGCTGCCGGCAACC	562
Db			

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 GTGAAGTGGATGGCGCC 1763
Db 17 GTGAAGTGGATGGCGCC 1

RESULT 548
LOCUS AR241816 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 104 from patent US 6472154.
ACCESSION AR241816
VERSION AR241816.1 GI:27287628
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 104 29-OCT-2002;
FEATURES
source
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATA 2840
Db 18 ATATATATATATATATA 2

RESULT 549
A95063/c
LOCUS A95063 19 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 5 from Patent WO9929866.
ACCESSION A95063
VERSION A95063.1 GI:6779218
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Bowler,C. and Mustilli,A.C.
TITLE NUCLEOTIDE SEQUENCES ENCODING THE TOMATO LIGHT HYPERSENSITIVE PHENOTYPE, ENCODED PROTEINS AND USES THEREOF
JOURNAL Patent: WO 9929866-A 5 17-JUN-1999;
BOWLER CHRIS (GB); STAZIONE ZOOL ANTON DOHRN (IT)
FEATURES
source
Location/Qualifiers
1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1291 GCCGTGAAGATGCTGAA 1307
Db 19 GCCGTGAAGATGATGAA 3

RESULT 550
LOCUS I26329 19 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 21 from patent US 5558988.
ACCESSION I26329
VERSION I26329.1 GI:1606199
KEYWORDS
SOURCE
ORGANISM

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AR072218
LOCUS AR072218 19 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 21 from patent US 5948611.
ACCESSION AR072218
VERSION AR072218.1 GI:9998982
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvaniemi,P., Baldwin,C., Hopkinson,I. and Ahmad,N.Nina.
TITLE Primers and methods for detecting mutations in the procollagen II gene (COL2A1) that indicate a genetic predisposition for a COL2A1-associated disease
JOURNAL Patent: US 5948611-A 21 07-SEP-1999;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2975 AGAGGACCAGGCGCTTTT 2991
Db 2 AGATGACCAGGCGCTTTT 18

RESULT 551
CQ802798/c
LOCUS CQ802798 19 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 36 from Patent WO2004035820.
ACCESSION CQ802798
VERSION CQ802798.1 GI:47109818
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kalm,E., Reinsch,N. and Schwarz,S.
TITLE Genetic markers for diagnosing the splay leg phenotype expression in domestic animals, breeding animals, and working animals
JOURNAL Patent: WO 2004035820-A 36 29-APR-2004;
FBF- Foerderverein Biologieforschung der Deutschen Schwein eproduktion e.V. (DE)
FEATURES
source
Location/Qualifiers
1..19
/organism="Sus scrofa"
/mol_type="unassigned DNA"
/db_xref="taxon:9823"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3212 CCCTCCAGCCTAAAG 3228
Db 19 CCCTCCAGCCTGAAAG 3

RESULT 552
LOCUS I26329 19 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 21 from patent US 5558988.
ACCESSION I26329
VERSION I26329.1 GI:1606199
KEYWORDS
SOURCE
ORGANISM

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REFERENCE 1 (bases 1 to 19)
AUTHORS Prockop,D.J., Ala-Kokko,L. and Ritvaniemi,P.
TITLE Primers and methods for detecting mutations in the procollagen II
        gene that indicate a genetic predisposition for osteoarthritis
JOURNAL Patent: US 558988-A 21 24-SEP-1996;
FEATURES Location/Qualifiers
source
    1..19
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2975 AGAGGACGAGGCTTTT 2991
    ||| ||||| ||||| |||||
Db 2 AGATGACGAGGCTTTT 18

RESULT 553
AR222435/c
LOCUS AR222435 19 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 5 from patent US 6429299.
ACCESSION AR222435
VERSION AR222435.1 GI:23329965
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Bowler,C. and Mustilli,A.C.
TITLE Nucleotide sequences encoding the tomato light hypersensitive
        phenotype, encoded proteins and uses thereof
JOURNAL Patent: US 6429299-A 5 06-AUG-2002;
FEATURES Location/Qualifiers
source
    1..19
    /organism="unknown"
    /mol_type="genomic DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1291 GCCGTGAAGATGCTGAA 1307
    ||| ||||| ||||| |||||
Db 19 GCCGTGAAGATGATGAA 3

RESULT 554
BD102783/c
LOCUS BD102783 19 bp DNA linear PAT 27-AUG-2002
DEFINITION Nucleotide sequence encoding tomato photosensitive phenotype,
        protein encoded thereby and utilization thereof.
ACCESSION BD102783
VERSION BD102783.1 GI:22648357
KEYWORDS JP 2001526034-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Bowler,C. and Mustilli,A.C.
TITLE Nucleotide sequence encoding tomato photosensitive phenotype,
        protein encoded thereby and utilization thereof
JOURNAL Patent: JP 2001526034-A 4 18-DEC-2001;
        STAZIONE ZOOLOGICA ANTON DOHRN
COMMENT OS Artificial Sequence
        PN JP 2001526034-A/4
        PD 18-DEC-2001
        PF 07-DEC-1998 JP 2000524438
        PR 09-DEC-1997 IT RM97A000760
        PI CHLIS BOWLER,ANNA CHIARA MUSTILLI
        PC C12N15/09,A01H5/00,C07K14/415,C12N15/00
        CC Nucleotide sequence encoding tomato photosensitive phenotype,

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CC protein
CC encoded thereby and utilization thereof
FH Key Location/Qualifiers
FT source
    1..19
    /organism="Artificial Sequence".
FEATURES Location/Qualifiers
source
    1..19
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1291 GCCGTGAAGATGCTGAA 1307
    ||| ||||| ||||| |||||
Db 19 GCCGTGAAGATGATGAA 3

RESULT 555
AR373540
LOCUS AR373540 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 110 from patent US 6602713.
ACCESSION AR373540
VERSION AR373540.1 GI:40075669
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt,J.
TITLE Antisense modulation of protein phosphatase 2 catalytic subunit
        beta expression
JOURNAL Patent: US 6602713-A 110 05-AUG-2003;
FEATURES Location/Qualifiers
source
    1..20
    /organism="unknown"
    /mol_type="genomic DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3465 TATATATCTATATATAT 3481
    ||| ||||| ||||| |||||
Db 1 TATATATGTATATATAT 17

RESULT 556
AR074776/c
LOCUS AR074776 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 73 from patent US 5955276.
ACCESSION AR074776
VERSION AR074776.1 GI:10001529
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante,M. and Vogel,J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
        polymorphisms
JOURNAL Patent: US 5955276-A 73 21-SEP-1999;
FEATURES Location/Qualifiers
source
    1..20
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2316 TCTGTGTGTGTGTGT 2332
Db 17 TATGTGTGTGTGTGT 1
RESULT 557
AR103195/c
LOCUS AR103195 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 89 from patent US 6087160.
ACCESSION AR103195
VERSION AR103195.1 GI:12814783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Yuan,J. and Miura,M.
TITLE Programmed cell death genes and proteins
JOURNAL Patent: US 6087160-A 89 11-JUL-2000;
FEATURES
    Location/Qualifiers
    1..20
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1353 GGAGATGATGAGATGA 1369
Db 20 GGAGTTGATGAGATGA 4
RESULT 558
AR199773/c
LOCUS AR199773 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 34 from patent US 6355482.
ACCESSION AR199773
VERSION AR199773.1 GI:20249847
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Freier,S.M.
TITLE Antisense inhibition of integrin beta 4 binding protein expression
JOURNAL Patent: US 6355482-A 34 12-MAR-2002;
FEATURES
    Location/Qualifiers
    1..20
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 721 ACCACCGACAGGAGCT 737
Db 20 ACCACCGACAGGAGCT 4
RESULT 559
AR214196/c
LOCUS AR214196 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 4 from patent US 6406890.
ACCESSION AR214196
VERSION AR214196.1 GI:23311726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mueller,M.W.
TITLE Process for the amplification of nucleic acid
JOURNAL Patent: US 6406890-A 4 18-JUN-2002;
FEATURES
    Location/Qualifiers
    1..20
    /organism="unknown"
    /mol_type="genomic DNA"
Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2835 TATATATATAACATATA 2851
Db 19 TTTATATATAACATATA 3
RESULT 560
AR214200/c
LOCUS AR214200 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6406890.
ACCESSION AR214200
VERSION AR214200.1 GI:23311730
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mueller,M.W.
TITLE Process for the amplification of nucleic acid
JOURNAL Patent: US 6406890-A 8 18-JUN-2002;
FEATURES
    Location/Qualifiers
    1..20
    /organism="unknown"
    /mol_type="genomic DNA"
Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2835 TATATATATAACATATA 2851
Db 19 TTTATATATAACATATA 3
RESULT 561
AX370498
LOCUS AX370498 20 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 17 from Patent WO0196371.
ACCESSION AX370498
VERSION AX370498.1 GI:18857540
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Broenner,G., Ciosek,T., Dohrmann,C., Haeder,T. and Rothe,M.
TITLE Adipose-related gene
JOURNAL Patent: WO 0196371-A 17 20-DEC-2001;
FEATURES
    Location/Qualifiers
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 254 ACAAGAAGCTGCTGCC 270
Db 4 ACAAGAAGCTGCTGCC 20
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RESULT 562
AX527818
LOCUS          AX527818          20 bp    DNA          linear          PAT 21-NOV-2002
DEFINITION     Sequence 72 from Patent WO0230974.
ACCESSION      AX527818
VERSION        AX527818.1  GI:25172322
KEYWORDS       synthetic construct
SOURCE          synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE      1
AUTHORS         Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Burgess,C.E., Mishra,V.,
                Kekuda,R., Li,L., Padigaru,M., Shimkets,R.A., Zerhusen,B.D.,
                Spytek,K.A., Edinger,S., Gerlach,V., Macdougall,J., Stone,D.,
                Gunther,E. and Ellerman,K.
TITLE           Proteins and nucleic acids encoding same
JOURNAL         Patent: WO 0230974-A 72 18-APR-2002;
                Curagen Corporation (US)
FEATURES       Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="oligonucleotide primer"
Query Match    0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 854 AGGAGGAGCTGTGGAG 870
Db 2 AGGAGGAGCTGTGGAG 18

RESULT 563
AX601143/c
LOCUS          AX601143          20 bp    DNA          linear          PAT 17-FEB-2003
DEFINITION     Sequence 238 from Patent WO02092851.
ACCESSION      AX601143
VERSION        AX601143.1  GI:28401216
KEYWORDS       synthetic construct
SOURCE          synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE      1
AUTHORS         Binns,M.M. and Swinburne,J.E.
TITLE           Genetic typing
JOURNAL         Patent: WO 02092851-A 238 21-NOV-2002;
                ANIMAL HEALTH TRUST (GB) ; The British Horseracing Board (GB)
FEATURES       Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Primer"
Query Match    0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 594 CCACTGCAAGGTGTACA 610
Db 20 CCACTGCAAGGTGTACA 4

RESULT 564
BD144226
LOCUS          BD144226          20 bp    DNA          linear          PAT 17-JAN-2003
DEFINITION     Method for examining allergic diseases.
ACCESSION      BD144226
VERSION        BD144226.1  GI:27849984
KEYWORDS       JP 2002119281-A/14.

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SOURCE          synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE      1  (bases 1 to 20)
AUTHORS         Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T. and Tsujimoto,K.
TITLE           Method for examining allergic diseases
JOURNAL         Patent: JP 2002119281-A 14 23-APR-2002;
                GENOX RESEARCH INC.THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT         OS Artificial Sequence
                PN JP 2002119281-A/14
                PD 23-APR-2002
                PF 11-OCT-2000  JP 2000311193
                PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA,KOZO
                PC TSUJIMOTO
                PC C12N15/09,A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P37/08,
                PC C12N5/10,
                PC C12Q1/02,C12Q1/68,G01N33/15,G01N33/50// (C12N15/09,C12R1:91),
                PC (C12N5/10,C12R1:91), (C12Q1/02,C12R1:91), C12N15/00,C12N5/00, PC
                PC (C12N15/00,C12R1:91), (C12N5/00,C12R1:91)
                CC Description of Artificial Sequence:an artificially synthesized
                Description of Artificial Sequence:an artificially synthesized

CC sequence     primer
CC key          Location/Qualifiers
FH key         1..20
FT source      /organism='Artificial Sequence'.
FT             Location/Qualifiers
             1..20
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

Query Match    0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1874 TGGAGGAGCTCTTCAAG 1890
Db 1 TGGAGGAGCTCTTCAAG 17

RESULT 565
AR177588
LOCUS          AR177588          21 bp    DNA          linear          PAT 17-DEC-2001
DEFINITION     Sequence 28 from patent US 632934.
ACCESSION      AR177588
VERSION        AR177588.1  GI:17919943
KEYWORDS       Unknown.
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE      1  (bases 1 to 21)
AUTHORS         Johnson,G.I.
TITLE           Human MEKK proteins, corresponding nucleic acid molecules, and uses
                therefor
JOURNAL         Patent: US 6312934-A 28 06-NOV-2001;
FEATURES       Location/Qualifiers
                source
                1..21
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match    0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2001 GCAGCTGTGGAGGACC 2017
Db 1 GGAGCTGTGGAGGACC 17

RESULT 566
CQ788487/c
LOCUS          CQ788487          21 bp    DNA          linear          PAT 24-MAR-2004

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DEFINITION Sequence 64 from Patent WO2004020619.
ACCESSION CQ788487
VERSION CQ788487.1 GI:45723252
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Constien,R., Mudde,G., Schroeder,A., Yu,P. and Hanke,P.
TITLE Modified phospholipase c-gamma-2, expression products, and
non-human animal models comprising said genes, and therapeutic uses
JOURNAL Patent: WO 2004020619-A 64 11-MAR-2004;
Ingenium Pharmaceuticals AG (DE)
FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer picg2-48"
Query Match 0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1559 TGTCTGTGCTACACAG 1575
DB 18 TGTCTGTGCTACACAG 2

RESULT 567
AX146144
LOCUS AX146144 21 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 335 from Patent WO0134840.
ACCESSION AX146144
VERSION AX146144.1 GI:14284662
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
TITLE Genetic compositions and methods
JOURNAL Patent: WO 0134840-A 335 17-MAY-2001;
GLAXO GROUP LIMITED (GB) ; Affymetrix, Inc. (US)
FEATURES
source
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
variation 1..21
/note="n' represents a polymorphic base"
Query Match 0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1820 TCCTGCTCTGGGAGATCT 1837
DB 4 TCCTCTNTGGGAGATCT 21

RESULT 568
AX539564
LOCUS AX539564 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 351 from Patent WO02059142.
ACCESSION AX539564
VERSION AX539564.1 GI:25273096
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Brekke,O.H., Stacy,J. and Kausmally,L.
TITLE Product
JOURNAL Patent: WO 03095491-A 5 20-NOV-2003;
Affitech AS (NO) ; Brekke, Ole Henrik (NO)
FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"

AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
JOURNAL Patent: WO 02059142-A 351 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="r = g or a"
Query Match 0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGATGGCACAGGCTGGTG 21
DB 2 GGGTGGCACRGTGCTGGTG 20

RESULT 569
AX539565/c
LOCUS AX539565 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 352 from Patent WO02059142.
ACCESSION AX539565
VERSION AX539565.1 GI:25273098
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
JOURNAL Patent: WO 02059142-A 352 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="y = c or t"
Query Match 0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGATGGCACAGGCTGGTG 21
DB 20 GGGTGGCACRGTGCTGGTG 2

RESULT 570
AX955606
LOCUS AX955606 21 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 5 from Patent WO03095491.
ACCESSION AX955606
VERSION AX955606.1 GI:40784264
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Brekke,O.H., Stacy,J. and Kausmally,L.
TITLE Product
JOURNAL Patent: WO 03095491-A 5 20-NOV-2003;
Affitech AS (NO) ; Brekke, Ole Henrik (NO)
FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 21;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGGTGAGGCT 873
Db 1 GAGGTGACGTGKTGGAGWCY 21

RESULT 571
AX042549
LOCUS AX042549 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 115 from Patent WO0065088.
ACCESSION AX042549
VERSION AX042549.1 GI:11341157
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 115 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="DPBI Homozygote primer sequence"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3264 TTTTATTTGCTTGTCTCTTTTCCAG 3288
Db 1 TTTTATTTTGTCTTGTCTCTTTTCCAG 25

RESULT 572
AX043230
LOCUS AX043230 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 796 from Patent WO0065088.
ACCESSION AX043230
VERSION AX043230.1 GI:11341838
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 796 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="DPBI Heterozygote Primer Sequence"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3264 TTTTATTTGCTTGTCTCTTTTCCAG 3288
Db 1 TTTTATTTTGTCTTGTCTCTTTTCCAG 25

RESULT 573
AX351715/c
LOCUS AX351715 30 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 11 from Patent WO0193902.
ACCESSION AX351715
VERSION AX351715.1 GI:18616998
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klimman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 11 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 30;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3310 TTTTCTTTTAGGAGATTATTTT 3334
Db 29 TTTTCTTTTAAAGCTTTT 5

RESULT 574
A08914/c
LOCUS A08914 31 bp DNA linear PAT 02-SEP-1993
DEFINITION H.sapiens (haplotype 3, allele MS32, isolate Mormon, serial number 2) minisatellite sequence.
ACCESSION A08914
VERSION A08914.1 GI:411836
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 31)
AUTHORS Jeffreys, A.J.
TITLE Extended nucleotide sequences
JOURNAL Patent: EP 0370719-A 97 30-MAY-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES
source
1. .31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 31;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3261 ATATTTTATTGCTTGTCTTTT 3285
Db 31 ATATTTTATTGCTTGTCTTTT 7

RESULT 575
AR029831
LOCUS AR029831 35 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5861244.
ACCESSION AR029831
VERSION AR029831.1 GI:5943045
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

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3401 ACGGTTTCCAGGGAGGGGCC 3420

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JOURNAL Patent: US 6271030-A 197 07-AUG-2001;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1478 GGCGCGGGCGGCCCGGGC 1497
Db 20 GGCGCGGGCGGCCCGGGC 1

RESULT 586
LOCUS AR170760/c 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6291742.
ACCESSION AR170760
VERSION AR170760.1 GI:17908719
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Somerville,C., Broun,P. and van de Loo,F.
TITLE Production of hydroxylated fatty acids in genetically modified
Plants
JOURNAL Patent: US 6291742-A 13 18-SEP-2001;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2982 CAGGGCTTTTCTGCGACCG 3001
Db 20 CAGGGCTTTTCTGCGTACCG 1

RESULT 587
LOCUS AR176139/c 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6310194.
ACCESSION AR176139
VERSION AR176139.1 GI:17917438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Somerville,C., Broun,P. and van de Loo,F.
TITLE Plant fatty acid hydroxylases
JOURNAL Patent: US 6310194-A 13 30-OCT-2001;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2982 CAGGGCTTTTCTGCGACCG 3001
Db 20 CAGGGCTTTTCTGCGTACCG 1

RESULT 588
LOCUS BD250269/c 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of p38 mitogen activated protein kinase
expression.
ACCESSION BD250269
VERSION BD250269.1 GI:33060039
KEYWORDS JP 2002540781-A/21.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Gaarde,W.A., Nero,P.S., Mckay,R. and Popoff,I.
TITLE Antisense modulation of p38 mitogen activated protein kinase
JOURNAL Patent: JP 2002540781-A 21 03-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002540781-A/21
PD 03-DEC-2002
PF 04-APR-2000 JP 2000609429
PR 06-APR-1999 US 09/286904
PI BRETT P MONIA, WILLIAM A GAARDE, PAMELA S NERO, ROBERT MCKAY, IAN
PI POPOFF
PC C12N15/09,A61K31/711,A61P19/02,A61P29/00,A61P37/06,
PC A61P43/00,
PC C12N5/10,C12N9/99,C12N15/00,C12N5/00
CC Antisense modulation of p38 mitogen activated protein kinase
expression
FH Key
FT source
FT Location/Qualifiers
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2321 GTGTGTGTGTGTGCGTGCT 2340
Db 20 GTTAGTGTGTGTGCGATGCT 1

RESULT 589
LOCUS CQ754256 20 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 6 from Patent WO2004001367.
ACCESSION CQ754256
VERSION CQ754256.1 GI:44845518
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Rapp,U.R. and Sedlacek,H.H.
TITLE Test system for identifying cancerous diseases
JOURNAL Patent: WO 2004001367-A 6 31-DEC-2003;
MEDINNOVA Gesellschaft fuer medizinische Innovationen aus;
akademischer Forschung mbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
    misc_feature
      1..20
        /note="primer"

Query Match
Best Local Similarity 0.4%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 3558 CTGGACTGCTACCTTTCAA 3577


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/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 925 TTCCTGTTTCATCTGCTGCT 944
    ||||| ||||| ||||| |||||
Db 20 TTCCTGTTTCATCTGCTGCT 1

RESULT 599
189428/c
LOCUS      189428      20 bp      DNA
DEFINITION Sequence 15 from patent US 5721352.
ACCESSION  189428
VERSION    189428.1 GI:3409368
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Moyer,R.W., Hall,R.L. and Gruidl,M.E.
TITLE      Entomopoxvirus expression system
JOURNAL    Patent: US 5721352-A 15 24-FEB-1998;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3715 GAGTGTCACCCAAACCGC 3734
    ||||| ||||| ||||| |||||
Db 20 GAGTGTTACCCACACGAGC 1

RESULT 600
AR199806/c
LOCUS      AR199806      20 bp      DNA
DEFINITION Sequence 67 from patent US 6355482.
ACCESSION  AR199806
VERSION    AR199806.1 GI:20249880
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Bennett,C.Frank. and Freier,S.M.
TITLE      Antisense inhibition of integrin beta 4 binding protein expression
JOURNAL    Patent: US 6355482-A 67 12-MAR-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2093 GTGGCCAGGACACCCCGAGC 2112
    ||||| ||||| ||||| |||||
Db 20 GTGGCCTGGACACACGAGC 1

RESULT 601
AR208740/c
LOCUS      AR208740      20 bp      DNA
DEFINITION Sequence 39 from patent US 6383808.
ACCESSION  AR208740
VERSION    AR208740.1 GI:21509974

/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 925 TTCCTGTTTCATCTGCTGCT 944
    ||||| ||||| ||||| |||||
Db 20 TTCCTGTTTCATCTGCTGCT 1

RESULT 599
189428/c
LOCUS      189428      20 bp      DNA
DEFINITION Sequence 15 from patent US 5721352.
ACCESSION  189428
VERSION    189428.1 GI:3409368
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Moyer,R.W., Hall,R.L. and Gruidl,M.E.
TITLE      Entomopoxvirus expression system
JOURNAL    Patent: US 5721352-A 15 24-FEB-1998;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3715 GAGTGTCACCCAAACCGC 3734
    ||||| ||||| ||||| |||||
Db 20 GAGTGTTACCCACACGAGC 1

RESULT 600
AR199806/c
LOCUS      AR199806      20 bp      DNA
DEFINITION Sequence 67 from patent US 6355482.
ACCESSION  AR199806
VERSION    AR199806.1 GI:20249880
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Bennett,C.Frank. and Freier,S.M.
TITLE      Antisense inhibition of integrin beta 4 binding protein expression
JOURNAL    Patent: US 6355482-A 67 12-MAR-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2093 GTGGCCAGGACACCCCGAGC 2112
    ||||| ||||| ||||| |||||
Db 20 GTGGCCTGGACACACGAGC 1

RESULT 601
AR208740/c
LOCUS      AR208740      20 bp      DNA
DEFINITION Sequence 39 from patent US 6383808.
ACCESSION  AR208740
VERSION    AR208740.1 GI:21509974

/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 925 TTCCTGTTTCATCTGCTGCT 944
    ||||| ||||| ||||| |||||
Db 20 TTCCTGTTTCATCTGCTGCT 1

RESULT 599
189428/c
LOCUS      189428      20 bp      DNA
DEFINITION Sequence 15 from patent US 5721352.
ACCESSION  189428
VERSION    189428.1 GI:3409368
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 39 07-MAY-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 489 GCAGACGTACACGCTGGACG 508
    ||||| ||||| ||||| |||||
Db 20 GCAGACGCACATGCTGGATG 1

RESULT 602
AR211982/c
LOCUS      AR211982      20 bp      DNA
DEFINITION Sequence 38 from patent US 6399378.
ACCESSION  AR211982
VERSION    AR211982.1 GI:21515448
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Ward,D.T. and Watt,A.T.
TITLE      Antisense modulation of RECQL2 expression
JOURNAL    Patent: US 6399378-A 38 04-JUN-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1357 ATGATGAAGATGATCGGAA 1376
    ||||| ||||| ||||| |||||
Db 20 ATGATGATGATGATCGGAA 1

RESULT 603
AR214733/c
LOCUS      AR214733      20 bp      DNA
DEFINITION Sequence 15 from patent US 6410221.
ACCESSION  AR214733
VERSION    AR214733.1 GI:23312643
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Moyer,R.W., Hall,R.L., Gruidl,M.E. and Li,Y.
TITLE      Entomopoxvirus expression system
JOURNAL    Patent: US 6410221-A 15 25-JUN-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 3715 GAGGTGTACCCAAACCGGC 3734
|||||
Db 20 GAGGTGTACCCAAACCGGC 1

RESULT 604
AR225997/c 20 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 60 from patent US 644465.
ACCESSION AR225997
VERSION AR225997.1 GI:27264151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt, J. and Freier, S.M.
TITLE Antisense modulation of Her-1 expression
JOURNAL Patent: US 644465-A 60 03-SEP-2002;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 GATCGCAGACTTCGGGCTGG 1690
|||||
Db 20 GATCACAGATTGTGGGCTGG 1

RESULT 605
AR228818/c 20 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 22 from patent US 6448079.
ACCESSION AR228818
VERSION AR228818.1 GI:27267957
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P., Gaarde, W.A., Nero, P., and McKay, R.
TITLE Antisense modulation of p38 mitogen activated protein kinase
expression
JOURNAL Patent: US 6448079-A 22 10-SEP-2002;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2321 GTGTGTGTGTGTGGTGTGT 2340
|||||
Db 20 GTTAGTGTGTGTGTGTGT 1

RESULT 606
AR264939 20 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 23 from patent US 6492121.
ACCESSION AR264939
VERSION AR264939.1 GI:29693326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)

AUTHORS Kurane, R., Kanagawa, T., Kanagata, Y., Kurata, S., Yamada, K.,
Yokomaku, T., Koyama, O. and Furusho, K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 23 10-DEC-2002;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3473 TATATATATAATTATTGAG 3492
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Db 1 TATATATATAATTATTGAG 20

RESULT 607
AR304132 20 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 6 from patent US 6544768.
ACCESSION AR304132
VERSION AR304132.1 GI:31693046
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buck, J. and Levin, L.R.
TITLE Mammalian soluble adenylyl cyclase
JOURNAL Patent: US 6544768-A 6 08-APR-2003;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1998 CAAGCAGCTGTGGAGGACC 2017
|||||
Db 1 CGAGCAGCTGTGGAGATCC 20

RESULT 608
AR305121/c 20 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 75 from patent US 6545137.
ACCESSION AR305121
VERSION AR305121.1 GI:31694431
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,
Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,
Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.
TITLE Receptor
JOURNAL Patent: US 6545137-A 75 08-APR-2003;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 157 GTCCTCATCTCGGAGATGA 176
Db 20 GCTGCATCTCTGGAGA 1

RESULT 609
LOCUS AR309225/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 75 from patent US 655654.
ACCESSION AR309225
VERSION AR309225.1 GI:31701230
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,
Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,
Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.
TITLE LDL-receptor
JOURNAL Patent: US 655654-A 75 29-APR-2003;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 157 GCTCCATCTCGGAGATGA 176
Db 20 GCTGCATCTCTGGAGA 1

RESULT 610
LOCUS AR399605 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 52 from patent US 6620623.
ACCESSION AR399605
VERSION AR399605.1 GI:40141777
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Yershov, G., Alferov, O. and Kukhtin, A.
TITLE Biochip reader with enhanced illumination and bioarray positioning
apparatus
JOURNAL Patent: US 6620623-A 52 16-SEP-2003;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGAGATGATGAGATGA 1369
Db 1 GATGATGATGATGATGA 20

RESULT 611
LOCUS AR399627 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 74 from patent US 6620623.
ACCESSION AR399627
VERSION AR399627.1 GI:40141812
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of vascular endothelial growth factor
receptor-1 expression
JOURNAL Patent: US 6710174-A 72 23-MAR-2004;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGAGATGATGAGATGA 1369
Db 1 GATGATGATGATGATGA 20

RESULT 612
LOCUS AR478220 20 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 23 from patent US 6699661.
ACCESSION AR478220
VERSION AR478220.1 GI:47236868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurane, R., Kanagawa, T., Kanagata, Y., Kurata, S., Yamada, K.,
Yokomaku, T., Koyama, O. and Furusho, K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 23 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3473 TATATATATATTTTGG 20
Db 1 TATATATATATTTTGG 20

RESULT 613
LOCUS AR489949/c 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 72 from patent US 6710174.
ACCESSION AR489949
VERSION AR489949.1 GI:47257062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of vascular endothelial growth factor
receptor-1 expression
JOURNAL Patent: US 6710174-A 72 23-MAR-2004;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1573 CAGGTGGCCGGGCGCATGGA 1592
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 Db 20 CAAAGTGGCCAGAGGCATGGA 1

RESULT 614
 LOCUS AR489951/c
 DEFINITION Sequence 74 from patent US 6710174.
 ACCESSION AR489951
 VERSION AR489951.1 GI:47257064
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Bennett,C.F. and Watt,A.T.
 TITLE Antisense inhibition of vascular endothelial growth factor receptor-1 expression
 JOURNAL Patent: US 6710174-A 74 23-MAR-2004;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1610 AGTGCATCCACAGGACCTG 1629
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 Db 20 AGTGCATTCATCGGACCTG 1

RESULT 615
 LOCUS AX035957/c
 DEFINITION Sequence 18 from Patent EP1035207.
 ACCESSION AX035957
 VERSION AX035957.1 GI:11191496
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Marquardt,A. and Weber,B.H.
 TITLE Cdna molecules of the members of gene family encoding human fatty acid desaturases and their use in diagnosis and therapy
 JOURNAL Patent: EP 1035207-A 18 13-SEP-2000;
 MULTIGENE BIOTECH GMBH (DE)
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
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 /db_xref="taxon:32630"
 /note="Description of Artificial Sequence: Primer"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
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 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2458 GAGGGGCTTTGTCTGGGG 2477
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 Db 20 GATGGGCTTTGTCTGAGG 1

RESULT 616
 LOCUS AX149223
 DEFINITION Sequence 425 from Patent WO0136625.
 ACCESSION AX149223

VERSION AX149223.1 GI:14347747
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Wright,J.A., Young,A.H. and Dugourd,D.
 TITLE Antisense oligonucleotide sequences derived from groel and groes as inhibitors of microorganisms
 JOURNAL Patent: WO 0136625-A 425 25-MAY-2001;
 Genesense Technologies Inc. (CA)
 FEATURES Location/Qualifiers
 source 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Antisense oligonucleotide"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3115 TTTTAATTTTAACTTATG 3134
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 Db 1 TTTTATTTTCACTTTG 20

RESULT 617
 LOCUS AX224921
 DEFINITION Sequence 75 from Patent WO0161030.
 ACCESSION AX224921
 VERSION AX224921.1 GI:15554994
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Gray,D.M. and Bollon,A.P.
 TITLE Libraries of optimum subsequence regions of mrna and genomic dna for control of gene expression
 JOURNAL Patent: WO 0161030-A 75 23-AUG-2001;
 Cytoclonal Pharmaceuticals, Inc. (US) ; University of Texas at Dallas, Dept. of Molecular and Cell Biology (US); Lab. of Experimental Carcinogenesis, National Cancer Institute/NIH (US)
 FEATURES Location/Qualifiers
 source 1..20
 /organism="Homo sapiens"
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Query Match 0.4%; Score 15.2; DB 1; Length 20;
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 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 528 CCGGGCCATCTCTGCAGCGG 547
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 Db 1 CCGGGCGACGCTGCAGCGG 20

RESULT 618
 LOCUS AX293956/c
 DEFINITION Sequence 5718 from Patent WO0179548.
 ACCESSION AX293956
 VERSION AX293956.1 GI:17055639
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.

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TITLE      Method of designing addressable array for detection of nucleic acid
JOURNAL    sequence differences using ligase detection reaction
           Patent: WO 0179548-A 5718 25-OCT-2001;
           CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
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Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 GCTGTGACCGAGGACAACG 1663
Db 20 GCTGGGACAGAGGTCAACG 1

RESULT 619
LOCUS      AX452336/c 20 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 22 from Patent WO0242441.
ACCESSION  AX452336
VERSION     AX452336.1 GI:21712247
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Leemle, B., Gerritsen, H.E., Furlan, M., Turecek, P., Schwarz, H.P.,
           Schneiflinger, F., Antoine, G., Kerschbaumer, R., Tagliavacca, L.,
           Zimmermann, K., and Voelkel, D.
           Von willibrand factor (wvf) cleaving protease polypeptide, nucleic
           acid encoding the polypeptide and use of polypeptide
JOURNAL    Patent: WO 0242441-A 22 30-MAY-2002;
           Baxter Aktiengesellschaft (AT)
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Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 182 ACGGGAGGACGAGGCTGAG 201
Db 20 ATGGGAGGACGAGGTGAG 1

RESULT 620
LOCUS      AX477161 20 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 252 from Patent WO0220848.
ACCESSION  AX477161
VERSION     AX477161.1 GI:22216414
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Bodnar, J.S., Castellani, L.W., Chatterjee, A., de Jong, P.,
           Lusis, A.J., Ohmen, J., Ross, D., Tafuri, S., and Wu, C.
           Gene and sequence variation associated with cancer
           Gene and sequence variation associated with cancer
JOURNAL    Patent: WO 0220848-A 252 14-MAR-2002;
           THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
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/mol_type="unassigned DNA"
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Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3651 CTTGCTTGCCTGCAGGGCCA 3670
Db 1 CTTGCATGCTGCAGGTGCA 20

RESULT 621
LOCUS      AX526537 20 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 252 from Patent WO0220847.
ACCESSION  AX526537
VERSION     AX526537.1 GI:25171344
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Bodnar, J.S., Castellani, L.W., Chatterjee, A., de Jong, P.,
           Lusis, A.J., Ohmen, J., Ross, D., Tafuri, S., and Wu, C.
           Gene and sequence variation associated with lipid disorder
           Gene and sequence variation associated with lipid disorder
JOURNAL    Patent: WO 0220847-A 252 14-MAR-2002;
           THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES
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    1..20
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    /db_xref="taxon:32630"
    /note="Synthetic Primer"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3651 CTTGCTTGCCTGCAGGGCCA 3670
Db 1 CTTGCATGCTGCAGGTGCA 20

RESULT 622
LOCUS      AX712200/c 20 bp DNA linear PAT 11-APR-2003
DEFINITION Sequence 34 from Patent WO03018810.
ACCESSION  AX712200
VERSION     AX712200.1 GI:29823423
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Chen, E. and Stacy, C.
           Modified cry3a toxins and nucleic acid sequences coding therefor
           Patent: WO 03018810-A 34 06-MAR-2003;
           Syngenta Participations AG (CH)
FEATURES
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Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1995 CTTCAAGCAGCTGTGTGAGG 2014
Db 1 CTTCAAGCAGCTGTGTGAGG 2014

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Db      20 CTTCTGGAGCAGGTGGAGG 1
RESULT 623
AX787161/c
LOCUS   AX787161 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 22 from Patent WO03013598.
ACCESSION AX787161
VERSION   AX787161.1 GI:32954361
KEYWORDS
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE
1 Lam,D.M., Zeng,F. and Leung,F.C.
  Novel vaccine compositions and methods of vaccine preparation for
  veterinary and human diseases
JOURNAL  Patent: WO 03013598-A 22 20-FEB-2003;
        Lam, Dominic M. K., VaxGene Corporation (CN) ; Zeng, Fanya, VaxGene
        Corporation (CN) ; Leung, Frederick C. VaxGene Corporation (CN)
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Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1537 CAGCTCACCTTCAAGGACCT 1556
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Db 20 CAGCTCAAGTTCGAGGACCT 1

RESULT 624
AX799916
LOCUS   AX799916 20 bp DNA linear PAT 08-OCT-2003
DEFINITION Sequence 2 from Patent WO03045995.
ACCESSION AX799916
VERSION   AX799916.1 GI:37605404
KEYWORDS
SOURCE    synthetic construct
ORGANISM  synthetic construct
          artificial sequences.
REFERENCE
1 Zeng,S., Bogner,F.M., Kunert,R., Mueller,D. and Unterluggauer,F.
  Cell culture process
JOURNAL  Patent: WO 03045995-A 2 05-JUN-2003;
        BIOCHEMIE Gesellschaft m.b.H. (AT)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3576 AAGCTTGGAGGGAAGCCGTG 3595
||||| ||||| |||||
Db 1 AAGCTTGTGGGAAGCCGTG 20

RESULT 625
BD072884
LOCUS   BD072884 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
ACCESSION BD072884
VERSION   BD072884.1 GI:22618487
KEYWORDS
SOURCE    and method for analyzing data obtained by that method.
ORGANISM  AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
REFERENCE
1 Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
  Yokomaku,T., Koyama,O. and Furusho,K.
  Method for assaying nucleic acid, nucleic acid probe used therefor,
  and method for analyzing data obtained by that method
JOURNAL  Patent: JP 2001286300-A 33 16-OCT-2001;
        JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
        NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
        AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT   OS Artificial Sequence
          PN JP 2001286300-A/33
          PD 16-OCT-2001
          PF 20-APR-2000 JP 2000120097

KEYWORDS JP 2001286300-A/22.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
          Yokomaku,T., Koyama,O. and Furusho,K.
          Method for assaying nucleic acid, nucleic acid probe used therefor,
          and method for analyzing data obtained by that method
TITLE     Patent: JP 2001286300-A 22 16-OCT-2001;
JOURNAL   JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
          NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
          AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT   OS Artificial Sequence
          PN JP 2001286300-A/33
          PD 16-OCT-2001
          PF 20-APR-2000 JP 2000120097

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Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3473 TATATATATATTTTTCGAG 3492
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Db 1 TATATATATATTTTTCGG 20

RESULT 626
BD072895/c
LOCUS   BD072895 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
ACCESSION BD072895
VERSION   BD072895.1 GI:22618498
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
          Yokomaku,T., Koyama,O. and Furusho,K.
          Method for assaying nucleic acid, nucleic acid probe used therefor,
          and method for analyzing data obtained by that method
TITLE     Patent: JP 2001286300-A 33 16-OCT-2001;
JOURNAL   JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
          NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
          AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT   OS Artificial Sequence
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          PD 16-OCT-2001
          PF 20-APR-2000 JP 2000120097

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PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
  KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU, OSAMU KOYAMA, KENTA FURUSHO
PC C12Q1/68, C12M1/00, C12N15/09, G01N31/22, G01N33/53, G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
  examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
  labeled with
CC BODIBY FL/C6 upon the hybridization of the
  probe with a target
CC nucleic
CC acid.
CC FH Key Location/Qualifiers
CC FT source 1..20
CC FT /organism="synthetic construct"
CC FT /mol_type="genomic DNA"
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Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
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QY 3473 TATATATATAATTATTGAG 3492
Db 20 TATATATATATTTTTTTGGG 1

RESULT 627
BD106032/c
LOCUS Novel LDL-receptor. 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel LDL-receptor.
ACCESSION BD106032
VERSION BD106032.1 GI:23200850
KEYWORDS JP 2002501376-A/47.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd J.A., Hess J.W., Caskey, C.T., Cox, R.D., Gerhold, D., Hammond, H.
and Hey, P.
TITLE Novel LDL-receptor
JOURNAL THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
INC
COMMENT PN JP 2002501376-A/47
PD 15-JAN-2002
PF 15-APR-1998 JP 1998543635
PR 15-APR-1997 US 60/043553, 05-JUN-1997 US 60/048740 PI
JOHN ANDREW TODD, JOHN WILFRED HESS, CHARLES THOMAS CASKEY, ROGER
PI DAVID COX,
PI DAVID GERHOLD, HOLLY HAMMOND, PATRICIA HEY
PC C12N15/12, C12N15/11, C12Q1/68, C07K14/705, C07K16/28, A61K38/17,
PC A61K39/395,
PC A61K48/00
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CC Topology: Linear;
CC Key Location/Qualifiers.
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Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 20 GCTGCATCTCTGGAGAAGA 1

RESULT 628
BD107511
LOCUS Novel quantitative polymorphism analysis method. 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107511
VERSION BD107511.1 GI:23202329
KEYWORDS JP 2002000275-A/20.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurane, R., Kanekawa, T., Kamagata, Y., Kurata, S., Yamada, K. and
Yokomaku, T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 20 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/20
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
  examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
  labeled with
CC BODIBY FL/C6 upon the hybridization of the
  probe with a target
CC nucleic
CC acid.
CC FH Key Location/Qualifiers
CC FT source 1..20
CC FT /organism="synthetic construct"
CC FT /mol_type="genomic DNA"
CC FT /db_xref="taxon:32630"

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Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3473 TATATATATAATTATTGAG 3492
Db 1 TATATATATATTTTTTTGGG 20

RESULT 629
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LOCUS Novel quantitative polymorphism analysis method. 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107522
VERSION BD107522.1 GI:23202340
KEYWORDS JP 2002000275-A/31.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurane, R., Kanekawa, T., Kamagata, Y., Kurata, S., Yamada, K. and
Yokomaku, T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 31 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL

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COMMENT
OS Artificial Sequence
PN JP 2002000275-A/31
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
   KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..20
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   /organism='synthetic construct'
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Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3473 TATATATATATTTATTGAG 3492
DB 20 TATATATATATTTTGGG 1

RESULT 630
BD138221/C
LOCUS
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138221
VERSION BD138221.1 GI:23233166
KEYWORDS JP 2002508944-A/147.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowser, L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 147 26-MAR-2002;
ISIS PHARMACEUTICALS INC
COMMENT
OS Unidentified
PN JP 2002508944-A/147
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3473 TATATATATATTTATTGAG 3492
DB 20 TATATATATATTTTGGG 1

RESULT 630
BD138221/C
LOCUS
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138221
VERSION BD138221.1 GI:23233166
KEYWORDS JP 2002508944-A/147.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowser, L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 147 26-MAR-2002;
ISIS PHARMACEUTICALS INC
COMMENT
OS Unidentified
PN JP 2002508944-A/147
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3473 TATATATATATTTATTGAG 3492
DB 20 TATATATATATTTTGGG 1

RESULT 632
BD145043
LOCUS
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145043
VERSION BD145043.1 GI:27850801
KEYWORDS JP 2002119291-A/24.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Kuran, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,
Yamada, K. and Yokomaku, T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 24 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED

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Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1346 CTCAGATGAGATGATGAAG 1365
DB 20 CTCAGATGAGATGATGAG 1

RESULT 631
BD138283/C
LOCUS
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138283
VERSION BD138283.1 GI:23233228
KEYWORDS JP 2002508944-A/209.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowser, L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 209 26-MAR-2002;
ISIS PHARMACEUTICALS INC
COMMENT
OS Unidentified
PN JP 2002508944-A/209
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3462 TTATATATATCTATATATAT 3481
DB 20 TTATATATTTCTACTATAT 1

RESULT 632
BD145043
LOCUS
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145043
VERSION BD145043.1 GI:27850801
KEYWORDS JP 2002119291-A/24.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Kuran, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,
Yamada, K. and Yokomaku, T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 24 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED

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INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/24
PD 23-APR-2002
PF RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..20
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1..20
Location/Qualifiers
/organism="synthetic construct"
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Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3473 TATATATATAATTATTGAG 3492
DB 20 TATATATATATTTTGGG 1
RESULT 634
BD166043
LOCUS
DEFINITION
20 bp DNA linear PAT 17-JAN-2003
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166043
VERSION
BD166043.1 GI:27871855
KEYWORDS
JP 2002191372-A/23.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL
Patent: JP 2002191372-A 23 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002191372-A/23
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58,G01N33/53,G01N33/566,PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
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source
1..20
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3473 TATATATATAATTATTGAG 3492
DB 1 TATATATATATTTTGGG 20
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/24
PD 23-APR-2002
PF RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
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source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3473 TATATATATAATTATTGAG 3492
DB 1 TATATATATATTTTGGG 20
RESULT 633
BD145054/c
LOCUS
DEFINITION
20 bp DNA linear PAT 17-JAN-2003
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION
BD145054
VERSION
BD145054.1 GI:27850812
KEYWORDS
JP 2002119291-A/35.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
Patent: JP 2002119291-A 35 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002119291-A/35
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of

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A28676/c
 LOCUS A28676 21 bp RNA linear PAT 04-JUN-1995
 DEFINITION dsRNA with central hinge (comp.).
 ACCESSION A28676
 VERSION A28676.1 GI:1248715
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
 TITLE Patent: WO 90/4090-A 4 29-NOV-1990;
 JOURNAL Location/Qualifiers
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 Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2920 GGGCGGGGGCTGGGGGGCG 2939
 Db |||||
 21 GGGCGGGGGCTGGGGGGGG 2
 RESULT 639
 AR073030/c
 LOCUS AR073030 21 bp DNA linear PAT 28-AUG-2000
 DEFINITION Sequence 3 from patent US 5948680.
 ACCESSION AR073030
 VERSION AR073030.1 GI:9999793
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Baker,B.F. and Cowert,L.M.
 TITLE Antisense inhibition of Elk-1 expression
 JOURNAL Patent: US 5948680-A 3 07-SEP-1999;
 FEATURES Location/Qualifiers
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 Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 860 AGCTGGTGGAGCTGACGAG 879
 Db |||||
 20 AGCTGGTGGAGCTGACGAGGAG 1
 RESULT 640
 AR084556
 LOCUS AR084556 21 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 45 from patent US 5981185.
 ACCESSION AR084556
 VERSION AR084556.1 GI:10011327
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
 TITLE Oligonucleotide repeat arrays
 JOURNAL Patent: US 5981185-A 45 09-NOV-1999;
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/mol_type="unassigned DNA"
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 QY 1351 ATGGAGATGATGAAGATGAT 1370
 Db |||||
 1 ATGGATGATGATGATGATGAT 20
 RESULT 641
 AR084560/c
 LOCUS AR084560 21 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 49 from patent US 5981185.
 ACCESSION AR084560
 VERSION AR084560.1 GI:10011331
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
 TITLE Oligonucleotide repeat arrays
 JOURNAL Patent: US 5981185-A 49 09-NOV-1999;
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
 Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1351 ATGGAGATGATGAAGATGAT 1370
 Db |||||
 21 ATGGATGATGATGATGATGAT 2
 RESULT 642
 AR084593/c
 LOCUS AR084593 21 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 82 from patent US 5981185.
 ACCESSION AR084593
 VERSION AR084593.1 GI:10011364
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
 TITLE Oligonucleotide repeat arrays
 JOURNAL Patent: US 5981185-A 82 09-NOV-1999;
 FEATURES Location/Qualifiers
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 Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1350 GATGGAGATGATGAAGATGA 1369
 Db |||||
 20 GATGGATGATGATGATGATGA 1
 RESULT 643
 AR084597
 LOCUS AR084597 21 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 86 from patent US 5981185.
 ACCESSION AR084597
 VERSION AR084597.1 GI:10011368

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KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE          Oligonucleotide repeat arrays/8.
JOURNAL        Patent: US 5981185-A 86 09-NOV-1999;
FEATURES       Location/Qualifiers
source         1..21
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Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGAGATGATGAAGATGA 1369
Db 2 GATGATGATGATGATGATGA 21

RESULT 644
LOCUS          BD250646/c
DEFINITION     Identification of genetic targets for modulation by
               oligonucleotides and generation of oligonucleotides for gene
               modulation.
ACCESSION      BD250646
VERSION        BD250646.1 GI:33060416
KEYWORDS       JP 2002511276-A/200.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Cowsett,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasmor,H.M.,
               Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,I.A.
TITLE          Identification of genetic targets for modulation by
               oligonucleotides and generation of oligonucleotides for gene
               modulation
JOURNAL        Patent: JP 2002511276-A 200 16-APR-2002;
               ISIS PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002511276-A/200
               PD 16-APR-2002
               PF 13-APR-1999 JP 2000543647
               PR 13-APR-1998 US 60/081483, 28-APR-1998 US 09/067638 PI
               LEX M COWSETT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
               M SASMOR,
               PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
               BORCHERS,
               PI TIMOTHY A VIKKARS
               PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
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Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 860 AGCTGGTGGAGGTGACGAG 879
Db 20 AGCTGGTGGATGACGAGGAG 1

KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE          Oligonucleotide repeat arrays/8.
JOURNAL        Patent: US 5981185-A 86 09-NOV-1999;
FEATURES       Location/Qualifiers
source         1..21
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Query Match      0.4%; Score 15.2; DB 1; Length 21;
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGAGATGATGAAGATGA 1369
Db 2 GATGATGATGATGATGATGA 21

RESULT 644
LOCUS          BD250646/c
DEFINITION     Identification of genetic targets for modulation by
               oligonucleotides and generation of oligonucleotides for gene
               modulation.
ACCESSION      BD250646
VERSION        BD250646.1 GI:33060416
KEYWORDS       JP 2002511276-A/200.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Cowsett,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasmor,H.M.,
               Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,I.A.
TITLE          Identification of genetic targets for modulation by
               oligonucleotides and generation of oligonucleotides for gene
               modulation
JOURNAL        Patent: JP 2002511276-A 200 16-APR-2002;
               ISIS PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002511276-A/200
               PD 16-APR-2002
               PF 13-APR-1999 JP 2000543647
               PR 13-APR-1998 US 60/081483, 28-APR-1998 US 09/067638 PI
               LEX M COWSETT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
               M SASMOR,
               PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
               BORCHERS,
               PI TIMOTHY A VIKKARS
               PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
               C12N15/00
               CC PCR Primer
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FEATURES       source
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Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 860 AGCTGGTGGAGGTGACGAG 879
Db 20 AGCTGGTGGATGACGAGGAG 1

RESULT 645
BD266134
LOCUS          BD266134
DEFINITION     Universal arrays.
ACCESSION      BD266134
VERSION        BD266134.1 GI:33075902
KEYWORDS       JP 2002539849-A/134.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 21)
AUTHORS        Pan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,E.S.,
               Lockhart,D.J., Ryder,T. and Sklar,P.
TITLE          Universal arrays
JOURNAL        Patent: JP 2002539849-A 134 26-NOV-2002;
               WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH,AFFYMETRIX INC
COMMENT        OS Homo sapiens (human)
               PN JP 2002539849-A/134
               PD 26-NOV-2002
               PF 27-MAR-2000 JP 2000608794
               PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
               JIAN BING FAN,JOEL N HIRSCHHORN,XIAOHUA
               HUANG,PAUL KAPLAN,ERIC
               PI S LANDER,
               PI DAVID J LOCKHART,THOMAS RYDER,PAMELA SKLAR
               PC C12Q1/68,C12M1/00,C12N15/09,C12N15/09,G01N33/53, PC
               G01N33/566,
               PC G01N37/00,C12N15/00,C12N15/00,C12N15/00
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Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 754 CACAACGTCACCTTTGAGGA 773
Db 1 CACAAGGTCARCATTGAGGA 20

RESULT 646
LOCUS          CQ769152
DEFINITION     Sequence 13 from Patent EP1386961.
ACCESSION      CQ769152
VERSION        CQ769152.1 GI:45112910
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Asako,H. and Shimizu,M.
TITLE          Modified reductase and its gene and use thereof
JOURNAL        Patent: EP 1386961-A 13 04-FEB-2004;
               Sumitomo Chemical Company, Limited (JP)
FEATURES       Location/Qualifiers
source         1..21
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Thu Oct 28 12:48:19 2004

QY 2443 TGGTGTGTCAGCACCAGGG 2462
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 Db 1 TGGTACTACAGCACCAGGG 20

RESULT 647
 CQ797933 21 bp DNA linear PAT 20-APR-2004
 LOCUS Sequence 31 from Patent WO2004029631.
 DEFINITION CQ797933
 ACCESSION CQ797933.1 GI:46426428
 VERSION
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Wolf, S., Jaeger, M., Bangsow, T., Bangsow, C., Jordan, D., Pelzer, B.
 and Oppolzer, T.
 TITLE Method for identifying bhs-specific proteins and fragments thereof
 JOURNAL Patent: WO 2004029631-A 31 08-APR-2004;
 Esplora GmbH, c/OTU Darmstadt Institut fuer Biochemie (DE)
 FEATURES Location/Qualifiers
 1..21
 source /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Beschreibung der k nstlichen Sequenz: Primer"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1007 TGCAAGATCTCCGCTTC 1026
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 Db 2 TGCTGAAGATCTCAGCTTC 21

RESULT 648
 E08187 21 bp DNA linear PAT 29-SEP-1997
 LOCUS Primer for isolation of the promoter in rice starch-branching
 DEFINITION enzyme.
 ACCESSION E08187
 VERSION E08187.1 GI:2176308
 KEYWORDS JP 1994261767-A/5.
 SOURCE unidentified
 ORGANISM unclassified.
 1 (bases 1 to 21)
 REFERENCE Baba, T. and Shimada, H.
 AUTHORS NEW RICE PLANT STARCH-BRANCHED ENZYMIC GENE
 TITLE Patent: JP 1994261767-A 5 20-SEP-1994;
 JOURNAL MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO:KK
 COMMENT OS None
 OC Artificial sequences.
 PN JP 1994261767-A/5
 PD 20-SEP-1994
 PF 22-OCT-1993 JP 92P 291719
 PR 29-OCT-1992 JP 92P 291719
 PI BABA TADASHI, SHIMADA HIROAKI
 PC C12N15/54,A01H5/00,C12N5/10,C12P19/16//A23L1/10,C12N9/10; CC
 strandedness: Single;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FH source 1..21
 FT /organism='Artificial sequences'.
 FT Location/Qualifiers
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 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
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 Db 2 GTGTGTGTGTGTGTGTGTGT 21

RESULT 649
 127608/c 21 bp DNA linear PAT 06-FEB-1997
 LOCUS Sequence 4 from patent US 5565334.
 DEFINITION I27608
 ACCESSION I27608
 VERSION I27608.1 GI:1818384
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Kufe, D. and Abe, M.
 TITLE Enhancer sequence for modulating expression in epithelial cells
 JOURNAL Patent: US 5565334-A 4 15-OCT-1996;
 FEATURES Location/Qualifiers
 1..21
 source /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3067 TCCACACCCCACTTCC 3086
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 Db 21 TCCCTCCCACTTCC 2

RESULT 650
 AR279803 21 bp DNA linear PAT 10-APR-2003
 LOCUS Sequence 49 from patent US 6518017.
 DEFINITION AR279803
 ACCESSION AR279803
 VERSION AR279803.1 GI:29714948
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Riley, T.A., Brown, B.D. and Arnold, L.J.
 TITLE Combinatorial antisense library
 JOURNAL Patent: US 6518017-A 49 11-FEB-2003;
 FEATURES Location/Qualifiers
 1..21
 source /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1434 GCTGTGTGTGTGTGTGTGTGT 1453
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 Db 1 GCTGTGTGTGTGTGTGTGTGT 20

RESULT 651
 AR351501/c 21 bp DNA linear PAT 17-AUG-2003
 LOCUS Sequence 82 from patent US 6586579.
 DEFINITION AR351501
 ACCESSION AR351501
 VERSION AR351501.1 GI:33753229
 KEYWORDS
 SOURCE Unknown.

ORGANISM	Unknown.	Query Match	0.4%; Score 15.2; DB 1; Length 21;	DB 1; Length 21;
REFERENCE	Unclassified.	Best Local Similarity	85.0%; Pred. No. 9.2e+02;	
AUTHORS	Huang, S.	Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
TITLE	PR-domain containing nucleic acids, polypeptides, antibodies and methods			
JOURNAL	Patent: US 6586579-A 82 01-JUL-2003;			
FEATURES	Location/Qualifiers			
source	1. .21			
	/organism="unknown"			
	/mol_type="genomic DNA"			
Query Match	0.4%; Score 15.2; DB 1; Length 21;			
Best Local Similarity	85.0%; Pred. No. 9.2e+02;			
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	1722 GAAGACAACACGCGCGGC 1741			
Db	21 GAAGACAATCAACAGCGGC 2			
RESULT 652				
LOCUS	AR483457			
DEFINITION	Sequence 166 from patent US 6703362.			
ACCESSION	AR483457			
VERSION	AR483457.1 GI:47246096			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 21)			
AUTHORS	Alvarez, V.L., O'Mahony, D.J., Lambkin, I.J., Patterson, C.A., Singleton, J., Belinka, B.A. Jr., Carter, J.M. and Cagney, G.M.			
TITLE	Random peptides that bind to gastro-intestinal tract (GIT) transport receptors and related methods			
JOURNAL	Patent: US 6703362-A 166 09-MAR-2004;			
FEATURES	Location/Qualifiers			
source	1. .21			
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	/mol_type="genomic DNA"			
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Best Local Similarity	85.0%; Pred. No. 9.2e+02;			
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	3651 CTTGCTTGCTGCAGGCGCA 3670			
Db	1 CTTGCATGCTGCAGGTCGA 20			
RESULT 653				
LOCUS	AX203590/c			
DEFINITION	Sequence 220 from Patent WO0153520.			
ACCESSION	AX203590			
VERSION	AX203590.1 GI:15393017			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	1			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	Cullen, P. and Seedorf, U.			
JOURNAL	Gene chip for neonate screening			
FEATURES	Patent: WO 0153520-A 220 26-JUL-2001;			
source	Cullen, Paul (DE) ; Seedorf, Udo (DE)			
	Location/Qualifiers			
	1. .21			
	/organism="Homo sapiens"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:9606"			

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	Huang,S.
TITLE	PR-domain containing nucleic acids, polypeptides, antibodies and methods
JOURNAL	Patent: US 6586579-A 82 01-JUL-2003;
FEATURES	Location/Qualifiers source 1..21 /organism="unknown" /mol_type="genomic DNA"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1722 GAAGACAACCAACGCGCGC 1741
Db	21 GAAGACAATCAACAGCGGC 2
RESULT 652	
LOCUS	AR483457
DEFINITION	Sequence 166 from patent US 6703362.
ACCESSION	AR483457
VERSION	AR483457.1 GI:47246096
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 21)
AUTHORS	Alvarez,V.L., O'Mahony,D.J., Lambkin,I.J., Patterson,C.A., Singletton,J., Belinka,B.A. Jr., Carter,J.M. and Cagney,G.M.
TITLE	Random peptides that bind to gastro-intestinal tract (GIT) transport receptors and related methods
JOURNAL	Patent: US 6703362-A 166 09-MAR-2004;
FEATURES	Location/Qualifiers source 1..21 /organism="unknown" /mol_type="genomic DNA"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	3651 CTTCCTTGCTGCGAGGCCA 3670
Db	1 CTTCGATGCTCGAGGTGA 20
RESULT 653	
LOCUS	AX203590/c
DEFINITION	Sequence 220 from Patent WO0153520.
ACCESSION	AX203590
VERSION	AX203590.1 GI:15393017
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Cullen,P. and Seedorf,U.
JOURNAL	Gene chip for neonate screening
FEATURES	Patent: WO 0153520-A 220 26-JUL-2001; Cullen, Paul (DE); Seedorf, Udo (DE) Location/Qualifiers source 1..21 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1119 CCCACGGTGGCCAATGCT 1138
Db	20 CCTCACGCTGGCAATACT 1
RESULT 654	
LOCUS	AX226447
DEFINITION	Sequence 103 from Patent WO0155179.
ACCESSION	AX226447
VERSION	AX226447.1 GI:15555682
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Prayaga,S.K., Padigar,M., Spytek,K.A., Li,L., Tchernev,V.T., Vernet,C.A., Peyman,J.A. and Macdougall,J.
TITLE	Nucleic acids encoding polypeptides with homology to olfactory receptors
JOURNAL	Patent: WO 0155179-A 103 02-AUG-2001;
FEATURES	Curagen Corporation (US) Location/Qualifiers source 1..21 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="NOV 12 Probe Primer Sequence"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1182 GGCCCGGCTGACCCTGGGCA 1201
Db	2 GGCCCGGCTGACCCTGCTCA 21
RESULT 655	
LOCUS	AX250034
DEFINITION	Sequence 33 from Patent WO0166747.
ACCESSION	AX250034
VERSION	AX250034.1 GI:15864493
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Vernet,C.A., Fernandes,E., Shimkets,R.A., Herrmann,J.L., Majumder,K., Macdougall,J., Mishra,V., Mezes,P.S. and Rastelli,L.
TITLE	Proteins named fctrx and nucleic acids encoding same
JOURNAL	Patent: WO 0166747-A 33 13-SEP-2001;
FEATURES	Curagen Corporation (US) Location/Qualifiers source 1..21 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Ag427 Probe Primer"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1182 GGCCCGGCTGACCCTGGGCA 1201
Db	2 GGCCCGGCTGACCCTGCTCA 21
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 21)
TITLE	Random peptides that bind to gastro-intestinal tract (GIT) transport receptors and related methods
JOURNAL	Patent: US 6703362-A 166 09-MAR-2004;
FEATURES	Location/Qualifiers source 1..21 /organism="unknown" /mol_type="genomic DNA"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	3651 CTTCCTTGCTGCGAGGCCA 3670
Db	1 CTTCGATGCTCGAGGTGA 20
RESULT 653	
LOCUS	AX203590/c
DEFINITION	Sequence 220 from Patent WO0153520.
ACCESSION	AX203590
VERSION	AX203590.1 GI:15393017
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Cullen,P. and Seedorf,U.
JOURNAL	Gene chip for neonate screening
FEATURES	Patent: WO 0153520-A 220 26-JUL-2001; Cullen, Paul (DE); Seedorf, Udo (DE) Location/Qualifiers source 1..21 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1119 CCCACGGTGGCCAATGCT 1138
Db	20 CCTCACGCTGGCAATACT 1
RESULT 654	
LOCUS	AX226447
DEFINITION	Sequence 103 from Patent WO0155179.
ACCESSION	AX226447
VERSION	AX226447.1 GI:15555682
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Prayaga,S.K., Padigar,M., Spytek,K.A., Li,L., Tchernev,V.T., Vernet,C.A., Peyman,J.A. and Macdougall,J.
TITLE	Nucleic acids encoding polypeptides with homology to olfactory receptors
JOURNAL	Patent: WO 0155179-A 103 02-AUG-2001;
FEATURES	Curagen Corporation (US) Location/Qualifiers source 1..21 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="NOV 12 Probe Primer Sequence"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	Huang,S.
TITLE	PR-domain containing nucleic acids, polypeptides, antibodies and methods
JOURNAL	Patent: US 6586579-A 82 01-JUL-2003;
FEATURES	Location/Qualifiers 1..21 /organism="unknown" /mol_type="genomic DNA"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1722 GAAGACAACACGCGCGGC 1741
Db	21 GAAGACAATCAACAGCGGC 2
RESULT 652	
LOCUS	AR483457
DEFINITION	Sequence 166 from patent US 6703362.
ACCESSION	AR483457
VERSION	AR483457.1 GI:47246096
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 21)
AUTHORS	Alvarez,V.L., O'Mahony,D.J., Lambkin,I.J., Patterson,C.A., Singleton,J., Belinka,B.A. Jr., Carter,J.M. and Cagney,G.M.
TITLE	Random peptides that bind to gastro-intestinal tract (GIT) transport receptors and related methods
JOURNAL	Patent: US 6703362-A 166 09-MAR-2004;
FEATURES	Location/Qualifiers 1..21 /organism="unknown" /mol_type="genomic DNA"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	3651 CTTCCTTGCTGCGAGGCCA 3670
Db	1 CTTCGATGCTCGAGGTGA 20
RESULT 653	
LOCUS	AX203590/c
DEFINITION	Sequence 220 from Patent WO0153520.
ACCESSION	AX203590
VERSION	AX203590.1 GI:15393017
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Cullen,P. and Seedorf,U.
JOURNAL	Gene chip for neonate screening
FEATURES	Patent: WO 0153520-A 220 26-JUL-2001; Cullen, Paul (DE); Seedorf, Udo (DE) Location/Qualifiers 1..21 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1119 CCCACGGTGGCCAATGTCT 1138
Db	20 CCTCACGCTGGCAATACT 1
RESULT 654	
LOCUS	AX226447
DEFINITION	Sequence 103 from Patent WO0155179.
ACCESSION	AX226447
VERSION	AX226447.1 GI:15555682
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Prayaga,S.K., Padigar,M., Spytek,K.A., Li,L., Tchernev,V.T., Vernet,C.A., Peyman,J.A. and Macdougall,J.
TITLE	Nucleic acids encoding polypeptides with homology to olfactory receptors
JOURNAL	Patent: WO 0155179-A 103 02-AUG-2001;
FEATURES	Curagen Corporation (US) Location/Qualifiers 1..21 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="NOV 12 Probe Primer Sequence"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1182 GGCCCGGCTGACCCTGGGCA 1201
Db	2 GGCCCGGCTGACCCTGCTCA 21
RESULT 655	
LOCUS	AX250034
DEFINITION	Sequence 33 from Patent WO0166747.
ACCESSION	AX250034
VERSION	AX250034.1 GI:15864493
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Vernet,C.A., Fernandes,E., Shimkets,R.A., Herrmann,J.L., Majumder,K., Macdougall,J., Mishra,V., Mezes,P.S. and Rastelli,L.
TITLE	Proteins named fctrx and nucleic acids encoding same
JOURNAL	Patent: WO 0166747-A 33 13-SEP-2001;
FEATURES	Curagen Corporation (US) Location/Qualifiers 1..21 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Ag427 Probe Primer"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1182 GGCCCGGCTGACCCTGGGCA 1201
Db	2 GGCCCGGCTGACCCTGCTCA 21
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 21)
TITLE	Random peptides that bind to gastro-intestinal tract (GIT) transport receptors and related methods
JOURNAL	Patent: US 6703362-A 166 09-MAR-2004;
FEATURES	Location/Qualifiers 1..21 /organism="unknown" /mol_type="genomic DNA"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	3651 CTTCCTTGCTGCGAGGCCA 3670
Db	1 CTTCGATGCTCGAGGTGA 20
RESULT 653	
LOCUS	AX203590/c
DEFINITION	Sequence 220 from Patent WO0153520.
ACCESSION	AX203590
VERSION	AX203590.1 GI:15393017
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Cullen,P. and Seedorf,U.
JOURNAL	Gene chip for neonate screening
FEATURES	Patent: WO 0153520-A 220 26-JUL-2001; Cullen, Paul (DE); Seedorf, Udo (DE) Location/Qualifiers 1..21 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1119 CCCACGGTGGCCAATGTCT 1138
Db	20 CCTCACGCTGGCAATACT 1
RESULT 654	
LOCUS	AX226447
DEFINITION	Sequence 103 from Patent WO0155179.
ACCESSION	AX226447
VERSION	AX226447.1 GI:15555682
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Prayaga,S.K., Padigar,M., Spytek,K.A., Li,L., Tchernev,V.T., Vernet,C.A., Peyman,J.A. and Macdougall,J.
TITLE	Nucleic acids encoding polypeptides with homology to olfactory receptors
JOURNAL	Patent: WO 0155179-A 103 02-AUG-2001;
FEATURES	Curagen Corporation (US) Location/Qualifiers 1..21 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="NOV 12 Probe Primer Sequence"
Query Match	0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 9.2e+02;
Matches	17; Conservative 0; M

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RESULT 656
AX740291
LOCUS AX740291 21 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 25 from Patent EP1300419.
ACCESSION AX740291
VERSION AX740291.1 GI:30523464
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Buettner,C., Schwarz,M., Knackmuss,S., Peter,K., Roettgen,P. and Little,M.
TITLE Antibody of human origin for inhibiting thrombocyte aggregation
JOURNAL Patent: EP 1300419-A 25 09-APR-2003;
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 854 AGGAGGAGCTGGTGGAGGCT 873
DB 2 AGTGACGCTGGTGGAGTCT 21

RESULT 657
BD140700
LOCUS BD140700 22 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods for the simultaneous identification of novel biological targets and lead structures for drug development.
ACCESSION BD140700
VERSION BD140700.1 GI:23235645
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Heefner,D.L., Zepp,C.M., Gao,Y. and Jones,S.W.
TITLE Methods for the simultaneous identification of novel biological targets and lead structures for drug development
JOURNAL Patent: JP 2002508507-A 2 19-MAR-2002;
COMMENT SEPRACOR INC
OS Artificial Sequence
PN JP 2002508507-A/2
PD 19-MAR-2002
PR 18-DEC-1998 JP 2000539165
PI DONALD L. HEEFNER, CHARLES M. ZEPP, YUN GAO, STEVEN W. JONES PC
GO1N33/542, C12Q1/04, C12Q1/68, C12Q1/70, G01N21/00, G01N21/76, PC
GO1N33/53,
PC GO1N33/566//C12N15/09, C12N15/00
CC Description of Artificial Sequence: construct FH Key
Location/Qualifiers
FT source
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/organism='Artificial Sequence'.
FT Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 658
AR438517/c
LOCUS AR438517/c 29 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7 from patent US 6664064.
ACCESSION AR438517
VERSION AR438517.1 GI:42663388
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive PCR products
JOURNAL Patent: US 6664064-A 7 16-DEC-2003;
FEATURES
source
1. .29
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 29;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3308 GATTTTCTTTAGGAGATTATTTTGTG 3335
DB 28 GATTTTCTTTTATTTTATTTTGTG 1

RESULT 659
AX430216/c
LOCUS AX430216/c 29 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 7 from Patent EP1207210.
ACCESSION AX430216
VERSION AX430216.1 GI:21655581
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive PCR products
JOURNAL Patent: EP 1207210-A 7 22-MAY-2002;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
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1. .29
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.2; DB 1; Length 29;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3308 GATTTTCTTTAGGAGATTATTTTGTG 3335
DB 28 GATTTTCTTTTATTTTATTTTGTG 1

RESULT 660
BD165919/c
LOCUS BD165919/c 29 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for melting curve analysis of repetitive PCR products.
ACCESSION BD165919
VERSION BD165919.1 GI:27871731
KEYWORDS JP 2002191384-A/7.
SOURCE unidentified
ORGANISM unidentified

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Unclassified.
1 (bases 1 to 15)
Morgante,M. and Vogel,J.Marie.
Compound microsatellite primers for the detection of genetic polymorphisms
Patent: US 5955276-A 7 21-SEP-1999;
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGT 2332
Db 15 TGTGTGTGTGTGTGT 1

RESULT 665
AR074711/c
LOCUS AR074711 15 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 8 from patent US 5955276.
ACCESSION AR074711
VERSION AR074711.1 GI:10001464
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 8 21-SEP-1999;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGT 2333
Db 15 GTGTGTGTGTGTGTGT 1

RESULT 666
AR074712
LOCUS AR074712 15 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 9 from patent US 5955276.
ACCESSION AR074712
VERSION AR074712.1 GI:10001465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 9 21-SEP-1999;
FEATURES Location/Qualifiers
source 1. .15
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGT 2333
Db 15 GTGTGTGTGTGTGTGT 1

RESULT 667
AR074713
LOCUS AR074713 15 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 10 from patent US 5955276.
ACCESSION AR074713
VERSION AR074713.1 GI:10001466
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 10 21-SEP-1999;
FEATURES Location/Qualifiers
source 1. .15
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGT 2333
Db 15 GTGTGTGTGTGTGTGT 1

RESULT 668
AR127803/c
LOCUS AR127803 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6180777.
ACCESSION AR127803
VERSION AR127803.1 GI:14114398
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Horn,T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 24 30-JAN-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGT 2333
Db 15 GTGTGTGTGTGTGTGT 1

RESULT 669
AX175252
LOCUS AX175252 15 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 16 from Patent WO014465.
ACCESSION AX175252
VERSION AX175252.1 GI:14598620
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.


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AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 16 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTG 2333
Db 1 GTGTGTGTGTGTGTG 15

RESULT 670
AX721631
LOCUS AX721631 15 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 10 from Patent EP1298221.
ACCESSION AX721631
VERSION AX721631.1 GI:30422164
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial construct.
REFERENCE 1
AUTHORS van der Kuyt,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1298221-A 10 02-APR-2003;
PrimaGen Holding B.V. (NL)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Tag with increased expression in SAGE libraries KS3
and KS4"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3704 CATGTGGCCAGG 3718
Db 1 CATGTGGCCAGG 15

RESULT 671
AR328668
LOCUS AR328668 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6070 from patent US 6566127.
ACCESSION AR328668
VERSION AR328668.1 GI:33714476
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6070 20-MAY-2003;
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/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 16 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTG 2333
Db 1 GTGTGTGTGTGTGTG 15

RESULT 672
AR074719
LOCUS AR074719 17 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 16 from patent US 5955276.
ACCESSION AR074719
VERSION AR074719.1 GI:10001472
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 16 21-SEP-1999;
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2320 TGTGTGTGTGTGTGC 2334
Db 17 TGTGTGTGTGTGTGC 3

RESULT 673
AX687933
LOCUS AX687933 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 665 from Patent EPI281758.
ACCESSION AX687933
VERSION AX687933.1 GI:29410631
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 665 05-FEB-2003;
Aeonica, Inc. (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1529 CCGAGGAGCAGCTCA 1543
Db 3 CCGAGGAGCAGCTCA 17

RESULT 674
AX687934
LOCUS AX687934 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 666 from Patent EPI281758.
ACCESSION AX687934
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VERSION AX687934.1 GI:29410632
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
 AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
 TITLE mdz12
 JOURNAL Patent: EP 1281758-A 666 05-FEB-2003;
 FEATURES Aeomica, Inc. (US)
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1529 CCGAGGAGCAGCTCA 1543
 Db 2 CCGAGGAGCAGCTCA 16

RESULT 675
 LOCUS AX687935 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 667 from Patent EP1281758.
 ACCESSION AX687935
 VERSION AX687935.1 GI:29410633
 KEYWORDS Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
 AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
 TITLE mdz12
 JOURNAL Patent: EP 1281758-A 667 05-FEB-2003;
 FEATURES Aeomica, Inc. (US)
 source 1. .17
 /organism="Homo sapiens"
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Query Match 0.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1529 CCGAGGAGCAGCTCA 1543
 Db 1 CCGAGGAGCAGCTCA 15

RESULT 676
 LOCUS AR076354 18 bp DNA linear PAT 30-AUG-2000
 DEFINITION Sequence 21 from patent US 5958772.
 ACCESSION AR076354
 VERSION AR076354.1 GI:10003100
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowsert,L.M.
 TITLE Antisense inhibition of cellular inhibitor of apoptosis-1 expression

JOURNAL Patent: US 5958772-A 21 28-SEP-1999;
 FEATURES Location/Qualifiers
 source 1. .18
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 /mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1606 CAGAAGTGCATCCAC 1620
 Db 17 CAGAAGTGCATCCAC 3

RESULT 677
 LOCUS BD234297 18 bp DNA linear PAT 17-JUL-2003
 DEFINITION Antisense modulation of expression of cellular inhibitor of apoptosis-1.
 ACCESSION BD234297
 VERSION BD234297.1 GI:33044067
 KEYWORDS JP 2002531469-A/21.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Bennett,F.C., Ackermann,E.A. and Cowsert,L.M.
 TITLE Antisense modulation of expression of cellular inhibitor of
 JOURNAL Patent: JP 2002531469-A 21 24-SEP-2002;
 COMMENT ISIS PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2002531469-A/21
 PD 24-SEP-2002
 PF 16-JUN-1999 JP 2000585447
 PR 03-DEC-1998 US 09/205204
 PI FRANK C BENNETT,ELIZABETH A ACKERMANN,LEX M COWSERT PC
 A61K48/00,A61K31/7115,A61K31/712,A61K31/7125,A61P29/00 PC
 ,A61P31/00,A61P35/00, C12N15/09,C12N15/00
 PC A61P37/02,A61P43/00
 CC Synthetic
 PH Key
 FT source 1. .18
 Location/Qualifiers
 FT /organism="Artificial Sequence".

Query Match 0.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1606 CAGAAGTGCATCCAC 1620
 Db 17 CAGAAGTGCATCCAC 3

RESULT 678
 LOCUS AR127806 19 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 27 from patent US 6180777.
 ACCESSION AR127806
 VERSION AR127806.1 GI:14114401
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Horn,T.
 TITLE Synthesis of branched nucleic acids
 JOURNAL Patent: US 6180777-A 27 30-JAN-2001;

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Query Match
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  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTG 2333
Db 19 GTGTGTGTGTGTGTG 5

RESULT 679
LOCUS AR163975 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 173 from patent US 6271030.
ACCESSION AR163975
VERSION AR163975.1 GI:16234857
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 20)
  Monia,B.P., Butler,M.M. and Wyatt,J.
  Antisense inhibition of C/EBP beta expression
  TITLE
  Antisense inhibition of C/EBP beta expression
  JOURNAL
  Patent: US 6271030-A 173 07-AUG-2001;
  LOCATION/Qualifiers
  1..20
  /organism="unknown"
  /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 15; DB 1; Length 20;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2639 TCCAGCACCTTGTGC 2653
Db 2 TCCAGCACCTTGTGC 16

RESULT 680
LOCUS AR208748 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 47 from patent US 6383808.
ACCESSION AR208748
VERSION AR208748.1 GI:21509984
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 20)
  Monia,B.P. and Freier,S.M.
  Antisense inhibition of clusterin expression
  TITLE
  Antisense inhibition of clusterin expression
  JOURNAL
  Patent: US 6383808-A 47 07-MAY-2002;
  LOCATION/Qualifiers
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Query Match
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  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 GGATCAAGCTGCGG 396
Db 2 GGATCAAGCTGCGG 16

RESULT 681
LOCUS AX482068 20 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 45 from Patent EPI225233.
ACCESSION AX482068
VERSION AX482068.1 GI:22316790
KEYWORDS
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
  ORGANISM
  van der Kuyl,A.C. and Cornelissen,M.
  Means and methods for treatment evaluation
  TITLE
  Patent: EP 1225233-A 45 24-JUL-2002;
  JOURNAL
  Amsterdam Support Diagnostics B.V. (NL)
  LOCATION/Qualifiers
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  /db_xref="taxon:32630"
  /note="TAG019"
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  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3704 CATGTGGCCAGG 3718
Db 6 CATGTGGCCAGG 20

RESULT 682
LOCUS AX511307 20 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 45 from Patent WO2059558.
ACCESSION AX511307
VERSION AX511307.1 GI:23392184
KEYWORDS
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
  ORGANISM
  van der Kuyl,A.C. and Cornelissen,M.
  Means and methods for treatment evaluation
  TITLE
  Patent: WO 02059558-A 45 01-AUG-2002;
  JOURNAL
  Amsterdam Support Diagnostics B.V. (NL)
  LOCATION/Qualifiers
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  /mod_base=i

Query Match
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  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3704 CATGTGGCCAGG 3718
Db 6 CATGTGGCCAGG 20

RESULT 683
LOCUS AX721667 20 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 46 from Patent EPI298221.
ACCESSION AX721667
VERSION AX721667.1 GI:30422200
KEYWORDS
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
  ORGANISM
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REFERENCE
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AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1298221-A 46 02-APR-2003;
PrimaGen Holding B.V. (NL)
FEATURES
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/mol_type="unassigned DNA"
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/note="primer used for tag confirmation"
misc_feature
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Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3704 CATGTGGCCAGG 3718
DB 6 CATGTGGCCAGG 20
RESULT 684
S61964/c
LOCUS S61964 23 bp DNA linear PRI 07-MAY-1993
DEFINITION (beta C)-beta-globin (5' region) [human, Genomic Mutant, 23 nt].
ACCESSION S61964
VERSION S61964.1 GI:236198
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 23)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Nucleotide sequence evidence of the uniceutric origin of the beta C
mutation in Africa
JOURNAL Hum. Genet. 87 (5), 597-601 (1991)
MEDLINE 92009838
PUBMED 1680789
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 61964] from the original journal article.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/allele="beta C"
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Best Local Similarity 78.3%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2822 GTATATATACATATATATATA 2844
DB 23 GAAAAAAATATATATATATA 1
RESULT 685
A87890
LOCUS A87890 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 38 from Patent WO9833904.
ACCESSION A87890
VERSION A87890.1 GI:6736460
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 38 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2920 GGGCGGGCGTGGGGGG 2937
DB 1 GGGCGGGCGGGGGGG 18
RESULT 686
A89857
LOCUS A89857 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 38 from Patent EP0856579.
ACCESSION A89857
VERSION A89857.1 GI:6738371
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 38 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 1 GGGCGGGCGGGGGGG 18
RESULT 687
A8187533
LOCUS A8187533 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 3021 from patent US 6346398.
ACCESSION A8187533
VERSION A8187533.1 GI:20233498
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 3021 12-FEB-2002;.
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Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1391 TCAACCTGCTGGCGCCT 1408
Db 1 TTAACCTGCTGGAGCCT 18

RESULT 688
LOCUS AR190756 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6244 from patent US 6346398.
ACCESSION AR190756
VERSION AR190756.1 GI:20236721
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6244 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 1 GACTTCGGCTGGCCCGG 18

RESULT 689
LOCUS AR219474 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 12 from patent US 6420346.
ACCESSION AR219474
VERSION AR219474.1 GI:23320656
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Karin,N.
TITLE Polynucleotides encoding MIP-1.alpha., MCP-1, MIP-1.beta., Rantes
and TNF-.alpha., and methods for treating rheumatoid arthritis
JOURNAL Patent: US 6420346-A 12 16-JUL-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 550 CTGCGGGCCACACGACG 567
Db 1 CTACCGGCGCAGACG 18

RESULT 690
LOCUS AR324047 18 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1449 from patent US 6566127.
ACCESSION AR324047
VERSION AR324047.1 GI:33709855
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1449 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1391 TCAACCTGCTGGCGCCT 1408
Db 1 TTAACCTGCTGGAGCCT 18

RESULT 691
LOCUS AR325602 18 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3004 from patent US 6566127.
ACCESSION AR325602
VERSION AR325602.1 GI:33711410
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3004 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 1 GACTTCGGCTGGCCCGG 18

RESULT 692
LOCUS AR336934 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 42 from patent US 6566131.
ACCESSION AR336934
VERSION AR336934.1 GI:33722788
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cowsert,L.M.
TITLE Antisense modulation of Smad6 expression
JOURNAL Patent: US 6566131-A 42 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 168 GCGAGATGACGAGACG 185
Db 1 GCGAGATGACGAGACG 185
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Db 1 GGGAGTTGACGAGATGG 18

RESULT 693
AX343688
LOCUS AX343688 18 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 5 from Patent WO0200864.
ACCESSION AX343688
VERSION AX343688.1 GI:18491773
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Pankratz, M.J., Zinke, I., Luemmen, P., Benting, J. and Gunkel, N.
TITLE Histone acetyltransferase inhibitors and their use as insecticides
JOURNAL Patent: WO 0200864-A 5 03-JAN-2002;
Aventis CropScience GmbH (DE)
FEATURES
source 1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="-"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2068 GGGCTTTTCGAGCAGTAC 2085
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Db 1 GGGCTTATCGAGCAGTAC 18

RESULT 694
AX773276/c
LOCUS AX773276 18 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 250 from Patent WO03045426.
ACCESSION AX773276
VERSION AX773276.1 GI:32485219
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ellendoorn, K., Baker, M., Williams, S. and Carr, F.J.
TITLE T-cell epitopes in carboxypeptidase g2
JOURNAL Patent: WO 03045426-A 250 05-JUN-2003;
MERCK PATENT GmbH (DE)
FEATURES
source 1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2754 TACCTTTTATGCAAAAGG 2771
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Db 18 TACCTTTTATGTAACGG 1

RESULT 695
AX773292
LOCUS AX773292 18 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 266 from Patent WO03045426.
ACCESSION AX773292
VERSION AX773292.1 GI:32485235
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL Patent: EP 1340818-A 592 03-SEP-2003;
Epigenomics AG (DE)
FEATURES
source 1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for APC"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1379 ACAAAAACATCATCAACC 1396
|||||
Db 18 ACAAAAACATCATCCCC 1

RESULT 697
AX826340/c
LOCUS AX826340 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 592 from Patent WO03072821.
ACCESSION AX826340
VERSION AX826340.1 GI:39751854
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL Patent: WO 03072821-A 592 04-SEP-2003;
Epigenomics AG (DE)

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FEATURES
source
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  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="Detection oligonucleotide for APC"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1379 ACAAAACATCATCAACC 1396
DB 18 ACAAAACATCATCCCC 1

RESULT 698
LOCUS BD065403 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065403
VERSION BD065403.1 GI:22611006
KEYWORDS JP 2001511000-A/38.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 38 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/38
PD 07-AUG-2001
PR 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101331.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source
FT 1..18
  Location/Qualifiers
  /organism="Unknown".

FEATURES
source
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  /organism="unidentified"
  /mol_type="genomic DNA"
  /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2920 GGGCGGGCGTGGGGG 2937
DB 1 GGGCGGGCGGGGGGGG 18

RESULT 699
A91634
LOCUS A91634 19 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 161 from Patent WO9824928.
ACCESSION A91634
VERSION A91634.1 GI:6740589
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Pallisgaard,N. and Hokland,P.
TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES
JOURNAL Patent: WO 9824928-A 161 11-JUN-1998;
FEATURES
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  /organism="unidentified"
  /mol_type="genomic DNA"
  /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 909 CTACGGGTGGGCTTCTT 926
DB 2 CTCGGTGGTGGGCTTCTT 19

RESULT 700
LOCUS A9129286 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6183969.
ACCESSION A9129286
VERSION A9129286.1 GI:14116948
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Gabriel,A.
TITLE Intron-based assay for detecting and characterizing chromosomal
  rearrangement
JOURNAL Patent: US 6183969-A 10 06-FEB-2001;
FEATURES
  Location/Qualifiers
  source
  1..19
  /organism="unknown"
  /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 GGAGTCCACGCGTCCAT 1067
DB 1 GGAGTCAATGCGTCCAT 18

RESULT 701
BD182533/c
LOCUS BD182533 19 bp DNA linear PAT 15-MAY-2003
DEFINITION Screening method.
ACCESSION BD182533
VERSION BD182533.1 GI:30793498
KEYWORDS WO 02093161-A/92.
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Mori,M., Shimomura,Y. and Goto,M.
TITLE Screening method
JOURNAL Patent: WO 02093161-A 92 21-NOV-2002;
  TAKEDA CHEMICAL INDUSTRIES LTD,MASAOKI MORI,YUKIO SHIMOMURA, MIKA
  GOTO
COMMENT OS Artificial Sequence
PN WO 02093161-A/92
PD 21-NOV-2002
PR 14-MAY-2002 WO 2002JP004635
PR 15-MAY-2001 JP 01P 145411
PI MASAOKI MORI,YUKIO SHIMOMURA,MIKA GOTO
PC GOIN33/15,GOIN33/50,C07K14/705,C07K14/435
CC Primer
FT Key
FT source
FT 1..19
  Location/Qualifiers
  /organism="Artificial Sequence".
  Location/Qualifiers
  1..19
  /organism="synthetic construct"
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Thu Oct 28 12:48:19 2004

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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1876 GAGGAGCTCTTCAAGCTG 1893
DB 19 GACGAGCTCTTCACGCTG 2

RESULT 702
BD196868
LOCUS      19 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Prostatic cancer gene.
ACCESSION      BD196868
VERSION      BD196868.1 GI:33006638
KEYWORDS      JP 2002516657-A/457.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 19)
AUTHORS      Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
TITLE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
PATENT      JP 2002516657-A 457 11-JUN-2002;
GENSET

COMMENT      OS Homo sapiens (human)
PN JP 2002516657-A/457
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19.
PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
C12N15/00,C12N5/00.
PC C12N5/00,C12N15/00
CC potential microsequencing oligo for 99-128-202.mis2 FH Key
FT primer bind 1..19.
LOCATION/Qualifiers
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source
1..19
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGTGTGTGTGTGT 2332
DB 1 GTATGTAATGTGTGTGTGTGTGTGTGT 18

RESULT 704
LOCUS      19 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION      Sequence 18 from patent US 5733732.
ACCESSION      I95651
VERSION      I95651.1 GI:3940121
KEYWORDS      Unknown.
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Campbell,K.P., Roberds,S.L., Sunada,Y., Piccolo,F., Jeanpierre,M.
and Kaplan,J.-C.
TITLE      Methods for detecting primary adhalinopathy
JOURNAL      Patent: US 5733732-A 18 31-MAR-1998;
FEATURES
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 752 TGCACAACTGTACCTTTG 769
DB 1 TGCTCAACGTCACTCTG 18

RESULT 705
LOCUS      19 bp      DNA      linear      PAT 15-MAY-2004
DEFINITION      Sequence 118 from patent US 6720137.
ACCESSION      AR493086
VERSION      AR493086.1 GI:47264497
KEYWORDS      Unknown.
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Roder,M., Plaschke,J. and Ganai,M.
TITLE      Microsatellite markers for plants of the species Triticum aestivum
and tribe triticeae and the use of said markers
JOURNAL      Patent: US 6720137-A 118 13-APR-2004;

/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3469 TATCTATATATATATATTT 3486
DB 1 TATCTATATATATATTT 18

RESULT 703
BD196931
LOCUS      19 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Prostatic cancer gene.
ACCESSION      BD196931
VERSION      BD196931.1 GI:33006701
KEYWORDS      JP 2002516657-A/520.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 19)
AUTHORS      Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
TITLE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
PATENT      JP 2002516657-A 520 11-JUN-2002;
GENSET

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Db	18	CGTCCAGTACTGTTACTG 1	19 bp	DNA	linear	PAT 15-FEB-2002
FEATURES						
source						
Query Match		0.4%; Score 14.8; DB 1; Length 19;				
Best Local Similarity		88.9%; Pred. No. 9.4e+02;				
Matches	16;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	404	AGTGAGCTGCTGCTGCTG 421				
Db	18	AGTGGATGCTGCTGCTG 1				
RESULT 706						
LOCUS	AX166727	19 bp	DNA	linear	PAT 22-JUN-2001	
DEFINITION	Sequence 218 from Patent WO0138503.					
ACCESSION	AX166727					
VERSION	AX166727.1	GI:14547002				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE						
AUTHORS	Planman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,					
TITLE	Novel human protein kinases and protein kinase-like enzymes					
JOURNAL	Patent: WO 0138503-A 218 31-MAY-2001;					
FEATURES						
source						
Query Match		0.4%; Score 14.8; DB 1; Length 19;				
Best Local Similarity		88.9%; Pred. No. 9.4e+02;				
Matches	16;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	503	TGGACGTGCTGAGCGCT 520				
Db	1	TGGCCGTGCTGAGCGCT 18				
RESULT 707						
LOCUS	AX353125/c	19 bp	DNA	linear	PAT 06-FEB-2002	
DEFINITION	Sequence 331 from Patent EPI174518.					
ACCESSION	AX353125					
VERSION	AX353125.1	GI:18618207				
KEYWORDS						
SOURCE						
ORGANISM	synthetic construct					
REFERENCE						
AUTHORS	Loukachov,V.V., van Gemen,B. and Goudsmit,J.					
TITLE	Collection of binding molecules					
JOURNAL	Patent: EP 1174518-A 331 23-JAN-2002;					
FEATURES						
source						
Query Match		0.4%; Score 14.8; DB 1; Length 19;				
Best Local Similarity		88.9%; Pred. No. 9.4e+02;				
Matches	16;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	3609	CGTCTGCTGCTGCTGCTG 3626				
Db	18	CGTCCAGTACTGTTACTG 1				
RESULT 708						
LOCUS	AX362970/c	19 bp	DNA	linear	PAT 15-FEB-2002	
DEFINITION	Sequence 331 from Patent WO0208463.					
ACCESSION	AX362970					
VERSION	AX362970.1	GI:18695110				
KEYWORDS						
SOURCE						
ORGANISM	synthetic construct					
REFERENCE						
AUTHORS	Loukachov,V.V., Goudsmit,J. and van Gemen,B.					
TITLE	Collection of binding molecules					
JOURNAL	Patent: WO 0208463-A 331 31-JAN-2002;					
FEATURES						
source						
Query Match		0.4%; Score 14.8; DB 1; Length 19;				
Best Local Similarity		88.9%; Pred. No. 9.4e+02;				
Matches	16;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	3609	CGTCTGCTGCTGCTGCTG 3626				
Db	18	CGTCCAGTACTGTTACTG 1				
RESULT 709						
LOCUS	AX539200/c	19 bp	DNA	linear	PAT 23-NOV-2002	
DEFINITION	Sequence 2 from Patent WO02064774.					
ACCESSION	AX539200					
VERSION	AX539200.1	GI:25272379				
KEYWORDS						
SOURCE						
ORGANISM	synthetic construct					
REFERENCE						
AUTHORS	Ben-Asouli,Y. and Osman,F.					
TITLE	Orientation-directed construction of plasmids					
JOURNAL	Patent: WO 02064774-A 2 22-AUG-2002;					
FEATURES						
source						
Query Match		0.4%; Score 14.8; DB 1; Length 19;				
Best Local Similarity		88.9%; Pred. No. 9.4e+02;				
Matches	16;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	3651	CTTGCTGCTGCTG				

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 19)
 TITLE Method for detecting abnormality in chromosome
 JOURNAL Patent: JP 2001505428-A 161 24-APR-2001;
 NEILLS PARISGARD
 COMMENT PN JP 2001505428-A/161
 PD 24-APR-2001 JP 1998525090
 PF 08-DEC-1997 JP 1998525090
 PI NEILLS PARISGARD, PATER HOKURANDO
 PC C12N15/09, C12Q1/68, G01N33/50, C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers.
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 source 1..19
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 9.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 909 CTCAGGGTGGCTTCTT 926
 Db 2 CTCGGTGGCTTCTT 19
 RESULT 711
 LOCUS BD089758 19 bp DNA linear PAT 27-AUG-2002
 DEFINITION A method of arraying genome clone.
 ACCESSION BD089758
 VERSION BD089758.1 GI:22635368
 KEYWORDS JP 2001321190-A/2002.
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Soeda,E.
 TITLE A method of arraying genome clone
 JOURNAL Patent: JP 2001321190-A 2002 20-NOV-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
 GENOTECHS
 COMMENT OS Artificial Sequence
 PN JP 2001321190-A/2002
 PD 20-NOV-2001
 PF 12-MAR-2001 JP 2001068285
 PI EIICHI SOEDA
 PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC
 C12N15/00,
 PC C12N15/00
 CC Description of Artificial Sequence:Synthetic DNA FH Key
 Location/Qualifiers
 FT source 1..19
 /organism="Artificial Sequence".
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 9.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1037 GACAGGTGTCCTGGAGT 1054
 Db 1 GACAGGTGACCTGTGT 18
 RESULT 713
 LOCUS AR214196 20 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 4 from patent US 6406890.
 ACCESSION AR214196
 VERSION AR214196.1 GI:23311726
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Mueller,M.W.
 TITLE Process for the amplification of nucleic acid
 JOURNAL Patent: US 6406890-A 4 18-JUN-2002;
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 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 9.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1037 GACAGGTGTCCTGGAGT 1054
 Db 1 GACAGGTGACCTGTGT 18

RESULT 712
 LOCUS AB068169 19 bp DNA linear SYN 21-MAY-2003
 DEFINITION Synthetic construct DNA, reverse primer for human STS sts-cos245-T3
 at 1p36.
 ACCESSION AB068169
 VERSION AB068169.1 GI:15128973
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Chen,Y.Z., Hayaishi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
 Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
 Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
 and Soeda,E.
 TITLE A BAC-based STS-content map spanning a 35-Mb region of human
 chromosome 1p35-p36
 JOURNAL Genomics 74 (1), 55-70 (2001)
 MEDLINE 21269192
 PUBMED 11374902
 REFERENCE 2 (bases 1 to 19)
 AUTHORS Horii,A.
 TITLE Direct Submission
 JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
 Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
 Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
 Tel:81-22-717-8042, Fax:81-22-717-8047)
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 B143P11, B380E2, B154M16, B154C10, Human BAC library
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 QY 1037 GACAGGTGTCCTGGAGT 1054
 Db 1 GACAGGTGACCTGTGT 18
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 LOCUS AR214196 20 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 4 from patent US 6406890.
 ACCESSION AR214196
 VERSION AR214196.1 GI:23311726
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Mueller,M.W.
 TITLE Process for the amplification of nucleic acid
 JOURNAL Patent: US 6406890-A 4 18-JUN-2002;
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Db 2 GTATATGTTATATATAA 19

RESULT 714
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LOCUS AR214200 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6406890.
ACCESSION AR214200
VERSION AR214200.1 GI:23311730
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mueller,M.W.
TITLE Process for the amplification of nucleic acid
JOURNAL Patent: US 6406890-A 8 18-JUN-2002;
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QY 2815 GTATATGGTATATATACA 2832
Db 2 GTATATGTTATATATAA 19

RESULT 715
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LOCUS AR029135 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5859221.
ACCESSION AR029135
VERSION AR029135.1 GI:5941108
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.
TITLE 2'-modified oligonucleotides
JOURNAL Patent: US 5859221-A 11 12-JAN-1999;
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Location/Qualifiers
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QY 2815 GTATATGGTATATATACA 2832
Db 2 GTATATGTTATATATAA 19

RESULT 716
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LOCUS AR036519 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5872232.
ACCESSION AR036519
VERSION AR036519.1 GI:5953187
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.

TITLE 2'-O-modified oligonucleotides
Patent: US 5872232-A 11 16-FEB-1999;
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QY 2815 GTATATGGTATATATACA 2832
Db 2 GTATATGTTATATATAA 19

RESULT 717
AR073957/c
LOCUS AR073957 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 26 from patent US 5952229.
ACCESSION AR073957
VERSION AR073957.1 GI:10000717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Boggs,R.T.
TITLE Antisense oligonucleotide modulation of raf gene expression
JOURNAL Patent: US 5952229-A 26 14-SEP-1999;
FEATURES
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Location/Qualifiers
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Db 2 GTATATGTTATATATAA 19

RESULT 718
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LOCUS AR074771 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 68 from patent US 5955276.
ACCESSION AR074771
VERSION AR074771.1 GI:10001524
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 68 21-SEP-1999;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2815 GTATATGGTATATATACA 2832
Db 2 GTATATGTTATATATAA 19
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RESULT 719
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LOCUS AR074785 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 82 from patent US 5955276.
ACCESSION AR074785
VERSION AR074785.1 GI:10001538
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 82 21-SEP-1999;
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Qy 2316 TCCTGTGTGTGTGTGTGTG 2333
Db 3 TATATGTGTGTGTGTGTG 20

RESULT 720
AR096052/c
LOCUS AR096052 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 11 from patent US 6005087.
ACCESSION AR096052
VERSION AR096052.1 GI:10024502
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.
TITLE 2'-modified oligonucleotides
JOURNAL Patent: US 6005087-A 11 21-DEC-1999;
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 844 CTGCAGCCGAGGAGGAG 861
Db 20 CTGCAGGAGGAGGAGGAG 3

RESULT 721
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LOCUS AR105512 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 12 from patent US 6096720.
ACCESSION AR105512
VERSION AR105512.1 GI:12819109
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Love,W.Guy., Nicklin,P.Leslie., Hamilton,K.Ophelia. and
Phillips,J. Ann.
TITLE Liposomal oligonucleotide compositions
JOURNAL Patent: US 6096720-A 12 01-AUG-2000;
FEATURES
    Location/Qualifiers

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Qy 844 CTGCAGCCGAGGAGGAG 861
Db 20 CTGCAGGAGGAGGAGGAG 3

RESULT 722
AR110470/c
LOCUS AR110470 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6114517.
ACCESSION AR110470
VERSION AR110470.1 GI:12826746
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Xu,X.S.
TITLE Methods of modulating tumor necrosis factor .alpha.-induced
expression of cell adhesion molecules
JOURNAL Patent: US 6114517-A 7 05-SEP-2000;
FEATURES
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1678 GACTTCGGGCTGGCCCGG 1695
Db 20 GACTTTGGCTGGCCCGG 3

RESULT 723
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LOCUS AR116450 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6133246.
ACCESSION AR116450
VERSION AR116450.1 GI:14096772
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
TITLE Antisense oligonucleotide compositions and methods for the
modulation of JNK proteins
JOURNAL Patent: US 6133246-A 31 17-OCT-2000;
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RESULT 724
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Query Match	0.4%;	Score 14.8;	DB 1;	Length 20;
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LOCUS	AR130129	Accession	AR130129	
DEFINITION	AR130129.1	GI:14118026		
AUTHORS	Unknown.			
TITLE	Unclassified.			
JOURNAL	1 (bases 1 to 20)			
FEATURES	Popoff, I., Brown-Driver, V.L. and Cowsert, L.M.			
source	Antisense inhibition of e2f transcription factor 1 expression			
Patent:	US 6187587-A 32 13-FEB-2001;			
Location/Qualifiers	1. .20			
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QY 620 AGCCCCACATCCAGTGGC 637				
DB	18	AGAACCATCCAGTGGC 1		
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LOCUS	AR130802	Accession	AR130802	
DEFINITION	AR130802.1	GI:14119127		
AUTHORS	Unknown.			
TITLE	Unclassified.			
JOURNAL	1 (bases 1 to 20)			
FEATURES	Bennett, C. Frank. and Cowsert, L.M.			
Antisense inhibition of protein kinase C-theta expression				
Patent:	US 6190869-A 53 20-FEB-2001;			
Location/Qualifiers	1. .20			
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QY 1872 TGTGAGGAGGCTCTTCAA 1889				
DB	18	TGAGGAGGAGCTCTTCCA 1		
RESULT 729				
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LOCUS	BD177203	Accession	BD177203	
DEFINITION	BD177203.1	GI:30014463		
AUTHORS	Antisense inhibition of e2f transcription factor 1 expression			
TITLE	Antisense inhibition of e2f transcription factor 1 expression			
JOURNAL	Patent: US 6187587-A 32 13-FEB-2001;			
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KEYWORDS JP 2002306169-A/16.
 SOURCE synthetic construct
 ORGANISM artificial construct
 REFERENCE 1 (bases 1 to 20)
 AUTHORS King,K.W., Madura,R.A. and Rosey,E.L.
 TITLE Nucleic acid and protein of mup3 gene of Mycoplasma hyopneumoniae
 JOURNAL and utilization thereof
 COMMENT Patent: JP 2002306169-A 16 22-OCT-2002;
 PFIZER PRODUCTS INC
 OS Artificial Sequence
 PN JP 2002306169-A/16
 PD 22-OCT-2002
 PF 30-MAR-2001 JP 2001101364
 PI KENDALL WAYNE KING,REBECCA ANN MADURA,EVERETT LEE ROSEY PC
 C12N15/09,A61K39/00,A61K48/00,A61P31/04,A61P31/04, PC
 C07K14/30,
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 DB 2 GCTCTCTAGTTTATAG 19
 RESULT 730
 LOCUS BD183264 20 bp DNA linear PAT 17-JUN-2003
 DEFINITION Method for estimating genotype of fertility restoration gene site
 against rice BT type male sterile cytoplasm.
 ACCESSION BD183264
 VERSION BD183264.1 GI:31875464
 KEYWORDS JP 2002345485-A/3.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Komori,T., Yamamoto,T., Nitta,N. and Takemori,N.
 TITLE Method for estimating genotype of fertility restoration gene site
 against rice BT type male sterile cytoplasm
 JOURNAL Patent: JP 2002345485-A 3 03-DEC-2002;
 JAPAN TORACCO INC,SYNGENTA LTD
 OS Artificial Sequence
 PN JP 2002345485-A/3
 PD 03-DEC-2002
 PF 17-AUG-2001 JP 2001247600
 PI TOSHIYUKI KOMORI,TOSHIO YAMAMOTO,NAOTO NITTA,NAOKI TAKEMORI PC
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 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2044 ACCGACGAGTACCTGGAC 2061
 DB 2 ATCGACGAGTACCTGAAC 19
 RESULT 731
 LOCUS BD237317 20 bp DNA linear PAT 17-JUL-2003
 DEFINITION Modulation method of induction expression of tumor necrosis
 factor-alpha of cell adhesion molecules.
 ACCESSION BD237317
 VERSION BD237317.1 GI:33047087
 KEYWORDS JP 2002531574-A/7.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Monia,B.P. and Xu,X.S.
 TITLE Modulation method of induction expression of tumor necrosis
 factor-alpha of cell adhesion molecules
 JOURNAL Patent: JP 2002531574-A 7 24-SEP-2002;
 ISIS PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2002531574-A/7
 PD 24-SEP-2002
 PF 08-DEC-1999 JP 2000586746
 PI BRETT P MONIA,XIAOXING S XU
 PC A61K45/00,A61K31/712,A61K31/7125,A61K48/00,A61P1/00,A61P3/10,
 PC A61P5/14,
 PC A61P17/04,A61P17/06,A61P29/00,A61P29/00,A61P31/00,A61P35/00,
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 DB 20 GACTTCGGCTGCGCCG 3
 RESULT 732
 LOCUS BD270713 20 bp DNA linear PAT 17-JUL-2003
 DEFINITION Selection system.
 ACCESSION BD270713
 VERSION BD270713.1 GI:33080481
 KEYWORDS JP 2002514413-A/40.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Riechmann,L., Kristensen,P., Jestin,J.L. and Winter,G.P.
 TITLE Selection system
 JOURNAL Patent: JP 2002514413-A 40 21-MAY-2002;
 DIVERSYS LTD
 OS Artificial Sequence
 PN JP 2002514413-A/40

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PD 21-MAY-2002
PF 13-MAY-1999 JP 2000548446
PR 13-MAY-1998 GB 9810223.9,13-MAY-1998 GB 9810228.8 PI
LUTZ RIECHMANN,PETER KRISTENSEN,JEAN LUC JESTIN,GREGORY PAUL PI
WINTER
PC C12N15/00,C12N7/02,C12N15/00
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Db 1 CTGACGGCGGGCTGCCG 18
RESULT 733
BD272876/c
LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of diagnosing Alzheimer's disease or its prognosis.
ACCESSION BD272876
VERSION BD272876.1 GI:33082644
KEYWORDS JP 2002531063-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nitsch,R. and Growdon,J.
TITLE Method of diagnosing Alzheimer's disease or its prognosis
JOURNAL Patent: JP 2002531063-A 2 24-SEP-2002;
COMMENT ROGER NITSCH
OS Artificial Sequence
PN JP 2002531063-A/2
PD 24-SEP-2002
PF 22-OCT-1999 JP 2000578661
PR 23-OCT-1998 US 60/105458,06-NOV-1998 US 60/107434 PR
26-JAN-1999 EP 99101377.2
PI ROGER NITSCH,JOHN GROWDON
PC C12N15/09,A61K38/46,A61K38/55,A61K45/00,A61K48/00,A61P25/28,
PC C12Q1/37,
PC C12Q1/68,G01N33/15,G01N33/50,G01N33/50,G01N33/50,G01N33/53, PC
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PC C12N15/00,A61K37/54,A61K37/64
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 19 TGGTGGGAGGCCCGCATGG 2
RESULT 734
CQ763625

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LOCUS CQ763625 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 2243 from Patent WO2004003201.
ACCESSION CQ763625
VERSION CQ763625.1 GI:44906861
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kane,C.D.
TITLE Antisense modulation of lrlh1 expression
JOURNAL Patent: WO 2004003201-A.2243 08-JAN-2004;
Pharmacia Corporation (US)
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 318 CCCCACTCCCTCAATCTC 335
Db 2 CCCCACTCCCAATCTC 19
RESULT 735
CQ764398
LOCUS 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 3016 from Patent WO2004003201.
ACCESSION CQ764398
VERSION CQ764398.1 GI:44907634
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kane,C.D.
TITLE Antisense modulation of lrlh1 expression
JOURNAL Patent: WO 2004003201-A.3016 08-JAN-2004;
Pharmacia Corporation (US)
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 318 CCCCACTCCCTCAATCTC 335
Db 3 CCCCACTCCCAATCTC 20
RESULT 736
CQ812580/c
LOCUS 20 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 4 from Patent WO2004038416.
ACCESSION CQ812580
VERSION CQ812580.1 GI:47602055
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Golz,S., Brueggemeier,U. and Summer,H.

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TITLE Diagnostics and therapeutics for diseases associated with human g-protein coupled receptor 6 (gpr6)
JOURNAL Patent: WO 2004038416-A 4 06-MAY-2004; Bayer HealthCare AG (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2015 ACCTGACCGTGTCTTA 2032
Db 19 ACTTGACCGTGTCCCTA 2
RESULT 737
LOCUS E40652 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Antihuman Fas humanized antibody-containing antirheumatic.
ACCESSION E40652
VERSION E40652.1 GI:18625145
KEYWORDS JP 2000154149-A/23.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 20)
REFERENCE Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.
AUTHORS Antihuman Fas humanized antibody-containing antirheumatic
TITLE Patent: JP 2000154149-A 23 06-JUN-2000;
JOURNAL SANKYO CO LTD
COMMENT OS Artificial Sequence
PN JP 2000154149-A/23
PD 06-JUN-2000
PF 17-SEP-1999 JP 1999263984
PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI KAORI
PR NAKAHARA,
PI SHIN YONEHARA
PC A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 604 GTGTACAGTGTGACGACAG 621
Db 3 GTGTACTGTGACTACAG 20
RESULT 738
LOCUS E41257 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Beta-Fructofuranosidase gene.
ACCESSION E41257
VERSION E41257.1 GI:18621976
KEYWORDS JP 2000342273-A/2.
SOURCE Arthrobacter sp.
REFERENCE Arthrobacter sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter.

REFERENCE 1 (bases 1 to 20)
AUTHORS Ito,T., Fujita,T., Hara,K., Tonozuka,T. and Sakano,Y.
TITLE Beta-Fructofuranosidase gene
JOURNAL Patent: JP 2000342273-A 2 13-DEC-2000;
SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES
COMMENT OS Arthrobacter sp.
PN JP 2000342273-A/2
PD 12-DEC-2000
PF 08-JUN-1999 JP 1999160416
PR TETSUYA ITO,TAKATERU FUJITA,KOZO HARA,TAKASHI TONOUZUKA, PI
YOSHIYUKI SAKANO
PC C12N15/09,C12N9/24//C12N15/09,C12R1:06),C12N15/00,(C12N15/00,
PC C12R1:06)
CC
FH Key Location/Qualifiers
FT source 1..20
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/organism="Arthrobacter sp."
/mol_type="genomic DNA"
/db_xref="taxon:1667"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 72.2%; Pred. No. 9.8e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 528 CCGGCCCATCTCGCAGGC 545
Db 19 CSGGSCCGTCTGAGSC 2
RESULT 739
LOCUS E49536 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Antisense oligonucleotide regulation of raft gene expression.
ACCESSION E49536
VERSION E49536.1 GI:18628117
KEYWORDS JP 2000152797-A/26.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 20)
P,M.B. and T.B.R.
TITLE Antisense oligonucleotide regulation of raft gene expression
JOURNAL Patent: JP 2000152797-A 26 06-JUN-2000;
ISIS PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2000152797-A/26
PD 06-JUN-2000
PF 18-JAN-2000 JP 2000008654
PR 31-MAY-1994 US 08/250856
PI MONIA BURETTO P,BOGGUZO RUSSELL T
PC C12N15/09,A61K31/7088,A61K48/00,A61P17/06,A61P35/00,A61P43/00,
PC C12N15/00,A
CC
FH Key Location/Qualifiers
FT source 1..20
/organism="Homo sapiens (human)".
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 844 CTGCCAGCCGAGGAGGAG 861
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Db          20 CTGCCAGCGGAGGAGGAG 3

RESULT 740
LOCUS      I27256
DEFINITION Sequence 26 from patent US 5563255.
ACCESSION  I27256
VERSION     I27256.1 GI:1818032
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Monia,B.P. and Boggs,R.T.
TITLE       Antisense oligonucleotide modulation of raf gene expression
JOURNAL     Patent: US 5563255-A 26 08-OCT-1996;
FEATURES    Location/Qualifiers
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                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      52 CGCTGTCAGGTGCTGAAT 69
Db      1 CGCTGCTGCTGCTGATT 18

RESULT 743
LOCUS      AR212285/c
DEFINITION Sequence 11 from patent US 6399754.
ACCESSION  AR212285
VERSION     AR212285.1 GI:21515819
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Cook,P.Dan.
TITLE       Sugar modified oligonucleotides
JOURNAL     Patent: US 6399754-A 11 04-JUN-2002;
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      844 CTGCCAGCGGAGGAGGAG 861
Db      20 CTGCCAGCGGAGGAGGAG 3

RESULT 744
LOCUS      AR215980/c
DEFINITION Sequence 27 from patent US 6410518.
ACCESSION  AR215980
VERSION     AR215980.1 GI:23314268
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Monia,B.P.
TITLE       Antisense oligonucleotide inhibition of raf gene expression
JOURNAL     Patent: US 6410518-A 27 25-JUN-2002;
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      844 CTGCCAGCGGAGGAGGAG 861
Db      20 CTGCCAGCGGAGGAGGAG 3

RESULT 745
LOCUS      AR211552
DEFINITION Sequence 14 from patent US 6399328.
ACCESSION  AR211552
VERSION     AR211552.1 GI:21514903
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Vournakis,J.N., Seth,A.K. and Papas,T.S.
TITLE       Methods and compositions for diagnosis and treatment of breast
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cancer
Patent: US 6399328-A 14 04-JUN-2002;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      52 CGCTGTCAGGTGCTGAAT 69
Db      1 CGCTGCTGCTGCTGATT 18

RESULT 743
LOCUS      AR212285/c
DEFINITION Sequence 11 from patent US 6399754.
ACCESSION  AR212285
VERSION     AR212285.1 GI:21515819
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Cook,P.Dan.
TITLE       Sugar modified oligonucleotides
JOURNAL     Patent: US 6399754-A 11 04-JUN-2002;
FEATURES    Location/Qualifiers
            source
              1..20
                /organism="unknown"
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Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      844 CTGCCAGCGGAGGAGGAG 861
Db      20 CTGCCAGCGGAGGAGGAG 3

RESULT 744
LOCUS      AR215980/c
DEFINITION Sequence 27 from patent US 6410518.
ACCESSION  AR215980
VERSION     AR215980.1 GI:23314268
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Monia,B.P.
TITLE       Antisense oligonucleotide inhibition of raf gene expression
JOURNAL     Patent: US 6410518-A 27 25-JUN-2002;
FEATURES    Location/Qualifiers
            source
              1..20
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Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      844 CTGCCAGCGGAGGAGGAG 861
Db      20 CTGCCAGCGGAGGAGGAG 3

RESULT 745
LOCUS      AR211552
DEFINITION Sequence 14 from patent US 6399328.
ACCESSION  AR211552
VERSION     AR211552.1 GI:21514903
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Vournakis,J.N., Seth,A.K. and Papas,T.S.
TITLE       Methods and compositions for diagnosis and treatment of breast
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AR231783/c
LOCUS AR231783 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6 from patent US 6455249.
ACCESSION AR231783
VERSION AR231783.1 GI:27273358
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hsu, I.-C., Highsmith, W.E. Jr. and Shih, J.
TITLE Method of amplifying DNA and RNA mismatch cleavage products
JOURNAL Patent: US 6455249-A 6 24-SEP-2002;
FEATURES
LOCATION/Qualifiers
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/mol_type="genomic DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2695 CCACCTCCACCCCTGCC 2712
Db 19 CCACCTGCCACCCCTGCAC 2
RESULT 746
AR281887/c
LOCUS AR281887 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 10 from patent US 6521407.
ACCESSION AR281887
VERSION AR281887.1 GI:29717815
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wardenius, H.M. and Seabra, L.A.
TITLE Methods for determining chemosensitivity of cancer cells based upon
expression of negative and positive signal transduction factors
JOURNAL Patent: US 6521407-A 10 18-FEB-2003;
FEATURES
LOCATION/Qualifiers
1..20
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2695 CCACCTCCACCCCTGCC 2712
Db 19 CCACCTGCCACCCCTGCAC 2
RESULT 747
AR296097/c
LOCUS AR296097 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7832 from patent US 6537751.
ACCESSION AR296097
VERSION AR296097.1 GI:31683381
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7832 25-MAR-2003;
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LOCATION/Qualifiers
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/organism="unknown"
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2974 CAGAGGACCAGGGCTTTT 2991
Db 20 CAGAGAACCGGGCTTGT 3
RESULT 748
AR315976/c
LOCUS AR315976 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6513 from patent US 6559294.
ACCESSION AR315976
VERSION AR315976.1 GI:31709402
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths, R., Hojseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6513 06-MAY-2003;
FEATURES
LOCATION/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 743 TTCTCTCTCTGCACACG 760
Db 19 TCCTCTCTCTAGCACACG 2
RESULT 749
AR489974
LOCUS AR489974 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 97 from patent US 6710174.
ACCESSION AR489974
VERSION AR489974.1 GI:47257087
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of vascular endothelial growth factor
receptor-1 expression
JOURNAL Patent: US 6710174-A 97 23-MAR-2004;
FEATURES
LOCATION/Qualifiers
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1352 TCGAGATGATGAAGATGA 1369
Db 1 TCGTGATGATGACGATGA 18
RESULT 750
AX018878/c
LOCUS AX018878 20 bp DNA linear PAT 07-SEP-2000

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DEFINITION Sequence 10 from Patent WO9942839.
ACCESSION AX018878
VERSION AX018878.1 GI:10042974
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Warenius,H.
TITLE Treating cancer
JOURNAL Patent: WO 9942839-A 10 26-AUG-1999;
THERYTE LIMITED (GB); WARENIVS HILMAR (GB)
FEATURES
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/db_xref="taxon:32630"
/note="PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTTCCACCCCTGCCAC 2

RESULT 751
AX018893/c
LOCUS AX018893 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9942834.
ACCESSION AX018893
VERSION AX018893.1 GI:10042989
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Seabra,L.A. and Warenius,H.
TITLE Treating cancer
JOURNAL Patent: WO 9942834-A 10 26-AUG-1999;
SEABRA LAURENCE ANTHONY (GB); THERYTE LIMITED (GB); WARENIVS HILMAR
(GB)
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/note="PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTTCCACCCCTGCCAC 2

RESULT 752
AX018910/c
LOCUS AX018910 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9942828.
ACCESSION AX018910
VERSION AX018910.1 GI:10043005
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Warenius,H.M.
TITLE Treating cancer
JOURNAL Patent: WO 9942828-A 10 26-AUG-1999;
THERYTE LIMITED (GB); WARENIVS HILMAR (GB)
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/note="PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
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QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTTCCACCCCTGCCAC 2

RESULT 753
AX018925/c
LOCUS AX018925 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9942821.
ACCESSION AX018925
VERSION AX018925.1 GI:10043020
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Seabra,L.A. and Warenius,H.M.
TITLE Treating cancer
JOURNAL Patent: WO 9942821-A 10 26-AUG-1999;
SEABRA LAURENCE ANTHONY (GB); THERYTE LIMITED (GB); WARENIVS HILMAR
(GB)
FEATURES
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/organism="synthetic construct"
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTTCCACCCCTGCCAC 2

RESULT 754
AX019039/c
LOCUS AX019039 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9942090.
ACCESSION AX019039
VERSION AX019039.1 GI:10043120
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Warenius,H.M.
TITLE Treating cancer
JOURNAL Patent: WO 9942090-A 10 26-AUG-1999;
THERYTE LIMITED (GB); WARENIVS HILMAR (GB)
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/db_xref="taxon:32630"
/note="PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTTCCACCCCTGCCAC 2
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Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTTCCACCCCTGCAC 2

RESULT 755
AX020774/c
LOCUS AX020774 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 274 from Patent WO9934016.
ACCESSION AX020774
VERSION AX020774.1 GI:10044473
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Vider, B.Z.
TITLE A method for identifying and characterizing cells and tissues
JOURNAL Patent: WO 9934016-A 274 08-JUL-1999;
GENEVA LTD (IL); VIDER BEN ZION (IL)
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1801 GACGTCGTGTCCTTGGG 1818
Db 18 GACGTCGTGTCCTTGGG 1

RESULT 756
AX084307
LOCUS AX084307 20 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 101 from Patent WO0110902.
ACCESSION AX084307
VERSION AX084307.1 GI:13185809
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Shimkets, R.A. and Fernandes, E.
TITLE Nucleic acids and secreted polypeptides encoded thereby
JOURNAL Patent: WO 0110902-A 101 15-FEB-2001;
Curagen Corporation (US)
FEATURES
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1495 GGCCTGGACTACTCTTC 1512
Db 3 GGCCTGGACTACTCTTC 20

RESULT 757
AX092588/c
LOCUS AX092588 20 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 22 from Patent EP1090995.
ACCESSION AX138974
VERSION AX138974.1 GI:14274669
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS King, K.W., Madura, R.A. and Rosey, E.L.
TITLE Mycoplasma hyopneumoniae antigen mhp3, gene encoding it and uses

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Sequence 2 from Patent WO0116364.
ACCESSION AX092588
VERSION AX092588.1 GI:13444646
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Richard, G.U. and Nitsch, R.
TITLE Methods of diagnosing or prognosticating age-related macular
degeneration
JOURNAL Patent: WO 0116364-A 2 08-MAR-2001;
EVOTEC Neurosciences GmbH (DE)
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2940 TGGAGGGAGGCCCCAGGG 2957
Db 19 TGGTGGGAGGCCCATGG 2

RESULT 758
AX104119/c
LOCUS AX104119 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 311 from Patent WO0122972.
ACCESSION AX104119
VERSION AX104119.1 GI:13920316
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 311 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DE)
FEATURES
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1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 20 GACTTCGGCTGGCCCGG 3

RESULT 759
AX138974
LOCUS AX138974 20 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 22 from Patent EP1090995.
ACCESSION AX138974
VERSION AX138974.1 GI:14274669
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS King, K.W., Madura, R.A. and Rosey, E.L.
TITLE Mycoplasma hyopneumoniae antigen mhp3, gene encoding it and uses

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thereof
Patent: EP 1090995-A 22 11-APR-2001;
Pfizer Products Inc. (US)
FEATURES
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3539 GCTTCTAGAGTTTATAG 3556
Db 2 GCTTCTCAGTTTATAG 19

RESULT 760
AX164692/c
LOCUS AX164692 20 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2 from Patent WO0134792.
ACCESSION AX164692
VERSION AX164692.1 GI:14545586
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Itoh,N. and Kavanaugh,M.W.
TITLE Human fgf-23 gene and gene expression products
JOURNAL Patent: WO 0134792-A 5 13-SEP-2001;
          CHIRON CORPORATION (US); Kyoto University (JP)
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGCCCGG 1695
Db 20 GACTTGGCTGCCCGG 3

RESULT 761
AX249751/c
LOCUS AX249751 20 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 5 from Patent WO0166596.
ACCESSION AX249751
VERSION AX249751.1 GI:15864370
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Itoh,N. and Kavanaugh,M.W.
TITLE Human fgf-23 gene and gene expression products
JOURNAL Patent: WO 0166596-A 5 13-SEP-2001;
          CHIRON CORPORATION (US); Kyoto University (JP)
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Sense PCR primer"

thereof
Patent: EP 1090995-A 22 11-APR-2001;
Pfizer Products Inc. (US)
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 825 CTCTGGCTGGCTGGTGGT 842
Db 18 CTCTGAGTGGCTGGTGGT 1

RESULT 762
AX250104/c
LOCUS AX250104 20 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 5 from Patent WO0166595.
ACCESSION AX250104
VERSION AX250104.1 GI:15864512
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Itoh,N. and Kavanaugh,M.W.
TITLE Human fgf-23 gene and gene expression products
JOURNAL Patent: WO 0166595-A 5 13-SEP-2001;
          CHIRON CORPORATION (US); Kyoto University (JP)
FEATURES
    source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Sense PCR primer"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 825 CTCTGGCTGGCTGGTGGT 842
Db 18 CTCTGAGTGGCTGGTGGT 1

RESULT 763
AX293716/c
LOCUS AX293716 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 5478 from Patent WO0179548.
ACCESSION AX293716
VERSION AX293716.1 GI:17055399
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Barany,P., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
          sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 5478 25-OCT-2001;
          CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
    source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Hypothetical Probe Sequence"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 365 CGAGCACCGCATTGGAGG 383
Db 19 CGAGCACCGCATTGCACG 2

RESULT 764
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AX295588
LOCUS AX295588 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 7350 from Patent WO0179548.
ACCESSION AX295588
VERSION AX295588.1 GI:17057277
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic sequences.

REFERENCE
1 Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
AUTHORS Method of designing addressable array for detection of nucleic acid
TITLE sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 7350 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 120 GCGGCTACTGTGCACTT 137
||| ||||| ||||| |||||
Db 2 GCGGCTACTGTGCACTT 19

RESULT 765
AX295703/c
LOCUS AX295703 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 7465 from Patent WO0179548.
ACCESSION AX295703
VERSION AX295703.1 GI:17057392
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1 Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
AUTHORS Method of designing addressable array for detection of nucleic acid
TITLE sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 7465 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..20
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 471 CAAGTTTGGCGACATCCG 488
||| ||||| ||||| |||||
Db 20 CAAGTTTGGCGACATCCG 3

RESULT 766
AX296579
LOCUS AX296579 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 8341 from Patent WO0179548.
ACCESSION AX296579
VERSION AX296579.1 GI:17058268
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1 Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
AUTHORS Method of designing addressable array for detection of nucleic acid
TITLE sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 8341 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 100 TGCAGCGACGGCTCAGC 117
||| ||||| ||||| |||||
Db 3 TGCAGCGACGGCTCAGC 20

RESULT 767
AX297158
LOCUS AX297158 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 8920 from Patent WO0179548.
ACCESSION AX297158
VERSION AX297158.1 GI:17058849
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1 Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
AUTHORS Method of designing addressable array for detection of nucleic acid
TITLE sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 8920 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1692 CCGGACGTCGACCACTT 1709
||| ||||| ||||| |||||
Db 2 CCGGACGTCGACCACTT 19

RESULT 768
AX355435/c
LOCUS AX355435 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 463 from Patent WO0197843.
ACCESSION AX355435
VERSION AX355435.1 GI:18620103
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1 Weiner,G. and Hartmann,G.
AUTHORS Methods for enhancing antibody-induced cell lysis and treating
TITLE cancer
JOURNAL Patent: WO 0197843-A 463 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"

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/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGCCCGG 1695
|||||
Db 20 GACTTTGGCTGCCCGG 3

RESULT 769
AX357565
LOCUS AX357565 20 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 36 from Patent WO0188200.
ACCESSION AX357565
VERSION AX357565.1 GI:18674589
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Wakeland,E.K., Wandstrat,A. and Morel,L.
TITLE Isolation of genes within sle-1b that mediate a break in immune
tolerance
JOURNAL Patent: WO 0188200-A 36 22-NOV-2001;
Board of Regents, The University of Texas System (US)
FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2325 GTGTGTGCTGGTGTGTGT 2342
|||||
Db 3 GGGTGTGTCATGTGTGT 20

RESULT 770
AX487479/c
LOCUS AX487479 20 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4779 from Patent WO02053728.
ACCESSION AX487479
VERSION AX487479.1 GI:22321627
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 4779 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
source
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/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 829 GCGTGGCTGGTGTGCTG 846

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGCCCGG 1695
|||||
Db 20 GACTTTGGCTGCCCGG 3

RESULT 771
AX547172/c
LOCUS AX547172 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 311 from Patent WO02053141.
ACCESSION AX547172
VERSION AX547172.1 GI:25812316
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 311 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic sequence"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGCCCGG 1695
|||||
Db 20 GACTTTGGCTGCCCGG 3

RESULT 772
AX552535
LOCUS AX552535 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 22 from Patent EP1245677.
ACCESSION AX552535
VERSION AX552535.1 GI:25896556
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS King,K.W., Madura,R.A. and Rosey,E.L.
TITLE Nucleic acids and proteins of the mycoplasma hyopneumoniae mhp3
JOURNAL Patent: EP 1245677-A 22 02-OCT-2002;
Pfizer Products Inc. (US)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3539 GCTTCTAGAGTTTATAG 3556
|||||
Db 2 GCTTCTTCAGTTTATAG 19

RESULT 773
AX613359
LOCUS AX613359 20 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 4384 from Patent WO02072882.
ACCESSION AX613359
VERSION AX613359.1 GI:28408788
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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     Cullen,P. and Seedorf,U.
AUTHORS      Coronary chip
JOURNAL      Patent: WO 02072882-A 4384 19-SEP-2002;
              OGHAM GmbH (DE)
FEATURES
  source      Location/Qualifiers
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  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
  /note="Oligonucleotide primer"

  Query Match      0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 9.8e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 368 AGCACCGCATTTGGAGGCA 385
  Db 1 AGACCGCCTTGGAGGCA 18

RESULT 774
AX708866
LOCUS      20 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 48 from Patent WO02101045.
ACCESSION AX708866
VERSION   AX708866.1 GI:29564596
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 Patapoutian,A., Song,C., Ganju,P., Peier,A., McIntyre,P. and
AUTHORS   Bevan,S.
TITLE     Vanilloid receptor-related nucleic acids and polypeptides
JOURNAL   Patent: WO 02101045-A 48 19-DEC-2002;
          Novartis AG (CH); IRM LLC (BM)
FEATURES
  source      Location/Qualifiers
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  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="Oligonucleotide primer"

  Query Match      0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 9.8e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 186 GGAGGACGAGGCTGAGGA 203
  Db 2 GGAGGACGAGGCTGAGGA 19

RESULT 775
AX708891/c
LOCUS      20 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 73 from Patent WO02101045.
ACCESSION AX708891
VERSION   AX708891.1 GI:29564621
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 Patapoutian,A., Song,C., Ganju,P., Peier,A., McIntyre,P. and
AUTHORS   Bevan,S.
TITLE     Vanilloid receptor-related nucleic acids and polypeptides
JOURNAL   Patent: WO 02101045-A 73 19-DEC-2002;
          Novartis AG (CH); IRM LLC (BM)

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  source      Location/Qualifiers
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  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="Oligonucleotide primer"

  Query Match      0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 9.8e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 186 GGAGGACGAGGCTGAGGA 203
  Db 19 GGAGGACGAGGCTGAGGA 2

RESULT 776
BD014728
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Nucleic acid and protein of mhp3 gene of Mycoplasma hypopneumoniae
              and use thereof.
ACCESSION BD014728
VERSION   BD014728.1 GI:22555511
KEYWORDS  JP 2001149085-A/16.
SOURCE    synthetic construct
ORGANISM  synthetic construct
              artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS   King,K.W., Madura,R.A. and Rosi,I.L.
TITLE     Nucleic acid and protein of mhp3 gene of Mycoplasma hypopneumoniae
              and use thereof
JOURNAL   Patent: JP 2001149085-A 16 05-JUN-2001;
              PFIZER PROD INC
COMMENT    OS Artificial Sequence
              PN JP 2001149085-A/16
              PD 05-JUN-2001
              PF 23-SEP-2000 JP 2000300778
              PR 23-SEP-1999 US 60/156602
              PI KENDALL WAIN KING,REBECCA ANNE MADURA,IBURETTO LEE ROSI PC
              C12N15/09,A61K39/02,A61P31/04,C07K14/30,C07K16/12,C07K19/00,PC
              C12N1/21,
              PC C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53//
              PC C12P21/08,
              PC
              (C12N15/09,C12R1:35),(C07K14/30,C12R1:19),(C07K19/00,C12R1:19),PC
              (C12N1/21,C12R1:19),(C12P21/02,C12R1:19),C12N15/00,(C12N15/00,PC
              C12R1:35)
              CC Description of Artificial Sequence:Oligonucleotide FH Key

  FT source      1..20
  FT Location/Qualifiers
  1..20
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

  Query Match      0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 9.8e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 3539 GCTTCTAGAGTTTATAG 3556
  Db 2 GCTTCTAGAGTTTATAG 19

RESULT 777
BD074607/c
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide composition and modulation method of JNK
              protein.
ACCESSION BD074607
VERSION   BD074607.1 GI:23620210

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KEYWORDS      JP 2001514905-A/31.
SOURCE        synthetic construct
ORGANISM      artificial construct
REFERENCE     1 (bases 1 to 20)
AUTHORS      McKay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
TITLE        Antisense oligonucleotide composition and modulation method of JNK
JOURNAL      Protein
COMMENT      Patent: JP 2001514905-A 31 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
            PN JP 2001514905-A/31
            PD 18-SEP-2001
            PF 07-AUG-1998 JP 2000509875
            PR 13-AUG-1997 US 08/910629
            PI ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO, WILLIAM A GAARDE
            PC C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC C12N15/00
            CC antisense sequence
            FH key Location/Qualifiers
            FT source 1..20
            FT /organism="Artificial Sequence".

FEATURES
source
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/organism="Artificial Sequence"
/mol_type="synthetic construct"
/db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 20 GACTTTGGCTGGCCCGG 3

RESULT 778
BD074618
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide composition and modulation method of JNK
            protein.
ACCESSION  BD074618.1 GI:22620221
VERSION     JP 2001514905-A/42.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     McKay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
TITLE       Antisense oligonucleotide composition and modulation method of JNK
JOURNAL     Protein
COMMENT     Patent: JP 2001514905-A 42 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
            PN JP 2001514905-A/42
            PD 18-SEP-2001
            PF 07-AUG-1998 JP 2000509875
            PR 13-AUG-1997 US 08/910629
            PI ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO, WILLIAM A GAARDE
            PC C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC C12N15/00
            CC control sequence (sense)
            FH key Location/Qualifiers
            FT source 1..20
            FT /organism="Artificial Sequence".

FEATURES
source
1..20 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 20 GACTTTGGCTGGCCCGG 3

RESULT 778
BD074618
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide composition and modulation method of JNK
            protein.
ACCESSION  BD074618.1 GI:22620221
VERSION     JP 2001514905-A/42.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     McKay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
TITLE       Antisense oligonucleotide composition and modulation method of JNK
JOURNAL     Protein
COMMENT     Patent: JP 2001514905-A 42 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
            PN JP 2001514905-A/42
            PD 18-SEP-2001
            PF 07-AUG-1998 JP 2000509875
            PR 13-AUG-1997 US 08/910629
            PI ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO, WILLIAM A GAARDE
            PC C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC C12N15/00
            CC control sequence (sense)
            FH key Location/Qualifiers
            FT source 1..20
            FT /organism="Artificial Sequence".

FEATURES
source
1..20 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 20 GACTTTGGCTGGCCCGG 18

RESULT 779
BD082094
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Reagents and methods useful for detecting diseases of the
            prostate,.
ACCESSION  BD082094.1 GI:22627704
VERSION     JP 20015233948-A/21.
KEYWORDS    Zea mays
SOURCE      Zea mays
ORGANISM    Zea mays
REFERENCE   1 (bases 1 to 20)
AUTHORS     Cohen,M., Friedman,P.N., Gordon,J., Hodges,S.C., Klass,M.R.,
            Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
TITLE       Reagents and methods useful for detecting diseases of the prostate
JOURNAL     Patent: JP 20015233948-A 21 27-NOV-2001;
            ABBOTT LABORATORIES
            PN JP 20015233948-A/21
            PD 27-NOV-2001
            PF 08-OCT-1997 JP 1998517758
            PR 08-OCT-1996 US 08/727688
            PI MAURICE COHEN,PAULA N FRIEDMAN,JULIAN GORDON,STEVEN C HODGES,
            PI MICHAEL R KLASS,JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C PI
            RUSSELL,
            PI STEVEN D STROUPE
            PC C12Q1/68,C07K14/47//C07K16/30,G01N33/574
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            CC Topology: Linear;
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            FT /db_xref="taxon:4577"

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Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 921 CTTCTTCCTGTTTCATCCT 938
Db 2 CTTCTTCCTTCCTTCCT 19

RESULT 780
BD084635
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for diagnosis and treatment of breast
            cancer.
ACCESSION  BD084635.1 GI:22630245
VERSION     JP 2001523096-A/13.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Vournakis,J.N., Seth,A.K. and Papas,T.S.
TITLE       Methods and compositions for diagnosis and treatment of breast
JOURNAL     Patent: JP 2001523096-A 13 20-NOV-2001;
            MUSC FOUNDATION FOR RESEARCH DEVELOPMENT
            OS Artificial Sequence

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BD141712
BD141712.1 GI:23236657
WO 0214506-A/3.
synthetic construct
artificial sequences.
1 (bases 1 to 20)
Komori,T., Yamamoto,T., Nitta,N. and Takemori,N.
Method of estimating genotype of fertility recovery locus for rice
Bt type male sterile cytoplasm
Patent: WO 0214506-A 3 21-FEB-2002;
JAPAN TOBACCO INC.SYNGENTA LTD.TOSHIYUKI KOMORI,TOSHIO YAMAMOTO,
NAOTO NITTA,NAOKI TAKEMORI
OS Artificial Sequence
FN WO 0214506-A/3
PD 21-FEB-2002
PF 16-AUG-2001 WO 2001JP007052
PR 17-AUG-2000 JP OOP 247204
PI TOSHIYUKI KOMORI,TOSHIO YAMAMOTO,NAOTO NITTA,NAOKI TAKEMORI PC
C12N15/09,C12Q1/68//A01H1/00
CC Oligonucleotide primer for amplification of G4003 HindIII CC
marker sequence.
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
Location/Qualifiers
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred.No.9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2044 ACCGACGAGTACTGGAC 2061
DB 2 ATCGACGAGTACTGAAC 19
RESULT 783
AB068811/c
LOCUS
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-DLS170 at
p36.
ACCSSION AB068811 GI:15129615 linear SYN 21-MAY-2003
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Ohita,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome lp35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 20)
AUTHORS Horii,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

misc_feature	1..20	notes=reverse primer for human STS sts-D1S170 at lp36 sts-D1S170 obtained from clones B13D23, B54P24, B311L3, B375N12, B99F6, B99C7, Human BAC library RPCI-11"	
Query Match	0.48; Score 14.8; DB 1; Length 20;		
Best Local Similarity	88.9%; Pred. No. 9.8e+02;		
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	999 CCCACCCTGCACAAAGAT 1016		
DB	20 CCACACCATGCACAAAGAT 3		
RESULT 784			
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LOCUS	AR014613	21 bp DNA	linear PAT 05-DEC-1998
DEFINITION	Sequence 46 from patent US 5773691.		
ACCESSION	AR014613		
VERSION	AR014613.1	GI:3972067	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Falco, S. Carl., Keeler, S. Jo. and Rice, J. Ann.		
TITLE	Chimeric genes and methods for increasing the lysine and threonine content of the seeds of plants		
JOURNAL	Patent: US 5773691-A 46 30-JUN-1998;		
FEATURES	Location/Qualifiers		
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Query Match	0.48; Score 14.8; DB 1; Length 21;		
Best Local Similarity	88.9%; Pred. No. 1e+03;		
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QY	1353 GGAGATGATGAAGATGAT 1370		
DB	18 GGAGAGATGAGAGAGAT 1		
RESULT 785			
BD223228/c			
LOCUS	BD223228	21 bp DNA	linear PAT 17-JUL-2003
DEFINITION	A novel plastid-targeting nucleic acid sequence, a novel beta-amylase sequence, a stimulus-responsive promoter and uses thereof.		
ACCESSION	BD223228		
VERSION	BD223228.1	GI:33032998	
KEYWORDS	JP 2002523040-A/5.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Kavanagh, T. A. and Lao, N. T.		
TITLE	A novel plastid-targeting nucleic acid sequence, a novel beta-amylase sequence, a stimulus-responsive promoter and uses		
JOURNAL	Patent: JP 2002523040-A 5 30-JUL-2002;		
COMMENT	ADVANCED TECHNOLOGIES LTD		
	OS Artificial Sequence		
	PN JP 2002523040-A/5		
	PD 30-JUL-2002		
	PF 13-AUG-1999 JP 2000566401		
	PR 19-AUG-1998 GB 9817959.1, 19-AUG-1998 GB 9817963.3 PR		
	OS-JUN-1999 GB 9913014.8		
	PI THOMAS ANTHONY KAVANAGH, NGA THI LAO		
	PC C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N15/00, C12N15/00, C12N15/00, C12R1/91		
	CC (C12N5/00, C12R1/91)		
	Description of Artificial Sequence: PCR Primers FH Key		
	Location/Qualifiers		

[illegible]

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ORGANISM unidentified
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 21)
TITLE Blasczyk,R.D.
JOURNAL A method for determining the histocompatibility locus antigen class
        II
        Patent: EP 0892069-A 94 20-JAN-1999;
        BIOTEST AG (DE)
FEATURES
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        Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
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Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2316 TCTGTGTGTGTGTGTGTG 2333
Db 18 TCTGAGTGTGTGTGTG 1

RESULT 797
AX020773/c
LOCUS AX020773 21 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 273 from Patent WO9934016.
ACCESSION AX020773
VERSION AX020773.1 GI:10044472
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Vider,B.Z.
TITLE A method for identifying and characterizing cells and tissues
JOURNAL Patent: WO 9934016-A 273 08-JUL-1999;
GENENA LTD (IL); VIDER BEN ZION (IL)
FEATURES
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                /organism="Homo sapiens"
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Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 1800 TGACGTCCTGCTCTTTGG 1817
Db 19 TGTGTGTGTCTTTGG 2

RESULT 798
AX092706
LOCUS AX092706 21 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 118 from Patent WO0115676.
ACCESSION AX092706
VERSION AX092706.1 GI:13444763
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and
        triglyceride levels
JOURNAL Patent: WO 0115676-A 118 08-MAR-2001;
        University of British Columbia (CA); Xenon Genetics Inc. (CA)
FEATURES
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/organism="Homo sapiens"
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Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 497 ACACGCTGGACGTGCTGG 514
Db 1 ACACGCTGGGGGTGCTGG 18

RESULT 799
AX095559/c
LOCUS AX095559 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 737 from Patent WO0118250.
ACCESSION AX095559
VERSION AX095559.1 GI:13511762
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
        McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 737 15-MAR-2001;
        WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
        Pharmaceuticals, Inc. (US)
FEATURES
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Best Local Similarity 80.0%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 16; Conservative 1; Mismatches 3;

QY 1386 CATCATCAACCTGCTGGCG 1405
Db 20 CAACATCCAYGTGCTGGCG 1

RESULT 800
AX154199
LOCUS AX154199 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 297 from Patent WO0138576.
ACCESSION AX154199
VERSION AX154199.1 GI:14535813
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 297 31-MAY-2001;
        WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
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Best Local Similarity 80.0%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
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QY 2009 TGGAGACCTGGACCGTGTG 2028

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RESULT 801
AX154392
LOCUS AX154392 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 490 from Patent WO0138576.
ACCESSION AX154392
VERSION AX154392.1 GI:14536006
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 490 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
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Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;
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QY 899 GCATCTCAGCTACGGGGTG 918
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2 GCATCCCACTCTCGGGTG 21

RESULT 802
AX154452
LOCUS AX154452 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 550 from Patent WO0138576.
ACCESSION AX154452
VERSION AX154452.1 GI:14536066
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 550 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
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/organism="Homo sapiens"
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Best Local Similarity 80.0%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 1; Mismatches 0; Gaps 0;
QY 905 TCAGCTACGGGGTGCGCTTC 924
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1 TCAGCTACTCGTGGGGCTC 20

RESULT 803
AX154453/c
LOCUS AX154453 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 551 from Patent WO0138576.
ACCESSION AX154453
VERSION AX154453.1 GI:14536067
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 551 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
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Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 1; Mismatches 0; Gaps 0;
QY 1242 GGAGGCCATCGCATTCACA 1261
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21 GGAGGTCTCTCGCAATGACA 2

RESULT 804
AX342717
LOCUS AX342717 21 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 21 from Patent WO0198511.
ACCESSION AX342717
VERSION AX342717.1 GI:18152095
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gallani,A.I., Imbert,G. and Krek,W.
TITLE Tumour-cell specific gene expression and its use in cancer therapy
JOURNAL Patent: WO 0198511-A 21 27-DEC-2001;
Novartis Forschungsstiftung Zweigniederlassung (CH)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; Mismatches 2; Indels 0; Gaps 0;
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QY 2700 TCCACCCCTGCCCTTCAG 2717
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3 TCCACCCCGGCACCTCAG 20

RESULT 805
AX428083/c
LOCUS AX428083 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 3 from Patent WO0233100.
ACCESSION AX428083
VERSION AX428083.1 GI:21538110
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liu,N. and Floeckner,J.
TITLE Regulation of human adenylate cyclase, type IV
JOURNAL Patent: WO 0233100-A 3 25-APR-2002;
BAYER AG (DE)
FEATURES
source
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Location/Qualifiers

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Primer: AC4-L1"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 868 GAGGCTGACGAGCGCGGC 885
Db 21 GGGCTGAGAGCGCGGC 4

RESULT 806
AX539458/c
LOCUS AX539458 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 245 from Patent WO02059142.
ACCESSION AX539458
VERSION AX539458.1 GI:25272897
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Brinkmann, U., Hoffmeyer, S. and Mornhinweg, E.
TITLE Polymorphisms in the human gene for the multidrug resistance-associated protein 1 (mrp-1) and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 02059142-A 245 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)

FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
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Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 2791 TACATTTCTATAATAGA 2808
Db 20 TCCATTTCTATAATTAGA 3

RESULT 807
AX539459
LOCUS AX539459 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 246 from Patent WO02059142.
ACCESSION AX539459
VERSION AX539459.1 GI:25272899
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Brinkmann, U., Hoffmeyer, S. and Mornhinweg, E.
TITLE Polymorphisms in the human gene for the multidrug resistance-associated protein 1 (mrp-1) and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 02059142-A 246 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)

FEATURES
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Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 2791 TACATTTCTATAATAGA 2808
Db 2 TCCATTTCTATAATTAGA 19

RESULT 808
AX53645/c
LOCUS AX53645 21 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 49 from Patent WO02074946.
ACCESSION AX53645
VERSION AX53645.1 GI:25897643
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Serup, P., Heimberg, H. and Gradwohl, G.
TITLE Method for generating insulin-secreting cells suitable for transplantation
JOURNAL Patent: WO 02074946-A 49 26-SEP-2002;
NOVO NORDISK A/S (DK)

FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 472 AAGTTTGGCAGCATCCGG 489
Db 18 AAGTTTGGCGTCATCCGG 1

RESULT 809
BD010405/c
LOCUS BD010405 21 bp DNA linear PAT 09-JAN-2004
DEFINITION Chimeric genes and methods for increasing the lysine content of the seeds of plants.

ACCESSION BD010405
VERSION BD010405.1 GI:18638778
KEYWORDS JP 2001502923-A/37.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 21)
AUTHORS Falco, S.C., Iii, R.E.M. and Epelbaum, S.U.
TITLE Chimeric genes and methods for increasing the lysine content of the seeds of plants
JOURNAL Patent: JP 2001502923-A 37 06-MAR-2001;
EI DU PONT DE NEMOURS AND CO

COMMENT OS Unidentified
PN JP 2001502923-A/37
PD 06-MAR-2001
PF 27-MAR-1998 JP 1998543284
PR 27-MAR-1997 US 08/824627
PI SAVORIO CARL FALCO, RAYMOND ERVIN MCDEVITT III, PI SABINE URSULA EPELBAUM
PC C12N9/06, C12N9/12, C12N9/88, C12P13/08, C12N15/82 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1353 GGAGATGATGAAGATGAT 1370
Db 18 GGAGATGATGAAGAT 1

RESULT 810
BD088877/c
LOCUS BD088877 21 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088877
VERSION BD088877.1 GI:22634487
KEYWORDS JP 2001321190-A/1121.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE Soeda,E.
AUTHORS A method of arraying genome clone
TITLE Patent: JP 2001321190-A 1121 20-NOV-2001;
JOURNAL THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
COMMENT GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1121
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source
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Query Match      0.4%; Score 14.8; DB 1; Length 21;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 19 ATGTGCTTGTCTCTTTT 2

RESULT 811
AR264922
LOCUS AR264922 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 6 from patent US 6492121.
ACCESSION AR264922
VERSION AR264922.1 GI:29693309
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 6 10-DEC-2002;
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Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTT 3284
Db 5 ATATTTTTTTTGTCTTTT 30

RESULT 812
AR264923
LOCUS AR264923 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 7 from patent US 6492121.
ACCESSION AR264923
VERSION AR264923.1 GI:29693310
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 7 10-DEC-2002;
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Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTT 3284
Db 5 ATATTTTTTTTGTCTTTT 30

RESULT 813
AR264928
LOCUS AR264928 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 12 from patent US 6492121.
ACCESSION AR264928
VERSION AR264928.1 GI:29693315
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 12 10-DEC-2002;
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Query Match      0.4%; Score 14.8; DB 1; Length 30;
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Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTT 3284
Db 5 ATATTTTTTTTGTCTTTT 30

RESULT 814
AR264928
LOCUS AR264928 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 12 from patent US 6492121.
ACCESSION AR264928
VERSION AR264928.1 GI:29693315
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 12 10-DEC-2002;
FEATURES Location/Qualifiers
source
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Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"
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AR478203
LOCUS       AR478203               30 bp      DNA          linear      PAT 14-MAY-2004
DEFINITION   Sequence 6 from patent US 6699661.
ACCESSION    AR478203
VERSION      AR478203.1 GI:47236851
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 30)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
              Yokomaku,T., Koyama,O. and Furusho,K.
TITLE        Method for determining a concentration of target nucleic acid
              molecules, nucleic acid probes for the method, and method for
              analyzing data obtained by the method
JOURNAL      Patent: US 6699661-A 6 02-MAR-2004;
FEATURES     Location/Qualifiers
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Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3284
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Db 5 ATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 815
BD072867
LOCUS       BD072867               30 bp      DNA          linear      PAT 27-AUG-2002
DEFINITION   Method for assaying nucleic acid, nucleic acid probe used therefor,
              and method for analyzing data obtained by that method.
ACCESSION    BD072867
VERSION      BD072867.1 GI:22618470
KEYWORDS     JP 2001286300-A/5.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 30)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
              Yokomaku,T., Koyama,O. and Furusho,K.
TITLE        Method for assaying nucleic acid, nucleic acid probe used therefor,
              and method for analyzing data obtained by that method
JOURNAL      Patent: JP 2001286300-A 5 16-OCT-2001;
              JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, DIRECTOR GENERAL OF
              NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
              AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
              OS Artificial Sequence
              PN JP 2001286300-A/5
              PD 16-OCT-2001
              PF 20-APR-2000 JP 2000120097
              PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
              KURATA,
              KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU, OSAMU KOYAMA, KENTA FURUSHO
              PC C12Q1/68, C12M1/60, C12N15/09, G01N31/22, G01N33/53, G01N33/542, PC
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              PC C12N15/00
              CC The base sequence was prepared synthetically on the aim of CC
              CC decrease in fluorescence emission of a nucleic acid probe CC
              CC labeled with
              CC BODIBY FL/C6 upon the hybridization of the
              CC probe with a target
              CC . nucleic
              CC acid.
              CC Key Location/Qualifiers
              FH Key 1..30
              FT source /organism='Artificial Sequence'.
              FT Location/Qualifiers
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             1..30
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3284
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Db 5 ATATTTTCTTTTCTTTTCTTTTCTTTT 30

AR478204
LOCUS       AR478204               30 bp      DNA          linear      PAT 14-MAY-2004
DEFINITION   Sequence 7 from patent US 6699661.
ACCESSION    AR478204
VERSION      AR478204.1 GI:47236852
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 30)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
              Yokomaku,T., Koyama,O. and Furusho,K.
TITLE        Method for determining a concentration of target nucleic acid
              molecules, nucleic acid probes for the method, and method for
              analyzing data obtained by the method
JOURNAL      Patent: US 6699661-A 7 02-MAR-2004;
FEATURES     Location/Qualifiers
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Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3284
      ||||| ||||| ||||| ||||| |||||
Db 5 ATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 816
BD072867
LOCUS       BD072867               30 bp      DNA          linear      PAT 14-MAY-2004
DEFINITION   Sequence 12 from patent US 6699661.
ACCESSION    AR478209
VERSION      AR478209.1 GI:47236857
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 30)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
              Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
              Yokomaku,T., Koyama,O. and Furusho,K.
TITLE        Method for determining a concentration of target nucleic acid
              molecules, nucleic acid probes for the method, and method for
              analyzing data obtained by the method
JOURNAL      Patent: US 6699661-A 7 02-MAR-2004;
FEATURES     Location/Qualifiers
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             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3284
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Db 5 ATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 816
BD072867
LOCUS       BD072867               30 bp      DNA          linear      PAT 14-MAY-2004
DEFINITION   Sequence 12 from patent US 6699661.
ACCESSION    AR478209
VERSION      AR478209.1 GI:47236857
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 30)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
              Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
              Yokomaku,T., Koyama,O. and Furusho,K.
TITLE        Method for determining a concentration of target nucleic acid
              molecules, nucleic acid probes for the method, and method for
              analyzing data obtained by the method
JOURNAL      Patent: US 6699661-A 7 02-MAR-2004;
FEATURES     Location/Qualifiers
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             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3284
      ||||| ||||| ||||| ||||| |||||
Db 5 ATATTTTCTTTTCTTTTCTTTTCTTTT 30
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RESULT 818
BD072873
LOCUS          30 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Method for assaying nucleic acid, nucleic acid probe used therefor,
               and method for analyzing data obtained by that method.
ACCESSION
VERSION       BD072873.1 GI:22618476
KEYWORDS      JP 2001286300-A/11.
SOURCE        synthetic construct
ORGANISM      artificial construct
REFERENCE     1 (bases 1 to 30)
AUTHORS      Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
               Yokomaku,T., Koyama,O. and Furusho,K.
TITLE        Method for assaying nucleic acid, nucleic acid probe used therefor,
               and method for analyzing data obtained by that method
JOURNAL       Patent: JP 2001286300-A 11 16-OCT-2001;
               JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
               NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
               AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
FEATURES      OS Artificial Sequence
               PN JP 2001286300-A/11
               PD 16-OCT-2001
               PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
               KURATA,
               PC KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
               PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53,G01N33/542,PC
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               PC C12N15/00
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               CC decrease in fluorescence emission of a nucleic acid probe CC
               CC labeled with
               CC BODIBY FL/C6 upon the hybridization of the
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               CC nucleic
               CC acid.
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               Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
               QY 3259 AGATATTTTATTCGTTTGTCTTTT 3284
               Db 5 ATATTTTTCCTTTTCTTTTTCCTTTT 30
RESULT 820
BD107500
LOCUS          30 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION    Novel quantitative polymorphism analysis method.
ACCESSION     BD107500
VERSION       BD107500.1 GI:23202318
KEYWORDS      JP 2002000275-A/9.
SOURCE        synthetic construct
ORGANISM      artificial construct
REFERENCE     1 (bases 1 to 30)
AUTHORS      Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
               Yokomaku,T.
TITLE        Novel quantitative polymorphism analysis method
JOURNAL       Patent: JP 2002000275-A 9 08-JAN-2002;
               JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
               & TECHNOL
FEATURES      OS Artificial Sequence
               PN JP 2002000275-A/9
               PD 08-JAN-2002
               PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
               KURATA,
               PC KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
               PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base
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               examining the
               CC decrease in fluorescence emission of a nucleic acid probe CC
               CC labeled with
               CC BODIBY FL/C6 upon the hybridization of the
               CC probe with a target
               CC nucleic
               CC acid.
               FH Key Location/Qualifiers
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               /db_xref='taxon:32630'
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               Query Match 0.4%; Score 14.8; DB 1; Length 30;
               Best Local Similarity 73.1%; Pred. No. 1.3e+03;
               Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
               QY 3259 AGATATTTTATTCGTTTGTCTTTT 3284
               Db 5 ATATTTTTCCTTTTCTTTTTCCTTTT 30
RESULT 819
BD107494
LOCUS          30 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION    Novel quantitative polymorphism analysis method.
ACCESSION     BD107494
VERSION       BD107494.1 GI:23202312
KEYWORDS      JP 2002000275-A/3.
SOURCE        synthetic construct
ORGANISM      artificial construct
REFERENCE     1 (bases 1 to 30)
AUTHORS      Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
               Yokomaku,T.
TITLE        Novel quantitative polymorphism analysis method
JOURNAL       Patent: JP 2002000275-A 3 08-JAN-2002;
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Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTGCTTTGTCCTTTT 3284
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Db 5 ATATTTTTTTTTTCTTTTTTTTTTTT 30

RESULT 821
BD145026        30 bp DNA linear PAT 17-JAN-2003
LOCUS           Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION      and method for analyzing data obtained by that method.
ACCESSION       BD145026
VERSION         BD145026.1 GI:27850784
KEYWORDS        JP 2002119291-A/7.
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1 (bases 1 to 30)
AUTHORS         Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
                Yamada,K. and Yokomaku,T.
TITLE           Method for assaying nucleic acid, nucleic acid probe used therefor,
                and method for analyzing data obtained by that method
JOURNAL         Patent: JP 2002119291-A 7 23-APR-2002;
                JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
                INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT         OS Artificial Sequence
                PN JP 2002119291-A/7
                PD 23-APR-2002
                PF 27-APR-2001 JP 2001133529
                PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
                TORIMURA,
                SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
                C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/ PC
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                G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
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                examining the
                decrease in fluorescence emission of
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Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTGCTTTGTCCTTTT 3284
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Db 5 ATATTTTTTTTTTCTTTTTTTTTTTT 30

RESULT 822
BD145032        30 bp DNA linear PAT 17-JAN-2003
LOCUS           Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION      and method for analyzing data obtained by that method.
ACCESSION       BD145032
VERSION         BD145032.1 GI:27850790
KEYWORDS        JP 2002119291-A/13.
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1 (bases 1 to 30)
AUTHORS         Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
                Yamada,K. and Yokomaku,T.
TITLE           Method for assaying nucleic acid, nucleic acid probe used therefor,
                and method for analyzing data obtained by that method
JOURNAL         Patent: JP 2002119291-A 13 23-APR-2002;
                JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
                INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT         OS Artificial Sequence
                PN JP 2002119291-A/13
                PD 23-APR-2002
                PF 27-APR-2001 JP 2001133529
                PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
                TORIMURA,
                SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
                C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/ PC
                53,
                G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
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                CC The base sequence was prepared synthetically on the aim of CC
                examining the
                decrease in fluorescence emission of
                a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
                hybridization of
                the probe with a target nucleic acid.
                FH Key Location/Qualifiers
                FT source 1. .30
                /organism='Artificial Sequence'.
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                1. .30
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTGCTTTGTCCTTTT 3284
    ||||| ||||| ||||| ||||| |||||
Db 5 ATATTTTTTTTTTCTTTTTTTTTTTT 30

RESULT 823
BD166027        30 bp DNA linear PAT 17-JAN-2003
LOCUS           Novel nucleic acid probes, method for determining concentrations of
DEFINITION      nucleic acid by using the probes, and method for analyzing data
                obtained by the method.
ACCESSION       BD166027
VERSION         BD166027.1 GI:27871839
KEYWORDS        JP 2002191372-A/7.
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 30)
AUTHORS         Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
                Yamada,K. and Yokomaku,T.
TITLE           Novel nucleic acid probes, method for determining concentrations of
                nucleic acid by using the probes, and method for analyzing data
                obtained by the method
JOURNAL         Patent: JP 2002191372-A 7 09-JUL-2002;
                NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
                KANKYO ENGINEERING CO LTD
COMMENT         OS Artificial Sequence

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PN JP 2002191372-A/7
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with the hybridization of the
probe with a target
nucleic
acid.
FH Key Location/Qualifiers
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FEATURES
source
Location/Qualifiers
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/mol_type='genomic DNA'
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Query Match 0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3284
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DB 5 ATATTTTTTTTGTGTTTTTTTTTTT 30

RESULT 824
BD166032
LOCUS 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166032
VERSION BD166032.1 GI:27871844
KEYWORDS JP 2002191372-A/12.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 12 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002191372-A/12
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
probe with a target
nucleic
acid.
FH Key Location/Qualifiers

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FT source 1..30
/organism='Artificial Sequence'.

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Location/Qualifiers
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3284
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DB 5 ATATTTTTTTTGTGTTTTTTTTTTT 30

RESULT 825
AR029830
LOCUS 35 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5861244.
ACCESSION AR029830
VERSION AR029830.1 GI:5943044
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 19 19-JAN-1999;
FEATURES Location/Qualifiers
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1..35
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 0.4%; Score 14.8; DB 1; Length 35;
Best Local Similarity 64.7%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3300 TTCTATAGGATTTTCTTTAGGAGATTTTATTTT 3333
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DB 1 TTTTCTATCTTTTCTTTTCTTTTCTTTTCTTTT 34

RESULT 826
I32405
LOCUS 42 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5587443.
ACCESSION I32405
VERSION I32405.1 GI:1823196
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 42)
AUTHORS Heiliger,L., Schmidt,A. and Probst,J.
TITLE Polymerizable emulsifiers and reactive groups and polymers of
emulsifiers and other monomers
JOURNAL Patent: US 5587443-A 2 24-DEC-1996;
FEATURES Location/Qualifiers
source
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/organism='unknown'
/mol_type='unassigned DNA'

Query Match 0.4%; Score 14.8; DB 1; Length 42;
Best Local Similarity 64.7%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3301 TCTATAGGATTTTCTTTAGGAGATTTTATTTT 3334
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DB 2 TCTACTGGCTCTTTTCTTTTCTTTTCTTTTCTTTT 35

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RESULT 827
AX287575
LOCUS AX287575 45 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 18 from Patent WO0177390.
ACCESSION AX287575
VERSION AX287575.1 GI:17049341
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS abarz A.P.
TITLE Process for allele discrimination utilizing primer extension
JOURNAL Patent: WO 0177390-A 18 OCT-2001;
Molecular Staging, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="P1 primer for use in allele discrimination"
Query Match 0.4%; Score 14.8; DB 1; Length 45;
Best Local Similarity 73.1%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3262 TATTTATTGCTTGTGCTTTTCA 3287
|||||
Db 12 TTTTATTTTATTTTATTTTATTTTCA 37

RESULT 828
AX287571
LOCUS AX287571 45 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 14 from Patent WO0177390.
ACCESSION AX287571
VERSION AX287571.1 GI:17049337
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS abarz A.P.
TITLE Process for allele discrimination utilizing primer extension
JOURNAL Patent: WO 0177390-A 14 OCT-2001;
Molecular Staging, Inc. (US)
FEATURES
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/db_xref="taxon:32630"
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Query Match 0.4%; Score 14.8; DB 1; Length 45;
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Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3262 TATTTATTGCTTGTGCTTTTCA 3287
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Db 12 TTTTATTTTATTTTATTTTATTTTCA 37

RESULT 829
AX287571/c
LOCUS AX287571/c 45 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 14 from Patent WO0177390.
ACCESSION AX287571
VERSION AX287571.1 GI:17049337
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS abarz A.P.
TITLE Process for allele discrimination utilizing primer extension
JOURNAL Patent: WO 0177390-A 14 OCT-2001;
Molecular Staging, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="P1 primer for use in allele discrimination"
Query Match 0.4%; Score 14.8; DB 1; Length 45;
Best Local Similarity 73.1%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3262 TATTTATTGCTTGTGCTTTTCA 3287
|||||
Db 12 TTTTATTTTATTTTATTTTATTTTCA 37
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REFERENCE
1
AUTHORS abarz A.P.
TITLE Process for allele discrimination utilizing primer extension
JOURNAL Patent: WO 0177390-A 14 OCT-2001;
Molecular Staging, Inc. (US)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="P1 primer for use in allele discrimination"
Query Match 0.4%; Score 14.8; DB 1; Length 45;
Best Local Similarity 59.5%; Pred. No. 1.5e+03;
Matches 25; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1353 GGAGATGATGAAGATGATCGGGAACACAAAACATCATCAA 1394
|||||
Db 45 GGAGAGGTGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 830
BD002050
LOCUS BD002050 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Agent for retarding the conversion of hormone-dependent cancer into hormone-independent cancer.
ACCESSION BD002050
VERSION BD002050.1 GI:18628790
KEYWORDS JP 2000178202-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 (bases 1 to 17)
AUTHORS Matsutani, T. and Naito, K.
TITLE Agent for retarding the conversion of hormone-dependent cancer into hormone-independent cancer.
JOURNAL Patent: JP 2000178202-A 1 27-JUN-2000;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Artificial Sequence
PN JP 2000178202-A/1
PD 27-JUN-2000
PF 07-OCT-1999 JP 1999286856
PR
PI TOSHIYA MATSUTANI, KENICHIRO NAITO
PC A61K38/04,A61K38/22,A61K45/00,A61P13/08,A61P35/00//C07K7/23 CC
PH Key Location/Qualifiers
FT source 1. .17
/organism='Artificial Sequence'.
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 14.6; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 9.1e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1618 CACAGGGACCTGGCTGC 1634
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Db 1 CAYMGGAAYTGGCHGC 17

RESULT 831
BD002052
LOCUS BD002052 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Agent for retarding the conversion of hormone-dependent cancer into hormone-independent cancer.
ACCESSION BD002052
VERSION BD002052.1 GI:18628792
KEYWORDS JP 2000178202-A/3.
SOURCE synthetic construct
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ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsutani, T. and Naito, K.
TITLE Agent for retarding the conversion of hormone-dependent cancer into hormone-independent cancer
JOURNAL Patent: JP 2000178202-A 3 27-JUN-2000;
COMMENT TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2000178202-A/3
PD 27-JUN-2000
PF 07-OCT-1999 JP 1999286956
PR
PI TOSHIYA MATSUTANI, KENICHIRO NAITO
PC A61K38/04, A61K38/22, A61K45/00, A61P13/08, A61P35/00//C07K7/23 CC

PH Key Location/Qualifiers
FT source 1..176
FT /organism='Artificial Sequence'.
FEATURES
source 1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.6; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 9.1e+02;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1618 CACAGGACCTGGCTGC 1534
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DB 1 CAYMGRGACVTKGWC 17

RESULT 832
LOCUS I29931/c
DEFINITION Sequence 44 from patent US 5578468.
ACCESSION I29931
VERSION I29931.1 GI:1820722
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Pickup, D.J., Patel, D. and Antczak, J.B.
TITLE Site-specific RNA cleavage
JOURNAL Patent: US 5578468-A 44 26-NOV-1996;
FEATURES
source 1..37
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.6; DB 1; Length 37;
Best Local Similarity 62.2%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 3299 TTCTCTAGGATTTCTTTAGGAGATTTATTTTGG 3335
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DB 37 TTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTG 1

RESULT 833
LOCUS AR222446/c
DEFINITION Sequence 4 from patent US 6429300.
ACCESSION AR222446
VERSION AR222446.1 GI:23329977
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)

AUTHORS Kurz, M., Lohse, P. and Wagner, R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 4 06-AUG-2002;
FEATURES
source 1..39
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.6; DB 1; Length 39;
Best Local Similarity 69.0%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3262 TATTTTATTTGCTTCTCCTTTTTCAGGA 3290
|||||
DB 35 TTTTNTTTTTTTTTTTTTTTTTTTTTTTAGAA 7

RESULT 834
LOCUS AR029978/c
DEFINITION Sequence 167 from patent US 5861244.
ACCESSION AR029978
VERSION AR029978.1 GI:5943192
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 167 19-JAN-1999;
FEATURES
source 1..16
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 923 TCTTCCTGTTTCATCCT 938
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DB 16 TCTTCCTCTTCATCCT 1

RESULT 835
LOCUS AR050989
DEFINITION Sequence 58 from patent US 5830644.
ACCESSION AR050989
VERSION AR050989.1 GI:5974353
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West, M.D., Shay, J. and Wright, W.E.
TITLE Method for screening for agents which increase telomerase activity in a cell
JOURNAL Patent: US 5830644-A 58 03-NOV-1999;
FEATURES
source 1..16
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTC 2333
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DB 1 TGGGTGTGTGTGTGTC 16

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RESULT 836
E32226/c
LOCUS          E32226          16 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for isolating satellite sequence.
ACCESSION      E32226
VERSION        E32226.1  GI:13021862
KEYWORDS       JP 2000060559-A/28.
SOURCE         Haliotis discus discus
ORGANISM       Haliotis discus discus
REFERENCE      1 (bases 1 to 16)
AUTHORS        Hideaki.T. and Masashi.S.
TITLE          Method for isolating satellite sequence
JOURNAL        Patent: JP 2000060559-A 28 29-FEB-2000;
               NATL INST OF AGRICULTURAL RESOURCES
COMMENT        OS Haliotis discus discus
               PN JP 2000060559-A/28
               PD 29-FEB-2000
               PF 18-AUG-1998  JP 1998232153
               PR
               PI HIDEAKI TAKAHASHI,MASASHI SEKINO
               PC C12N15/09,C12Q1/68,C12N15/00
               CC
               FH Key
               FT source
               FT Location/Qualifiers
FEATURES       source
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               /db_xref="taxon:91233"
Query Match    0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2316 TCTGTGTGTGTGTGTG 2331
Db 16 TCTGTGTGTGTGTGTG 1
RESULT 837
I33563
LOCUS          I33563          16 bp      DNA          linear          PAT 06-FEB-1997
DEFINITION     Sequence 2 from patent US 5593834.
ACCESSION      I33563
VERSION        I33563.1  GI:1824354
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Lane,M.J., Benight,A.S. and Paldasz,B.D.
TITLE          Method of preparing DNA sequences with known ligand binding
JOURNAL        Patent: US 5593834-A 2 14-JAN-1997;
               Location/Qualifiers
FEATURES       source
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               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match    0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2316 TCTGTGTGTGTGTGTG 2331
Db 16 TCTGTGTGTGTGTGTG 1
RESULT 838
I33563/c
LOCUS          I33563          16 bp      DNA          linear          PAT 06-FEB-1997
DEFINITION     Sequence 2 from patent US 5593834.
ACCESSION      I33563
VERSION        I33563.1  GI:1824354
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Lane,M.J., Benight,A.S. and Paldasz,B.D.
TITLE          Method of preparing DNA sequences with known ligand binding
JOURNAL        Patent: US 5593834-A 2 14-JAN-1997;
               Location/Qualifiers
FEATURES       source
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               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match    0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3464 ATATATATCTATATAT 3479
Db 16 ATATATAGCTATATAT 1
RESULT 839
I38642
LOCUS          I38642          16 bp      DNA          linear          PAT 13-MAY-1997
DEFINITION     Sequence 2 from patent US 5614617.
ACCESSION      I38642
VERSION        I38642.1  GI:2084696
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Cook,P.D. and Sanghvi,Y.S.
TITLE          Nuclease resistant, pyrimidine modified oligonucleotides that
               detect and modulate gene expression
JOURNAL        Patent: US 5614617-A 2 25-MAR-1997;
               Location/Qualifiers
FEATURES       source
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               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match    0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2824 ATATATACATATATAT 2839
Db 1 ATATATATATATATAT 16
RESULT 840
I38642/c
LOCUS          I38642          16 bp      DNA          linear          PAT 13-MAY-1997
DEFINITION     Sequence 2 from patent US 5614617.
ACCESSION      I38642
VERSION        I38642.1  GI:2084696
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Cook,P.D. and Sanghvi,Y.S.
TITLE          Nuclease resistant, pyrimidine modified oligonucleotides that
               detect and modulate gene expression
JOURNAL        Patent: US 5614617-A 2 25-MAR-1997;
               Location/Qualifiers
FEATURES       source
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Query Match    0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3464 ATATATATCTATATAT 3479
Db 1 ATATATAGCTATATAT 16

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Query Match
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  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2824 ATATATACATATATAT 2839
Db 16 ATATATATATATAT 1

RESULT 841
LOCUS I51790 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 58 from patent US 5645986.
ACCESSION I51790
VERSION I51790.1 GI:2472991
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 16)
  West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
  Wright,W.E., Blackburn,E.H. and Vaziri,H.
  Therapy and diagnosis of conditions related to telomere length
  and/or telomerase activity
  JOURNAL Patent: US 5645986-A 58 08-JUL-1997;
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      1. .16
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTG 2333
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 842
LOCUS I84399 16 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 57 from patent US 5695932.
ACCESSION I84399
VERSION I84399.1 GI:3021919
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 16)
  West,M.D., Shay,J., Wright,W., Blackburn,E.H. and McEachern,M.J.
  Telomerase activity assays for diagnosing pathogenic infections
  JOURNAL Patent: US 5695932-A 57 09-DEC-1997;
  FEATURES
    Location/Qualifiers
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      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTG 2333
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 843
LOCUS I51790 16 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 58 from patent US 5645986.
ACCESSION I51790
VERSION I51790.1 GI:2472991
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 16)
  West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
  Wright,W.E., Blackburn,E.H. and Vaziri,H.
  Therapy and diagnosis of conditions related to telomere length
  and/or telomerase activity
  JOURNAL Patent: US 5645986-A 58 08-JUL-1997;
  FEATURES
    Location/Qualifiers
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      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTG 2333
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 844
LOCUS AR307317 16 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 80 from patent US 6551774.
ACCESSION AR307317
VERSION AR307317.1 GI:31697844
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 16)
  West,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
  Shay,J., Wright,W.E., Blackburn,E.H., Kim,N.W. and Vaziri,H.
  Diagnostic methods for conditions associated with elevated cellular
  levels of telomerase activity
  JOURNAL Patent: US 6551774-A 80 22-APR-2003;
  FEATURES
    Location/Qualifiers
      1. .16
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTG 2333
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 845
LOCUS AR328417 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5819 from patent US 6566127.
ACCESSION AR328417
VERSION AR328417.1 GI:33714225
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 16)
  Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
  JOURNAL Patent: US 6566127-A 5819 20-MAY-2003;
  FEATURES
    Location/Qualifiers
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/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1295 TCAAGATGCTGAAGA 1310
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Db 1 TGAATGCTGAAGA 16

RESULT 846
AR328446
LOCUS
DEFINITION
Sequence 5848 from patent US 6566127.
ACCESSION
AR328446
VERSION
AR328446.1 GI:33714254
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6566127-A 5848 20-MAY-2003;
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 ACAACGTGTGAAGAT 1673
|||||
Db 1 ACAACGTGTGAAGAT 16

RESULT 847
AR328669
LOCUS
DEFINITION
Sequence 6071 from patent US 6566127.
ACCESSION
AR328669
VERSION
AR328669.1 GI:33714477
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6566127-A 6071 20-MAY-2003;
FEATURES
Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2321 GTGTGTGTGTGGT 2336
|||||
Db 1 GTGTGTGTGTGGT 16

RESULT 848
AX067878/c

source
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1295 TCAAGATGCTGAAGA 1310
|||||
Db 1 TGAATGCTGAAGA 16

RESULT 846
AR328446
LOCUS
DEFINITION
Sequence 5848 from patent US 6566127.
ACCESSION
AR328446
VERSION
AR328446.1 GI:33714254
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6566127-A 5848 20-MAY-2003;
FEATURES
Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 ACAACGTGTGAAGAT 1673
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Db 1 ACAACGTGTGAAGAT 16

RESULT 847
AR328669
LOCUS
DEFINITION
Sequence 6071 from patent US 6566127.
ACCESSION
AR328669
VERSION
AR328669.1 GI:33714477
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6566127-A 6071 20-MAY-2003;
FEATURES
Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2321 GTGTGTGTGTGGT 2336
|||||
Db 1 GTGTGTGTGTGGT 16

RESULT 848
AX067878/c

LOCUS
AX067878
DEFINITION
Sequence 19 from Patent WO0077205.
ACCESSION
AX067878
VERSION
AX067878.1 GI:12329735
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1
AUTHORS
Barber,G.N., Saunders,L. and Perkins,D.
TITLE
Human nuclear factors associated with dsrna (nfmr)
JOURNAL
Patent: WO 0077205-A 19 21-DEC-2000;
Barber, Glen N. (US); Saunders, Laura (US); Perkins, Darren (US)
FEATURES
Location/Qualifiers
source
1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2673 GCCTCCCTACCTCCAG 2688
|||||
Db 16 GCCTCCCTACCTCCAG 1

RESULT 849
AX135452
LOCUS
DEFINITION
Sequence 9 from Patent EP1113080.
ACCESSION
AX135452
VERSION
AX135452.1 GI:14271800
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Wang,X.B.
TITLE
Personal gene library
JOURNAL
Patent: EP 1113080-A 9 04-JUL-2001;
Wang, Xiao Bing (US); Morisawa, Shinkatsu (JP)
FEATURES
Location/Qualifiers
source
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 GTGCTGTGACCGAGG 1657
|||||
Db 1 GTGCTGTGACCGAGG 16

RESULT 850
BD002055/c
LOCUS
DEFINITION
Agent for retarding the conversion of hormone-dependent cancer into
hormone-independent cancer.
ACCESSION
BD002055
VERSION
BD002055.1 GI:18628795
KEYWORDS
JP 2000178202-A/6.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Matsutani,T. and Naito,K.
```

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TITLE      Agent for retarding the conversion of hormone-dependent cancer into
JOURNAL    hormone-independent cancer
COMMENT    Patent: JP 2000178202-A 6 27-JUN-2000;
          TAKEDA CHEMICAL INDUSTRIES LTD
          OS Artificial Sequence
          PN JP 2000178202-A/6
          PD 27-JUN-2000
          PF 07-OCT-1999 JP 1999286956
          PR TOSHIYA MATSUTANI,KENICHIRO NAITO
          PC A61K38/04,A61K38/22,A61K45/00,A61P13/08,A61P35/00//C07K7/23 CC

FH Key      Location/Qualifiers
FT source   1..16
FT          /organism='Artificial Sequence'.
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    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match      0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 9.2e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1798 AGTGAGCTGTGGTCCT 1813
Db 16 AGVGAGTGTGGTCYT 1

RESULT 851
LOCUS      BD016424
DEFINITION Personal gene library.
ACCESSION  BD016424
VERSION     BD016424.1 GI:22557562
KEYWORDS   JP 2001186882-A/9.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS    Wang,X.
TITLE      Personal gene library
JOURNAL    Patent: JP 2001186882-A 9 10-JUL-2001;
          XIAOBING WANG,SHINKATSU MORISAWA
COMMENT    OS Unidentified
          PN JP 2001186882-A/9
          PD 10-JUL-2001
          PF 17-NOV-2000 JP 2000350702
          PR 01-DEC-1999 US 60/168297,09-NOV-2000 US 09/708493 PI
          PC C12N15/09,C12N15/00,C12M1/00,C12Q1/68,C12N15/00,C12N15/00 CC
          Strandedness: Single;
          CC Topology: Linear;
          CC Personal gene library
          FH Key      Location/Qualifiers
          FT source   1..16
          FT          /organism='Unidentified'.
FEATURES
  source
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    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

Query Match      0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 GTGCTGTGACCGAGG 1657
Db 1 GTGCTGTGACCGAGG 16

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RESULT 852
LOCUS      AR046263/c
DEFINITION Sequence 1056 from patent US 5817796.
ACCESSION  AR046263
VERSION     AR046263.1 GI:5967728
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myd ribozymes having 2'-5'-linked adenylyate residues
JOURNAL     Patent: US 5817796-A 1056 06-OCT-1998;
          Location/Qualifiers
FEATURES
  source
    1..17
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2833 TATATATATATACAT 2848
Db 17 TATATATATATAAAT 2

RESULT 853
LOCUS      AR057459
DEFINITION Sequence 1663 from patent US 5837542.
ACCESSION  AR057459
VERSION     AR057459.1 GI:5983036
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS     Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
          Draper,K.G.
TITLE       Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL     Patent: US 5837542-A 1663 17-NOV-1998;
          Location/Qualifiers
FEATURES
  source
    1..17
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 GGAGCTCTTCAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16

RESULT 854
LOCUS      AR057807
DEFINITION Sequence 2011 from patent US 5837542.
ACCESSION  AR057807
VERSION     AR057807.1 GI:5983384
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS     Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
          Draper,K.G.
TITLE       Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL     Patent: US 5837542-A 2011 17-NOV-1998;
          Location/Qualifiers
FEATURES

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source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16

RESULT 855
LOCUS AR115217 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1663 from patent US 6132967.
ACCESSION AR115217
VERSION AR115217.1 GI:14095539
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1663 17-OCT-2000;
FEATURES
source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16

RESULT 856
LOCUS AR115565 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2011 from patent US 6132967.
ACCESSION AR115565
VERSION AR115565.1 GI:14095887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 2011 17-OCT-2000;
FEATURES
source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16
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RESULT 857
LOCUS CQ617262/c 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2002 from Patent WO0192524.
ACCESSION CQ617262
VERSION CQ617262.1 GI:41667480
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2002 06-DEC-2001;
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3194 CCCCGGAGCTGGAGGA 3209
Db 17 CCCCGGGGCTGGAGGA 2

RESULT 858
LOCUS CQ617263/c 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2003 from Patent WO0192524.
ACCESSION CQ617263
VERSION CQ617263.1 GI:41667481
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2003 06-DEC-2001;
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3194 CCCCGGAGCTGGAGGA 3209
Db 16 CCCCGGGGCTGGAGGA 1

RESULT 859
LOCUS CQ617265/c 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2005 from Patent WO0192524.
ACCESSION CQ617265
VERSION CQ617265.1 GI:41667483
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2005 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
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                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1487 GGCCCCCGGGCTGGA 1502
Db 17 GGCCCCCGGGCTGGA 2
RESULT 860
CQ617266/c
LOCUS       CQ617266             17 bp    DNA             linear     PAT 02-FEB-2004
DEFINITION Sequence 2006 from Patent WO0192524.
ACCESSION  CQ617266
VERSION    CQ617266.1 GI:41667484
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2006 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
              1..17
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1487 GGCCCCCGGGCTGGA 1502
Db 16 GGCCCCCGGGCTGGA 1
RESULT 861
CQ623255
LOCUS       CQ623255             17 bp    DNA             linear     PAT 02-FEB-2004
DEFINITION Sequence 7995 from Patent WO0192524.
ACCESSION  CQ623255
VERSION    CQ623255.1 GI:41673473
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 7995 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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source
  1..17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1992 CACCTTCAAGCAGCTG 2007
Db 2 CACCATCAAGCAGCTG 17
RESULT 862
CQ623257
LOCUS       CQ623257             17 bp    DNA             linear     PAT 02-FEB-2004
DEFINITION Sequence 7997 from Patent WO0192524.
ACCESSION  CQ623257
VERSION    CQ623257.1 GI:41673475
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 7997 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
              1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1993 ACCTTCAAGCAGCTGG 2008
Db 1 ACCATCAAGCAGCTGG 16
RESULT 863
I53315/c
LOCUS       I53315              17 bp    DNA             linear     PAT 07-OCT-1997
DEFINITION Sequence 1056 from patent US 5646042.
ACCESSION  I53315
VERSION    I53315.1 GI:2474518
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE      C-myb targeted ribozymes
JOURNAL    Patent: US 5646042-A 1056 08-JUL-1997;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
              1..17
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2833 TATATATATATACAT 2848
Db 17 TATATATATATANAAT 2
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JOURNAL Patent: US 6566127-A 4753 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1393 AACCTGCTGGCGCCT 1408
Db 2 AACCTGCTGGAGCCT 17
RESULT 867
LOCUS AR329330 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 6732 from patent US 6566127.
ACCESSION AR329330
VERSION AR329330.1 GI:33715138
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6732 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1619 ACAGGGACCTGGCTGC 1634
Db 1 ACAGGGACCTGGCGGC 16
RESULT 868
LOCUS AR458325/c 17 bp DNA PAT 20-FEB-2004
DEFINITION Sequence 2002 from patent US 6686188.
ACCESSION AR458325
VERSION AR458325.1 GI:42693382
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2002 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3194 CCCCAGCTGGAGGA 3209
Db 17 CCCCAGCTGGAGGA 2

RESULT 864
LOCUS AR190295 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 5783 from patent US 6346398.
ACCESSION AR190295
VERSION AR190295.1 GI:20236260
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5783 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1608 GAAGTGCATCCACAGG 1623
Db 2 GAAGTGCATCCACAGG 17
RESULT 865
LOCUS AR325248 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 2650 from patent US 6566127.
ACCESSION AR325248
VERSION AR325248.1 GI:33711056
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2650 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1608 GAAGTGCATCCACAGG 1623
Db 2 GAAGTGCATCCACAGG 17
RESULT 866
LOCUS AR327351 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 4753 from patent US 6566127.
ACCESSION AR327351
VERSION AR327351.1 GI:33713159
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

RESULT 869
AR458326/c
LOCUS AR458326 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2003 from patent US 6686188.
ACCESSION AR458326
VERSION AR458326.1 GI:42693383
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2003 03-FEB-2004;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3194 CCCCGGAGCTGGAGGA 3209
Db 16 CCCCGGGGCTGGAGGA 1

RESULT 870
AR458328/c
LOCUS AR458328 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2005 from patent US 6686188.
ACCESSION AR458328
VERSION AR458328.1 GI:42693385
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2005 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1487 GGCCCCCGGGCGCTGGA 1502
Db 17 GGCCCCCGGGCGCTGGA 2

RESULT 871
AR458329/c
LOCUS AR458329 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2006 from patent US 6686188.
ACCESSION AR458329
VERSION AR458329.1 GI:42693386
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

Shannon, M.E.
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
Patent: US 6686188-A 2006 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1487 GGCCCCCGGGCGCTGGA 1502
Db 16 GGCCCCCGGGCGCTGGA 1

RESULT 872
AR464318
LOCUS AR464318 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7995 from patent US 6686188.
ACCESSION AR464318
VERSION AR464318.1 GI:42699375
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7995 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1992 CACCTTCAAGCAGCTG 2007
Db 2 CACCATCAAGCAGCTG 17

RESULT 873
AR464320
LOCUS AR464320 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7997 from patent US 6686188.
ACCESSION AR464320
VERSION AR464320.1 GI:42699377
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7997 03-FEB-2004;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1487 GGCCCCCGGGCGCTGGA 1502
Db 17 GGCCCCCGGGCGCTGGA 2

RESULT 874
AR464322/c
LOCUS AR464322 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2007 from patent US 6686188.
ACCESSION AR464322
VERSION AR464322.1 GI:42693387
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

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QY      1993 ACCTCAAGCAGCTGG 2008
Db      1 ACCATCAAGCAGCTGG 16

RESULT 874
LOCUS   AX216365                17 bp  RNA
DEFINITION
Sequence 1807 from Patent WO0159103.
ACCESSION
AX216365
VERSION
AX216365.1 GI:15526426
KEYWORDS
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 1807 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      501 GCTGAGCTGCTGGAG 516
Db      2 GCTGAGCTGCTGGAG 17

RESULT 875
LOCUS   AX217982                17 bp  RNA
DEFINITION
Sequence 3424 from Patent WO0159103.
ACCESSION
AX217982
VERSION
AX217982.1 GI:15528043
KEYWORDS
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 3424 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3754 CAGCGAGCAACTTCC 3769
Db      2 CAGAGCAACTTCC 17

RESULT 876
LOCUS   AX272813                17 bp  RNA
DEFINITION
Sequence 382 from Patent WO0162911.
ACCESSION
AX272813
VERSION
AX272813.1 GI:16545550
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
Ellis, J.H.
TITLE
Method and reagent for the inhibition of grid
JOURNAL
Patent: WO 0162911-A 382 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      45 GCCCCAGCGCTGCAG 60
Db      1 GCCCCAGCAGCTGCAG 16

RESULT 877
LOCUS   AX273076                17 bp  RNA
DEFINITION
Sequence 645 from Patent WO0162911.
ACCESSION
AX273076
VERSION
AX273076.1 GI:16545813
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
Ellis, J.H.
TITLE
Method and reagent for the inhibition of grid
JOURNAL
Patent: WO 0162911-A 645 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2006 TGGTGAGGACCTGGA 2021
Db      1 TGGTGAGGCTCTGGA 16

RESULT 878
LOCUS   AX273311                17 bp  RNA
DEFINITION
Sequence 880 from Patent WO0162911.
ACCESSION
AX273311
VERSION
AX273311.1 GI:16546048
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Meswigen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 880 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
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1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2006 TGGTGGAGGACCTGGA 2021
Db 2 TGGTGGAGGTCCTGGA 17

RESULT 879
AX530932
LOCUS AX530932 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 441 from Patent EPI239051.
ACCESSION AX530932
VERSION AX530932.1 GI:25253654
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 441 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 546 GGGGCTGCGGCGCAAC 561
Db 2 GCGCTGCTCGCGCCAAC 17

RESULT 880
AX530934
LOCUS AX530934 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 443 from Patent EPI239051.
ACCESSION AX530934
VERSION AX530934.1 GI:25253658
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 443 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 547 GGGCTGCGCGCCAACC 562
Db 1 GCGCTGCGCGCCAACC 16

RESULT 881
AX530935
LOCUS AX530935 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 444 from Patent EPI239051.
ACCESSION AX530935
VERSION AX530935.1 GI:25253660
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 444 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 549 GCTGCGCGCCAACCAG 564
Db 2 GCTGCGCGCCAACCTG 17

RESULT 882
AX530936
LOCUS AX530936 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 445 from Patent EPI239051.
ACCESSION AX530936
VERSION AX530936.1 GI:25253662
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 445 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 549 GCTGCGCGCCAACCAG 564
Db 1 GCTGCGCGCCAACCTG 16

RESULT 883
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Thu Oct 28 12:48:19 2004

AX634548
LOCUS AX634548 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1687 from Patent EP1260586.
ACCESSION AX634548
VERSION AX634548.1 GI:28470162
KEYWORDS
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
AUTHORS Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Weidler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL Patent: EP 1260586-A 1687 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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/organism="unclassified"
/mol_type="unassigned RNA"
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Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16
RESULT 884
AX634866
LOCUS AX634866 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 2005 from Patent EPI260586.
ACCESSION AX634866
VERSION AX634866.1 GI:28470480
KEYWORDS
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
AUTHORS Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Weidler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL Patent: EP 1260586-A 2005 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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/organism="unclassified"
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/db_xref="taxon:32644"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16
RESULT 885
AX687397
LOCUS AX687397 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 129 from Patent EPI281758.
ACCESSION AX687397
VERSION AX687397.1 GI:29410091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1 Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE mdz12
JOURNAL Patent: EP 1281758-A 129 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1295 TGAAGATGCTGAAGA 1310
Db 2 TGAAGATGCTTAAGA 17
RESULT 886
AX687398
LOCUS AX687398 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 130 from Patent EPI281758.
ACCESSION AX687398
VERSION AX687398.1 GI:29410092
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE mdz12
JOURNAL Patent: EP 1281758-A 130 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1295 TGAAGATGCTGAAGA 1310
Db 2 TGAAGATGCTTAAGA 17
RESULT 887
AX734671/c
LOCUS AX734671/c 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 261 from Patent WO03025177.
ACCESSION AX734671
VERSION AX734671.1 GI:30513948
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Telerman,A., Amson,R. and Tuijnder,M.

FEATURES	Location/Qualifiers
source	1. 17

Qy 1599 GGCTTCCAGAAGTGC 1614

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Db      3  GTCCTCCAGAGTGC 18

RESULT 892
LOCUS   A87891/c
DEFINITION Sequence 39 from Patent WO9833904.
ACCESSION A87891
VERSION   A87891.1 GI:6736461
SOURCE   unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch, W. and Schlingsiepen, K.
TITLE   AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 39 06-AUG-1998;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2160 CCCGGCCCCCAGC 2175
Db 18 CCCGGCCCCCAGC 3

RESULT 893
LOCUS   A89858/c
DEFINITION Sequence 39 from Patent EP0856579.
ACCESSION A89858
VERSION   A89858.1 GI:6738372
SOURCE   unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch, W.D. and Schlingsiepen, K.D.
TITLE   An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 39 05-AUG-1998;
BIOGOSTIK GES (DE)
FEATURES
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    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2160 CCCGGCCCCCAGC 2175
Db 18 CCCGGCCCCCAGC 3

RESULT 894
LOCUS   AR035673
DEFINITION Sequence 12 from patent US 5871922.
ACCESSION AR035673
VERSION   AR035673.1 GI:5952341
SOURCE   Unknown.
ORGANISM Unclassified.

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2160 CCCGGCCCCCAGC 2175
Db 18 CCCGGCCCCCAGC 3

RESULT 895
LOCUS   AR104208
DEFINITION Sequence 24 from patent US 6093545.
ACCESSION AR104208
VERSION   AR104208.1 GI:12816916
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Goodearl, A.D.J. and Glucksmann, M. Alexandra.
TITLE   Methods for detecting nucleic acid molecules encoding a member of
        the muscarinic family of receptors
JOURNAL Patent: US 6093545-A 24 25-JUL-2000;
FEATURES
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    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3658 GCCTCCAGGCGCATGG 3673
Db 1 GCCTCCAGGCGCATGG 16

RESULT 896
LOCUS   AR134314/c
DEFINITION Sequence 2739 from patent US 6194150.
ACCESSION AR134314
VERSION   AR134314.1 GI:14123219
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stinchcomb, D.T., Jarvis, T. and McSwiggen, J.
TITLE   Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 2739 27-FEB-2001;
FEATURES
    source
    1..18
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3658 GCCTCCAGGCGCATGG 3673
Db 1 GCCTCCAGGCGCATGG 16

RESULT 897
LOCUS   AR134314
DEFINITION Sequence 2739 from patent US 6194150.
ACCESSION AR134314
VERSION   AR134314.1 GI:14123219
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stinchcomb, D.T., Jarvis, T. and McSwiggen, J.
TITLE   Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 2739 27-FEB-2001;
FEATURES
    source
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3658 GCCTCCAGGCGCATGG 3673
Db 1 GCCTCCAGGCGCATGG 16

RESULT 898
LOCUS   AR134314
DEFINITION Sequence 2739 from patent US 6194150.
ACCESSION AR134314
VERSION   AR134314.1 GI:14123219
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stinchcomb, D.T., Jarvis, T. and McSwiggen, J.
TITLE   Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 2739 27-FEB-2001;
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3658 GCCTCCAGGCGCATGG 3673
Db 1 GCCTCCAGGCGCATGG 16
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QY      2899 ACAGGAGGCGAGCATG 2914
DB      16 ACAGGAGGCGAGGCATG 1
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RESULT 897
LOCUS   AR165360
DEFINITION Sequence 6 from patent US 6274790.
ACCESSION AR165360
VERSION  AR165360.1 GI:16238940
KEYWORDS
SOURCE  Unknown.
ORGANISM
    Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS  Kunst, L. and Millar, A.A.
TITLE    Nucleic acids encoding a plant enzyme involved in very long chain
          fatty acid synthesis
JOURNAL  Patent: US 6274790-A 6 14-AUG-2001;
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3106 GCGGAGAGTTTAAAT 3121
DB      2 GTCGGAGAGTTTAAAT 17
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RESULT 898
LOCUS   BD175407
DEFINITION Secretary and transmembrane polypeptide and nucleic acid encoding
          the same.
ACCESSION BD175407.1 GI:291211103
VERSION   JP 2002253280-A/189.
KEYWORDS  synthetic construct
SOURCE    artificial sequences.
ORGANISM  1 (bases 1 to 18)
REFERENCE 1 (bases 1 to 18)
AUTHORS   Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
          Yuan, J.
TITLE     Secretary and transmembrane polypeptide and nucleic acid encoding
          the same
JOURNAL   Patent: JP 2002253280-A 189 10-SEP-2002;
          GENENTECH INC
COMMENT   OS Artificial Sequence
          PN JP 2002253280-A/189
          PD 10-SEP-2002
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          17-SEP-1997 US 60/059119, 17-SEP-1997 US 60/059263 PR
          18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
          17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
          21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR
          24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR
          24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR
          24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR
          27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR
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          28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR
          28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR
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          29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR

QY      29-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR
          31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR
          07-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR
          17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR
          21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066364 PR
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          24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR
          24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PR
          WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
          JIAN ZHENG,
          PI JEAN YUAN
          PC C12N15/09, A61K45/00, A61P1/00, A61P13/12, A61P17/00, A61P17/06, PC
          A61P25/00,
          PC A61P25/16, A61P25/28, A61P31/12, A61P35/00, C07K14/47, C07K16/18,
          PC C07K19/00,
          PC C12N1/19, C12N1/21, C12N5/10/A61K38/00, A61K39/395, A61K39/395,
          PC A61P43/00,
          PC C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19), (C12N5/10,
          PC C12R1:91),
          PC C12N15/00, C12N5/00, A61K37/02, (C12N5/00, C12R1:91) CC
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1101 GCTGTCCTCAGGGGAG 1116
DB      3 GCTGTCCACAGGGGAG 18
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RESULT 899
LOCUS   AR410785
DEFINITION Sequence 229 from patent US 6635468.
ACCESSION AR410785
VERSION   AR410785.1 GI:40162285
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS   Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,
          Filvaroff, E., Fong, S., Gao, W.-O., Gerber, H., Gerritsen, M.E.,
          Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,
          Kijavini, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,
          Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
          Secreted and transmembrane polypeptides and nucleic acids encoding
          the same
          Patent: US 6635468-A 229 21-OCT-2003;
          JOURNAL   Patent: US 6635468-A 229 21-OCT-2003;
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1101 GCTGTCCTCAGGGGAG 1116
DB      3 GCTGTCCACAGGGGAG 18
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RESULT 900

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AR439149
LOCUS AR439149 18 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 229 from patent US 6664376.
ACCESSION AR439149
VERSION AR439149.1 GI:42664998
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6664376-A 229 16-DEC-2003;
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/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1101 GCTGTCTCTCAGGGGAG 1116
Db 3 GCTGTCTCAGGGGAG 18
RESULT 901
AR473169
LOCUS AR473169 18 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 229 from patent US 6686451.
ACCESSION AR473169
VERSION AR473169.1 GI:42708544
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Mather, J.P., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6686451-A 229 03-FEB-2004;
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Query Match 0.4%; Score 14.4; DB 1; Length 18;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1101 GCTGTCTCTCAGGGGAG 1116
Db 3 GCTGTCTCAGGGGAG 18
RESULT 902
AR352818
LOCUS AR352818 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 24 from Patent EP1174518.
ACCESSION AR352818
VERSION AR352818.1 GI:18617900
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1

AUTHORS Loukachov, V.V., van Gemen, B. and Goudsmit, J.
TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 24 23-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
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/db_xref="taxon:32630"
/note="position 41"
Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2845 ACATATATGGAAGG 2860
Db 3 ACATTTATGGAAGG 18
RESULT 903
AX362663
LOCUS AX362663 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 24 from Patent WO0208463.
ACCESSION AX362663
VERSION AX362663.1 GI:18694803
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Loukachov, V.V., Goudsmit, J. and van Gemen, B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 24 31-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
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Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2845 ACATATATGGAAGG 2860
Db 3 ACATTTATGGAAGG 18
RESULT 904
AX683709/c
LOCUS AX683709 18 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 26 from Patent WO03006504.
ACCESSION AX683709
VERSION AX683709.1 GI:29370739
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Thomson, A.M. and Dunbar, D.R.
TITLE Allelic variants of gpr50
JOURNAL Patent: WO 03006504-A 26 23-JAN-2003;
Akzo Nobel N.V. (NL)
FEATURES
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1356 GATGATGAAGATGATC 1371
Db 16 GATGTTGAAGATGATC 1

RESULT 905
AX697638
LOCUS AX697638 18 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 229 from Patent WO0104311.
ACCESSION AX697638
VERSION AX697638.1 GI:29498731
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.O., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J.,
Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0104311-A 229 18-JAN-2001;
Genentech Inc. (US)
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/note="Synthetic Oligonucleotide Probe"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1101 GCTGTCCTCAGGGGAG 1116
Db 3 GCTGTCACAGGGGAG 18

RESULT 906
AX773279
LOCUS AX773279 18 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 253 from Patent WO03045426.
ACCESSION AX773279
VERSION AX773279.1 GI:32485222
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ellendoorn,K., Baker,M., Williams,S. and Carr,F.J.
TITLE T-cell epitodes in carboxypeptidase g2
JOURNAL Patent: WO 03045426-A 253 05-JUN-2003;
MERCK PATENT GmbH (DE)
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Location/Qualifiers
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/db_xref="taxon:32630"
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1295 TGAAGATGCTGAAGA 1310
Db 1295 TGAAGATGCTGAAGA 1310
17 TGAAGATGCTGAAGA 2

RESULT 907
AX773295/c
LOCUS AX773295 18 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 269 from Patent WO03045426.
ACCESSION AX773295
VERSION AX773295.1 GI:32485238
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ellendoorn,K., Baker,M., Williams,S. and Carr,F.J.
TITLE T-cell epitodes in carboxypeptidase g2
JOURNAL Patent: WO 03045426-A 269 05-JUN-2003;
MERCK PATENT GmbH (DE)
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source
Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1295 TGAAGATGCTGAAGA 1310
Db 17 TGAAGATGCTGAAGA 2

RESULT 908
BD065404/c
LOCUS BD065404 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065404
VERSION BD065404.1 GI:22611007
KEYWORDS JP 2001511000-A/39.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingsiefen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 39 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/39
PD 07-AUG-2001
PF 30-JAN-1998 JP 198532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGSIEFEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2160 CCGGCCCCACCCAGC 2175
Db 18 CCGGCCCCACCCAGC 3
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RESULT 909
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LOCUS      BD075556               18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding
ACCESSION  BD075556
VERSION     BD075556.1 GI:22621159
KEYWORDS   JP 2001516580-A/189.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
TITLE       Secretory and transmembrane polypeptide and nucleic acid encoding
JOURNAL
COMMENT     Patent: JP 2001516580-A 189 02-OCT-2001;
            GENENTECH INC
            OS Artificial Sequence
            PN JP 2001516580-A/189
            PD 02-OCT-2001
            PF 16-SEP-1998 JP 2000511867
            PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
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            25-NOV-1997 US 60/066840
            PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI
            JEAN CHEN,
            PC C12N15/09,C07K14/47,C07K16/18,C07K16/28,C07K19/00,
            PC C12N1/19,
            PC C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02,C12P21/08, PC
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            PC C12N15/00,C12N5/00
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1101 GCTGTCCTCAGGGGAG 1116
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DB 3 GCTGTCCACAGGGGAG 18

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RESULT 910
BD086292
LOCUS      BD086292               18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION G protein-coupled receptor and utilization thereof.
ACCESSION  BD086292
VERSION     BD086292.1 GI:22631902
KEYWORDS   JP 2001525174-A/8.
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Goodearl,A.D.J., Glucksmann,A.M., Xie,M. and Distefano,P.
TITLE       G protein-coupled receptor and utilization thereof
JOURNAL     Patent: JP 2001525174-A 8 11-DEC-2001;
            MILLENNIUM PHARMACEUTICALS INC
            OS Unidentified
            PN JP 2001525174-A/8
            PD 11-DEC-2001
            PF 04-DEC-1997 US 08/985090,17-MAR-1998 US 09/042780 PI
            PR 04-DEC-1997 US 08/985090,17-MAR-1998 US 09/042780 PI
            ANDREW D J GOODEARL,ALEXANDRA M GLUCKSMANN,MICHAEL XIE,PETER PI
            DISTEFANO
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            CC Topology: Linear;
            CC G protein-coupled receptor and utilization thereof FH Key
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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3658 GCCTGCAGGCCATGG 3673
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DB 1 GCCTGCTGGCCATGG 16

RESULT 911
BD172416
LOCUS      BD172416               18 bp      DNA      linear      PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
            the same.
ACCESSION  BD172416
VERSION     BD172416.1 GI:28413716
KEYWORDS   JP 200223786-A/189.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
            Yuan,J.
TITLE       Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
JOURNAL     Patent: JP 200223786-A 189 13-AUG-2002;
            GENENTECH INC
            OS Artificial Sequence
            PN JP 200223786-A/189
            PD 13-AUG-2002
            PF 18-DEC-2001 JP 2001385135
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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
C12N5/10,
C12P21/02//C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:91), PC
(C12P21/02,C12R1:645),C12N15/00,C12N5/00
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QY 1101 GCTGTCCTCAGGGGAG 1116
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Db 3 GCTGTCACAGGGGAG 18

RESULT 912
BD172735
LOCUS BD172735 18 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
BD172735
ACCESSION BD172735.1 GI:28414039
VERSION JP 2002238586-A/189.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238586-A 189 27-AUG-2002;
GENENTECH INC
COMMENT OS Artificial Sequence
PN JP 2002238586-A/189
PD 27-AUG-2002
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
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PI JEAN YUAN
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C12N5/10,
C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),
PC
(C12N5/10,C12R1:91),(C12P21/02,C12R1:91),(C12P21/02,C12R1:645), PC
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Best Local Similarity 93.8%; Pred. No. 1e+03;
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Db 3 GCTGTCACAGGGGAG 18

RESULT 913
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LOCUS BD173054 18 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
BD173054
ACCESSION BD173054.1 GI:28414360
VERSION JP 2002238587-A/189.
KEYWORDS JP 2002238587-A/189.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238587-A 189 27-AUG-2002;
GENENTECH INC
COMMENT OS Artificial Sequence
PN JP 2002238587-A/189
PD 27-AUG-2002
PR 18-DEC-2001 JP 2001385248

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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
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PC C12P21/02,C12P21/08/(C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC
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Qy 1101 GCTGTCTCTCAGGGGAG 1116
Db 3 GCTGTCCACAGGGGAG 18
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LOCUS BD173373 18 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
ACCESSION BD173373
VERSION BD173373.1 GI:28414684
KEYWORDS JP 2002238588-A/189.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238588-A 189 27-AUG-2002;
GENENTECH INC
COMMENT OS Artificial Sequence
PN JP 2002238588-A/189
PD 27-AUG-2002

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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
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PC C12P21/02/C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1101 GCTGTCTCTCAGGGGAG 1116
Db 3 GCTGTCCACAGGGGAG 18
RESULT 915
AR131366
LOCUS AR131366 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 18 from patent US 6194142.
ACCESSION AR131366
VERSION AR131366.1 GI:14120269
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Montcany,M. and Montagnier,L.
TITLE Nucleotide sequences derived from the genome of retroviruses of the
HIV-1, HIV-2, and SIV type, and their uses in particular for the
amplification of the genomes of these retroviruses and for the in
vitro diagnosis of the diseases due to these viruses
Patent: US 6194142-A 18 27-FEB-2001;
JOURNAL Location/Qualifiers
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Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2632 CCACATGTCACGACC 2647
Db 1 CCACATTCCAGCACC 16

RESULT 916
LOCUS CQ785575 19 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 17 from Patent EP1398632.
ACCESSION CQ785575
VERSION CQ785575.1 GI:45720505
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kauschat,D. and Froehlen,B.
TITLE P2y11 receptor agonists and the use in the field of erythropoiesis
JOURNAL Patent: EP 1398632-A 17 17-MAR-2004;
Bayer HealthCare AG (DE)
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Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3706 TGGTGCCACGAGGTGT 3721
Db 3 TGGTGCCACGAGGTGT 18

RESULT 917
LOCUS E09395/c 19 bp DNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotide primer for biotin carboxyl carrier
protein(BCCP1-BCCP4).
ACCESSION E09395
VERSION E09395.1 GI:22026022
KEYWORDS JP 1995143887-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Yanai,Y., Shimada,H. and Ichikawa,N.
TITLE ACETYL COA CARBOXYLASE GENE OF PLANT
JOURNAL Patent: JP 1995143887-A 16 06-JUN-1995;
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
COMMENT OS None
OC Artificial sequences.
PN JP 1995143887-A/16
PD 06-JUN-1995
PF 28-JUN-1994 JP 1994146827
PR 17-AUG-1993 JP 93P 203477
PI YANAI YUKIHIRO, SHIMADA HIROAKI, ICHIKAWA NORIO PC
C12N15/09,A01H5/00/C12N5/10,C12N9/00;
CC strandedness: Double;
CC topology: Linear;
FH key Location/Qualifiers
FT source 1..19
FT /organism='Artificial sequences'.
FEATURES
source 1..19

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGAGATGATC 1371 -
Db 19 GARGTTATGAGATGATC 2

RESULT 918
LOCUS AR482127/c 19 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 6 from patent US 6699985.
ACCESSION AR482127
VERSION AR482127.1 GI:47244096
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Burcoglu,A.
TITLE Method of treating HIV infection and related secondary infections thereof
JOURNAL Patent: US 6699985-A 6 02-MAR-2004;
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/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2814 TGTATATGATATATAT 2829
Db 19 TGTATATGATATATTT 4

RESULT 919
LOCUS AX117795/c 19 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2918 from Patent WO0129262.
ACCESSION AX117795
VERSION AX117795.1 GI:14034746
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2918 26-APR-2001;
Orchid BioSciences, Inc. (US)
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source 1..19
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Query Match      0.4%; Score 14.4; DB 1; Length 19;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2736 CCTGAAGATGGAGGCC 2751
Db 19 CTTGAAGATGGAGGCC 4
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RESULT 920
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LOCUS      19 bp      DNA      linear      PAT 15-MAY-2001
DEFINITION Sequence 2314 from Patent WO0130362.
ACCESSION AX131096
VERSION    AX131096.1 GI:14137401
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1. Robbins,J.M. and Tricz,R.
AUTHORS    Robbins,J.M. and Tricz,R.
TITLE      Ribozyme therapy for the treatment of proliferative skin and eye
JOURNAL    diseases
FEATURES   Patent: WO 0130362-A 2314 03-MAY-2001;
source     IMMUSOL, INC. (US)
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2868 TGGTACACGAGGCC 2883
DB 16 TGGTACACGAGGCC 1

RESULT 921
BD001771
LOCUS      19 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Immunogenic compounds containing a translation product of
           nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
           types.
ACCESSION BD001771
VERSION    BD001771.1 GI:18626330
KEYWORDS   JP 2000093187-A/18.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Moncany,M. and Montagnier,L.
TITLE      Immunogenic compounds containing a translation product of
           nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
           types
JOURNAL    Patent: JP 2000093187-A 18 04-APR-2000;
COMMENT    INST PASTEUR, INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL
           OS Artificial Sequence
           PN JP 2000093187-A/18
           PD 04-APR-2000
           PF 24-SEP-1999 JP 1999270165
           PR 02-JUN-1989 FR 89/07354,20-SEP-1989 FR 89/12371 PI
           MAURICE MONCANY, LUC MONTAGNIER
           PC C12N15/09,A61K39/21,A61K48/00,A61P31/18,C07H21/04,C07K14/155,
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Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;

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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2632 CCACATGCTCCAGCAC 2647
DB 1 CCACATTCAGCAC 16

RESULT 922
AR020466
LOCUS      20 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5789165.
ACCESSION AR020466
VERSION    AR020466.1 GI:3975081
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Oku,Y. and Toyoda,N.
TITLE      Method and reagent for simultaneously assaying one or more ligands
           in a group of preselected ligands
JOURNAL    Patent: US 5789165-A 3 04-AUG-1998;
FEATURES   Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3651 CTTGCTTCCTGCAGG 3666
DB 4 CTTGCATGCTGCAGG 19

RESULT 923
AR026501
LOCUS      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5856099.
ACCESSION AR026501
VERSION    AR026501.1 GI:5937341
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L., Bennett,C.,Frank., Dean,N. and Geiger,T.
TITLE      Antisense compositions and methods for modulating type I
           interleukin-1 receptor expression
JOURNAL    Patent: US 5856099-A 8 05-JAN-1999;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2587 GCGCTCGGCCCTCC 2602
DB 2 GCGCTCGGCTCCTCC 17

RESULT 924
AR063688/c
LOCUS      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5846718.
ACCESSION AR063688
VERSION    AR063688.1 GI:5992996
KEYWORDS   Unknown.
SOURCE     Unknown.

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QY	1908	CCGCATGGACAAGCCC	1923
Db	18	CCGCATGGACAATCCC	3
RESULT 927			
LOCUS	BD233551	20 bp	DNA
DEFINITION	Targeted integration into chromosome by using retrovirus vector.		
ACCESSION	BD233551		
VERSION	BD233551.1	GI:33043321	
KEYWORDS	JP 2002519069-A/20		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Guenzburg W., Salmons B., Goller S. and Klein D.		
TITLE	Targeted integration into chromosome by using retrovirus vector		
JOURNAL	Patent: JP 2002519069-A 20 02-JUL-2002;		
COMMENT	AUSTRIAN NORDIC BIOTHERAPEUTICS AG		
	OS	Artificial Sequence	
	PN	JP 2002519069-A/20	
	PD	02-JUL-2002	
	PF	30-JUN-1999	JP 2000558225
	PR	01-JUL-1998	DK PA 199801016
	PI	WALTER GUENZBURG, BRIAN SALMONS, SABINE GOLLER, DIETER KLEIN PC	
	C12N15/09	A61K48/00	A61P31/12, A61P43/00, C12N5/00, C12N7/00, PC
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	PC	C12N5/00	
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Matches	15;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
QY	3781	ACACCTGGTGTCTAAC	3796
Db	16	ACACCTGGTGTCTGAC	1
RESULT 928			
LOCUS	I25851	20 bp	DNA
DEFINITION	Sequence 11 from patent US 5552526.		
ACCESSION	I25851		
VERSION	I25851.1	GI:1605721	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Nakamura, Y. and Emi, M.		
TITLE	MDC proteins and DNAs encoding the same		
JOURNAL	Patent: US 5552526-A 11 03-SEP-1996;		
FEATURES	Location/Qualifiers		
	1..20	/organism='unknown'	
	/mol_type='unassigned DNA'		
Query Match	0.4%	Score 14.4	DB 1; Length 20;
Best Local Similarity	93.8%	Pred. No. 1.1e+03;	
Matches	15;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
QY	2097	CCAGGACACCCCGAC	2112
Db	18	CCGATGGACAATCCC	3
RESULT 927			
LOCUS	BD233551	20 bp	DNA
DEFINITION	Targeted integration into chromosome by using retrovirus vector.		
ACCESSION	BD233551		
VERSION	BD233551.1	GI:33043321	
KEYWORDS	JP 2002519069-A/20		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Guenzburg W., Salmons B., Goller S. and Klein D.		
TITLE	Targeted integration into chromosome by using retrovirus vector		
JOURNAL	Patent: JP 2002519069-A 20 02-JUL-2002;		
COMMENT	AUSTRIAN NORDIC BIOTHERAPEUTICS AG		
	OS	Artificial Sequence	
	PN	JP 2002519069-A/20	
	PD	02-JUL-2002	
	PF	30-JUN-1999	JP 2000558225
	PR	01-JUL-1998	DK PA 199801016
	PI	WALTER GUENZBURG, BRIAN SALMONS, SABINE GOLLER, DIETER KLEIN PC	
	C12N15/09	A61K48/00	A61P31/12, A61P43/00, C12N5/00, C12N7/00, PC
	C12N15/00		
	PC	C12N5/00	
	CC	Description of Artificial Sequence: Primer	
	PH	Key	Location/Qualifiers
	FT	source	1..20
FEATURES	Location/Qualifiers		
	1..20	/organism='Artificial Sequence'.	
	/organism='synthetic construct'		
	/mol_type='genomic DNA'		
	/db_xref='taxon:32630'		
Query Match	0.4%	Score 14.4	DB 1; Length 20;
Best Local Similarity	93.8%	Pred. No. 1.1e+03;	
Matches	15;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
QY	3781	ACACCTGGTGTCTAAC	3796
Db	16	ACACCTGGTGTCTGAC	1
RESULT 928			
LOCUS	I25851	20 bp	DNA
DEFINITION	Sequence 11 from patent US 5552526.		
ACCESSION	I25851		
VERSION	I25851.1	GI:1605721	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS			

QY	1908	CCGCATGGACAAGCCC	1923
Db	18	CCGCATGGACAATCCC	3
LOCUS	BD233551	Targeted integration into chromosome by using retrovirus vector.	20 bp DNA linear PAT 17-JUL-2003
DEFINITION	BD233551		
ACCESSION	BD233551		
VERSION	BD233551.1	GI:33043321	
KEYWORDS	JP 2002519069-A/20		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Guenzburg W., Salmans B., Goller S. and Klein D.		
TITLE	Targeted integration into chromosome by using retrovirus vector		
JOURNAL	Patent: JP 2002519069-A 20 02-JUL-2002;		
COMMENT	AUSTRIAN NORDIC BIOTHERAPEUTICS AG		
	OS Artificial Sequence		
	PN JP 2002519069-A/20		
	PD 02-JUL-2002		
	PP 30-JUN-1999 JP 2000558225		
	PR 01-JUL-1998 DK PA 199801016		
	PI WALTER GUENZBURG, BRIAN SALMONS, SABINE GOLLER, DIETER KLEIN PC		
	C12N15/09, A61K48/00, A61P31/12, A61P43/00, C12N5/00, C12N7/00, PC		
	C12N15/00,		
	PC C12N5/00		
	CC Description of Artificial Sequence: Primer		
	PH Key	Location/Qualifiers	
	FT source	1..20	
FEATURES	Location/Qualifiers	/organism='Artificial Sequence'.	
source	1..20	/organism='synthetic construct'	
	/mol_type='genomic DNA'		
	/db_xref='taxon:32630'		
Query Match	0.4%;	Score 14.4;	DB 1; Length 20;
Best Local Similarity	93.8%;	Pred. No. 1.1e+03;	
Matches	15;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
QY	3781	ACACCTGGTGTCTAAC	3796
Db	16	ACACCTGGTGTCTGAC	1
LOCUS	I25851	Sequence 11 from patent US 5552526.	20 bp DNA linear PAT 07-OCT-1996
DEFINITION	I25851		
ACCESSION	I25851		
VERSION	I25851.1	GI:1605721	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Nakamura, Y. and Emi, M.		
TITLE	MDC proteins and DNAs encoding the same		
JOURNAL	Patent: US 5552526-A 11 03-SEP-1996;		
FEATURES	Location/Qualifiers		
source	1..20	/organism='unknown'	
	/mol_type='unassigned DNA'		
Query Match	0.4%;	Score 14.4;	DB 1; Length 20;
Best Local Similarity	93.8%;	Pred. No. 1.1e+03;	
Matches	15;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
QY	2097	CCAGGACACCCCGAC	2112
Db	18	CCGATGGACAATCCC	3
LOCUS	BD233551	Targeted integration into chromosome by using retrovirus vector.	20 bp DNA linear PAT 17-JUL-2003
DEFINITION	BD233551		
ACCESSION	BD233551		
VERSION	BD233551.1	GI:33043321	
KEYWORDS	JP 2002519069-A/20		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Guenzburg W., Salmans B., Goller S. and Klein D.		
TITLE	Targeted integration into chromosome by using retrovirus vector		
JOURNAL	Patent: JP 2002519069-A 20 02-JUL-2002;		
COMMENT	AUSTRIAN NORDIC BIOTHERAPEUTICS AG		
	OS Artificial Sequence		
	PN JP 2002519069-A/20		
	PD 02-JUL-2002		
	PP 30-JUN-1999 JP 2000558225		
	PR 01-JUL-1998 DK PA 199801016		
	PI WALTER GUENZBURG, BRIAN SALMONS, SABINE GOLLER, DIETER KLEIN PC		
	C12N15/09, A61K48/00, A61P31/12, A61P43/00, C12N5/00, C12N7/00, PC		
	C12N15/00,		
	PC C12N5/00		
	CC Description of Artificial Sequence: Primer		
	PH Key	Location/Qualifiers	
	FT source	1..20	
FEATURES	Location/Qualifiers	/organism='Artificial Sequence'.	
source	1..20	/organism='synthetic construct'	
	/mol_type='genomic DNA'		
	/db_xref='taxon:32630'		
Query Match	0.4%;	Score 14.4;	DB 1; Length 20;
Best Local Similarity	93.8%;	Pred. No. 1.1e+03;	
Matches	15;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
QY	3781	ACACCTGGTGTCTAAC	3796
Db	16	ACACCTGGTGTCTGAC	1
LOCUS	I25851	Sequence 11 from patent US 5552526.	20 bp DNA linear PAT 07-OCT-1996
DEFINITION	I25851		
ACCESSION	I25851		
VERSION	I25851.1	GI:1605721	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Nakamura, Y. and Emi, M.		
TITLE	MDC proteins and DNAs encoding the same		
JOURNAL	Patent: US 5552526-A 11 03-SEP-1996;		
FEATURES	Location/Qualifiers		
source	1..20	/organism='unknown'	
	/mol_type='unassigned DNA'		
Query Match	0.4%;	Score 14.4;	DB 1; Length 20;
Best Local Similarity	93.8%;	Pred. No. 1.1e+03;	
Matches	15;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
QY	2097</		

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Db      1  CCAGGACAGCCCCAGC 16

RESULT 929
I43488
LOCUS      I43488
DEFINITION Sequence 11 from patent US 5631351.
ACCESSION  I43488
VERSION     I43488.1 GI:2468732
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Nakamura, Y. and Emi, M.
TITLE      Antibodies to MDC proteins
JOURNAL    Patent: US 5631351-A 11 20-MAY-1997;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2097 CCAGGACAGCCCCAGC 2112
            |||||
            1 CCAGGACAGCCCCAGC 16

Db

RESULT 930
AR208766/c
LOCUS      AR208766
DEFINITION Sequence 65 from patent US 6383808.
ACCESSION  AR208766
VERSION     AR208766.1 GI:21510006
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Monia, B.P. and Freier, S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 65 07-MAY-2002;
FEATURES   Location/Qualifiers
            source
            1..20
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            /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2097 CCAGGACAGCCCCAGC 2112
            |||||
            1 CCAGGACAGCCCCAGC 16

Db

RESULT 931
AR435720/c
LOCUS      AR435720
DEFINITION Sequence 20 from patent US 6656727.
ACCESSION  AR435720
VERSION     AR435720.1 GI:40198796
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Gunzburg, W.H., Salmons, B., Goller, S. and Klein, D.
TITLE      Targeted integration into chromosomes using retroviral vectors
JOURNAL    Patent: US 6656727-A 20 02-DEC-2003;

FEATURES   Location/Qualifiers
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            1..20
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer"

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2407 CTGGGTGTCCCGCTG 2422
            |||||
            20 CTGGGTGTCCCGCTG 5

Db

RESULT 932
AR475721/c
LOCUS      AR475721
DEFINITION Sequence 88 from patent US 6692960.
ACCESSION  AR475721
VERSION     AR475721.1 GI:42715204
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Bennett, C.F. and Freier, S.M.
TITLE      Antisense modulation of sphingosine-1-phosphate lyase expression
JOURNAL    Patent: US 6692960-A 88 17-FEB-2004;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3007 TTGTTTAAACTGGA 3022
            |||||
            20 TTGTTTAAAGACTGGA 5

Db

RESULT 933
AX006846/c
LOCUS      AX006846
DEFINITION Sequence 20 from Patent WO0001835.
ACCESSION  AX006846
VERSION     AX006846.1 GI:9994862
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Goller, S., Klein, D., Guenzburg, W. and Salmons, B.
TITLE      Targeted integration into chromosomes using retroviral vectors
JOURNAL    Patent: WO 0001835-A 20 13-JAN-2000;
            GOLLE SABINE (AT); KLEIN DIETER (AT); GUENZBURG WALTER (AT);
            SALMONS BRIAN (DE); BAVARIAN NORDIC RES INST AS (DK)

FEATURES   Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer"

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3781 ACACCTGGTTGCTAAC 3796
            |||||
            16 ACACCTGGTTGCTGAC 1
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RESULT 934
AX078019
LOCUS AX078019 20 bp DNA linear PAT 23-FEB-2001
DEFINITION Sequence 33 from Patent WO0105435.
ACCESSION AX078019
VERSION AX078019.1 GI:13157774
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gleave, M.
TITLE Antisense therapy for hormone-regulated tumors
JOURNAL Patent: WO 0105435-A 33 25-JAN-2001;
THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)
FEATURES
source
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2618 CCTGCAGGGAAGCCCC 2633
Db 1 CTTGCAGGAGGAGCTC 16
RESULT 935
AX304783
LOCUS AX304783 20 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 18 from Patent EP1158045.
ACCESSION AX304783
VERSION AX304783.1 GI:17644464
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Schneider, Y.J. and Burteau, N.
TITLE Culture conditions allowing to modulate the expression of cyp3a4 in
JOURNAL caco2 cells
Patent: EP 1158045-A 18 28-NOV-2001;
UNIVERSITE CATHOLIQUE DE LOUVAIN (BE)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide"
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1188 GCTGACCTGGGGAAG 1203
Db 2 GCTGACCTGGGGAAG 17
RESULT 936
AX404665/c
LOCUS AX404665 20 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 39 from Patent WO224745.
ACCESSION AX404665
VERSION AX404665.1 GI:21437946
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Abken, H. and Schinkoethe, T.
TITLE Method for detecting tumor cells
JOURNAL Patent: WO 0224745-A 39 28-MAR-2002;
Abken, Hinrich (DE)
FEATURES
source
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3651 CTTGCTTGCTGCAGG 3666
Db 17 CTTGCATGCTGCAGG 2
RESULT 937
AX494234/c
LOCUS AX494234 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 10 from Patent WO02059379.
ACCESSION AX494234
VERSION AX494234.1 GI:23339844
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Shuber, A.P.
TITLE Methods for detecting, grading or monitoring an H. pylori infection
JOURNAL Patent: WO 02059379-A 10 01-AUG-2002;
EXACT SCIENCES CORP (US)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="APC forward primer"
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 856 GAGGAGCTGCTGCAGG 871
Db 18 GAGGAGCTGCTGCAGG 3
RESULT 938
AX553634/c
LOCUS AX553634 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 38 from Patent WO02074946.
ACCESSION AX553634
VERSION AX553634.1 GI:25897632
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Serup, P., Heinberg, H. and Gradwohl, G.
TITLE Method for generating insulin-secreting cells suitable for
JOURNAL transplantation
Patent: WO 02074946-A 38 26-SEP-2002;
NOVO NORDISK A/S (DK)
FEATURES
source
1. .20
/organism="Homo sapiens"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TGTACCGTAGCGGTG 1296
DB 17 TGTACCGTGGCGGTG 2

RESULT 939
LOCUS AX740160/c
DEFINITION Sequence 2 from Patent WO03000927.
ACCESSION AX740160
VERSION AX740160.1 GI:30519337
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
SOURCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baird,D.M.
TITLE Method for the determination of telomere length
JOURNAL Patent: WO 03000927-A 2 03-JAN-2003;
University of Wales College of Medicine (GB)
FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3782 CACCTGGTTGCTAACC 3797
DB 16 CACCTGGTTGCTAACC 1

RESULT 940
LOCUS AX785898
DEFINITION Sequence 407 from Patent WO03050299.
ACCESSION AX785898
VERSION AX785898.1 GI:32953518
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
SOURCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cullen,P. and Seedorf,U.
TITLE Method for analysing hereditary masculine infertility
JOURNAL Patent: WO 03050299-A 407 19-JUN-2003;
OGHAM GmbH (DE)
FEATURES
source
1..20
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2051 AGTACTGGACCTGTC 2066
DB 1 ACTACTGGACCTGTC 16

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TGTACCGTAGCGGTG 1296
DB 17 TGTACCGTGGCGGTG 2

RESULT 941
LOCUS AX926289/c
DEFINITION Sequence 31 from Patent WO03085112.
ACCESSION AX926289
VERSION AX926289.1 GI:40245622
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Meyer,U.A., Frazer,D.J., Kaufmann,M.R., Podvinec,M. and Zumsteg,A.
TITLE Enhancer sequence of the 5-aminolevulinic synthase gene
JOURNAL Patent: WO 03085112-A 31 16-OCT-2003;
Universitaet Basel (CH)
FEATURES
source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Forward PCR primer"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2145 CCAGCAGCTGCTGCC 2160
DB 17 CCTGACCTGCTGCC 2

RESULT 942
LOCUS AX926579
DEFINITION Sequence 31 from Patent WO03085113.
ACCESSION AX926579
VERSION AX926579.1 GI:40246517
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Meyer,U.A., Frazer,D.J., Kaufmann,M.R., Podvinec,M. and Zumsteg,A.
TITLE Enhancer sequence of the 5-aminolevulinic acid synthase gene
JOURNAL Patent: WO 03085113-A 31 16-OCT-2003;
Universitaet Basel (CH)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Forward PCR primer"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2145 CCAGCAGCTGCTGCC 2160
DB 17 CCTGACCTGCTGCC 2

RESULT 943
LOCUS BD074593
DEFINITION Antisense oligonucleotide composition and modulation method of JNK
protein.
ACCESSION BD074593
VERSION BD074593.1 GI:22620196
KEYWORDS JP 2001514905-A/17.
SOURCE synthetic construct
ORGANISM synthetic construct
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Thu Oct 28 12:48:19 2004

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ACCESSION E33560
VERSION E33560.1 GI:18624133
KEYWORDS JP 2000078977-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Tsujimoto,Y., Izawa,S., Inoue,Y., Kimura,H. and Sato,N.
TITLE Stress-responsive gene promoter
JOURNAL Patent: JP 2000078977-A 5 21-MAR-2000;
MARUHA CORP
OS Artificial Sequence
PN JP 2000078977-A/5
PD 21-MAR-2000
PF 04-SEP-1998 JP 1998251390
PR YOSHIYUKI TSUJIMOTO,SHINGO IZAWA,YOSHIHARU INOUE,HIKARU
PI KIMURA, NOBUYUKI SATO
PC C12N15/09,C12N1/19,C12P21/02///(C12N15/09,C12R1:865),(C12N1/19,
C12R1:865),
PC (C12P21/02,C12R1:865),C12N15/00,(C12N15/00,C12R1:865) CC
FH Key Location/Qualifiers
FT source 1..36
FT Location/Qualifiers
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 14.4; DB 1; Length 26;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3113 AGTTTAAATTATTAACCTATTGAC 3136
Db 2 ATTTTATTTTATTTTCTTTT 25
RESULT 948
AR264927
LOCUS AR264927 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 11 from patent US'6492121.
ACCESSION AR264927
VERSION AR264927.1 GI:29693314
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 11 10-DEC-2002;
FEATURES
source
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Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATAATTATTGAGTTTTT 24
RESULT 949
AR478208
LOCUS AR478208 30 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 11 from patent US 6699661.
ACCESSION AR478208
VERSION AR478208.1 GI:47236856
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 11 02-MAR-2004;
FEATURES
source
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Location/Qualifiers
/organism="unknown"
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Query Match 0.4%; Score 14.4; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATAATTATTGAGTTTTT 24
RESULT 950
BD072872
LOCUS BD072872 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072872
VERSION BD072872.1 GI:22618475
KEYWORDS JP 2001286300-A/10
SOURCE synthetic construct
ORGANISM
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 10 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/10
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINVA PI
KURATA,
PC KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
CC
FH Key Location/Qualifiers
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FT Location/Qualifiers
/organism="Artificial Sequence".
FEATURES
source
1..30
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
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Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3474 ATATATATAATTTATTGAGTTTTT 3497
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Db 1 ATATATATTTTTTTTTTCTTTTTT 24

RESULT 951
BD107499
LOCUS
DEFINITION Novel quantitative polymorphism analysis method. PAT 18-SEP-2002
ACCESSION BD107499
VERSION BD107499.1 GI:23202317
KEYWORDS JP 2002000275-A/8.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 8 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/8
PD 08-JAN-2002
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA
PI KURATA,
PC C12N15/09,C12M1/00,C12Q1/68,C12Q1/68,G01N1/28,G01N1/28,G01N33/
PC The base sequence was prepared synthetically on the aim of CC
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CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC acid.
CC Key Location/Qualifiers
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FT /organism="synthetic construct"
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/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 30;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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||||| ||||| ||||| |||||
Db 1 ATATATATTTTTTTTTTCTTTTTT 24

RESULT 952
BD145031
LOCUS
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method. PAT 17-JAN-2003
ACCESSION BD145031
VERSION BD145031.1 GI:27850789
KEYWORDS JP 2002119291-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct

/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 30;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3474 ATATATATAATTTATTGAGTTTTT 3497
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Db 1 ATATATATTTTTTTTTTCTTTTTT 24

RESULT 953
BD166031
LOCUS
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166031
VERSION BD166031.1 GI:27871843
KEYWORDS JP 2002191372-A/11.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 11 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/11
PD 09-JUL-2002
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC

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artificial sequences.
1 (bases 1 to 30)
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
Patent: JP 2002119291-A 12 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/12
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/
PC 53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FT Key Location/Qualifiers
FT source 1..30
FT /organism="Artificial Sequence".
FEATURES
source Location/Qualifiers
1..30
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/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 30;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3474 ATATATATAATTTATTGAGTTTTT 3497
||||| ||||| ||||| |||||
Db 1 ATATATATTTTTTTTTTCTTTTTT 24

RESULT 953
BD166031
LOCUS
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166031
VERSION BD166031.1 GI:27871843
KEYWORDS JP 2002191372-A/11.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 11 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/11
PD 09-JUL-2002
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC

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C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examine the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
/organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..30
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/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 14.4; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 1 ATATATATTTTATTTTCTTTT 24
RESULT 954
AR051291
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 32)
AUTHORS
Soares,M.B. and Efstratiadis,A.
TITLE
Method for construction of normalized cDNA libraries
JOURNAL
Patent: US 5830662-A 8 03-NOV-1998;
FEATURES
Location/Qualifiers
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Db 1 TTTTCTTTAATAATTTT 24
RESULT 955
I16939
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 32)
AUTHORS
Soares,M.B. and Efstratiadis,A.
TITLE
Method for construction of normalized cDNA libraries
JOURNAL
Patent: US 5482845-A 8 09-JAN-1996;
FEATURES
Location/Qualifiers
1..32
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Query Match 0.4%; Score 14.4; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 1 TTTTCTTTAATAATTTT 24
RESULT 956
I45733
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 32)
AUTHORS
Soares,M.B. and Efstratiadis,A.
TITLE
Normalized cDNA libraries
JOURNAL
Patent: US 5637685-A 8 10-JUN-1997;
FEATURES
Location/Qualifiers
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/mol_type='unassigned DNA'
Query Match 0.4%; Score 14.4; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 1 TTTTCTTTAATAATTTT 24
RESULT 957
BD170449/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Artificial Sequence
PN WO 0250307-A/4
PD 27-JUN-2002
PF 12-DEC-2001 WO 2001JP010892
PR 12-DEC-2000 JP 00P 378091
PI HIDEOTOSHI INOKO,GEN TAMIYA,KENJI NAKAJIMA,NAOKI KIMURA,RENPEI
PI NAGASHIMA,
PI MINORU MORIKAWA,KOICHI OKAMOTO
PC C12N15/09,G01N33/53,G01N27/62,G01N33/566,C12M1/00 CC
Description of Artificial Sequence:an artificially synthesized CC
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FT source 1..40
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Location/Qualifiers
1..40
source

RESULT 962

RESULT 964

A56651
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
exon

A44390
Sequence 20 from Patent EP0653439.
A44390
A44390.1 GI:2299219
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Peyman,A.D., Uhlmann,E.D., Mag,M., Kretschmar,G.D., Helsberg,M.D.
and Winkler,I.D.
Stabilized oligonucleotides and the use thereof
Patent: EP 0653439-A 20 17-MAY-1995;
HOECHST AG (DE)
Other publication JP 7194385 950801
Other publication CA 2135591 950513
Other publication AU 779994 950518
Other publication DE 438704 950518.
Location/Qualifiers
1..19
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/note="P53 TUMORSUPPRESSOR"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGACGAGCTGAGG 202
|||||
Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 963

A47177
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
exon

A47177
Sequence 20 from Patent EP0680969.
A47177
A47177.1 GI:2301219
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Seela,F.P. and Lampe,S.D.
Modified oligonucleotides, their preparation and their use
Patent: EP 0680969-A 20 08-NOV-1995;
HOECHST AG (DE)
Other publication JP 8003186 960109
Other publication AU 1778295 951109
Other publication DE 4415370 951109.
Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGACGAGCTGAGG 202
|||||
Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 964

A56651
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
exon

A56651
Sequence 18 from Patent EP0739898.
A56651
A56651.1 GI:3712696
unidentified
unidentified
unclassified.
Peyman,A.D., Uhlmann,E.D., Breipohl,G.D. and Wallmeier,H.D.
Phosphonomonoester nucleic acids, methods for their preparation and
their use
Patent: EP 0739898-A 18 30-OCT-1996;
HOECHST AG (DE)
Other publication CZ 9600743 961016
Other publication CN 1138588 961225
Other publication PL 313207 960916
Other publication JP 8259579 961008
Other publication NO 961006 960916
Other publication CA 2171589 960914
Other publication AU 4802896 960926
Other publication DE 19508923 960919.
Location/Qualifiers
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Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGACGAGCTGAGG 202
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Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 965

A80372
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
exon

A80372
Sequence 18 from Patent EP0726274.
A80372
A80372.1 GI:6093099
unidentified
unidentified
unclassified.
Peyman,A.D. and Uhlmann,E.D.
G-CAP STABILIZED OLIGONUCLEOTIDES
Patent: EP 0726274-A 18 14-AUG-1996;
HOECHST AG (DE)
Location/Qualifiers
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/organism="unidentified"
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/db_xref="taxon:32644"
1..19

Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 966

AR111775
LOCUS

AR111775
Sequence 19 bp
DNA
linear
PAT 14-FEB-2001

DEFINITION Sequence 18 from patent US 6127346.
ACCESSION AR111775
VERSION AR111775.1 GI:12828623
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Feynman,A., Uhlmann,E., Breipohl,G. and Wallmeier,H.
TITLE Phosphonomonoester nucleic acids process for their preparation and their use
JOURNAL Patent: US 6127346-A 18 03-OCT-2000;
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Db 1 GGGAGGAGGAGGATGAGG 19
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RESULT 967
LOCUS AR179815 19 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 18 from patent US 6326487.
ACCESSION AR179815
VERSION AR179815.1 GI:20221370
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Feynman,A., Uhlmann,E. and Carolus,C.
TITLE 3 modified oligonucleotide derivatives
JOURNAL Patent: US 6326487-A 18 04-DEC-2001;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 184 GGGAGGACGAGGCTGAGG 202
|||||
Db 1 GGGAGGAGGAGGATGAGG 19
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RESULT 968
LOCUS BD266251 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Universal arrays.
ACCESSION BD266251
VERSION BD266251.1 GI:33076019
KEYWORDS JP 2002539849-A/251.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Fan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,E.S., Lockhart,D.J., Ryder,T. and Sklar,P.
TITLE Universal arrays
JOURNAL Patent: JP 2002539849-A 251 26-NOV-2002;
COMMENT WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
OS Artificial Sequence
PN JP 2002539849-A/251
PD 26-NOV-2002

PF 27-MAR-2000 JP 2000608794
PR 26-MAR-1999 US 60/126473,23-JUN-1999 US 60/140359 P1
JIAN BING FAN,JOEL N HIRSCHHORN,XIAOHUA
HUANG,PAUL KAPLAN,ERIC
PI S LANDER,
PI DAVID J LOCKHART,THOMAS RYDER,PAMELA SKLAR
PC C12Q1/68,C12N1/00,C12N15/09,C12N15/09,C12N15/09,G01N33/53, PC
GOIN33/566,
PC GOIN37/00,C12N15/00,C12N15/00,C12N15/00
CC Primer
FH Key Location/Qualifiers
FT source 1..19
/Organism='Artificial Sequence'.
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Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
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QY 2191 ACGTGAAGGCCACTGCTC 2209
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Db 1 AAGAGAATGCCCACTGCTC 19
-
RESULT 969
LOCUS CQ800200 19 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 25 from Patent WO2004031411.
ACCESSION CQ800200
VERSION CQ800200.1 GI:46849118
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Nakamura,Y. and Katagiri,T.
TITLE Genes and polypeptides relating to human pancreatic cancers
JOURNAL Patent: WO 2004031411-A 25 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by The President of the University of Tokyo (JP)
FEATURES Location/Qualifiers
source
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="target sequence for sirna"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2046 CGACGAGTACCTGGACCTG 2064
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Db 1 CGACAAGCACCTGGACGTG 19
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RESULT 970
LOCUS I46926 19 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 19 from patent US 5639655.
ACCESSION I46926
VERSION I46926.1 GI:2470891
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE PML-RARA targeted ribozymes

JOURNAL Patent: US 5639655-A 19 17-JUN-1997;
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 860 AGCTGCTGAGGCTGACGA 878
 ||||| ||||| ||||| ||||| |||||
 Db 1 AGCTGCTGAGGCTGTGGA 19

RESULT 971
 184730 184730 19 bp DNA linear PAT 04-APR-1998
 DEFINITION Sequence 18 from patent US 5696248.
 ACCESSION 184730
 VERSION 184730.1 GI:3022250
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Feynman,A., Uhlmann,E. and Carolus,C.
 TITLE 3'-modified oligonucleotide derivatives
 JOURNAL Patent: US 5696248-A 18 09-DEC-1997;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGGAGGACGAGGCTGAGG 202
 ||||| ||||| ||||| ||||| |||||
 Db 1 GGGGAGGAGGAGGATGAGG 19

RESULT 972
 AR193516 184730 19 bp DNA linear PAT 20-APR-2002
 LOCUS AR193516
 DEFINITION Sequence 20 from patent US 6348312.
 ACCESSION AR193516
 VERSION AR193516.1 GI:20240108
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Peyman,A., Uhlmann,E., Mag,M., Kretzschmar,G., Helsberg,M. and Winkler,I.
 TITLE Stabilized oligonucleotides and their use
 JOURNAL Patent: US 6348312-A 20 19-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGGAGGACGAGGCTGAGG 202
 ||||| ||||| ||||| ||||| |||||
 Db 1 GGGGAGGAGGAGGATGAGG 19

RESULT 973
 AR193516 184730 19 bp DNA linear PAT 20-APR-2002
 LOCUS AR193516
 DEFINITION Sequence 20 from patent US 6348312.
 ACCESSION AR193516
 VERSION AR193516.1 GI:20240108
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Peyman,A., Uhlmann,E., Mag,M., Kretzschmar,G., Helsberg,M. and Winkler,I.
 TITLE Stabilized oligonucleotides and their use
 JOURNAL Patent: US 6348312-A 20 19-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGGAGGACGAGGCTGAGG 202
 ||||| ||||| ||||| ||||| |||||
 Db 1 GGGGAGGAGGAGGATGAGG 19

RESULT 974
 AR292967 184730 19 bp DNA linear PAT 12-JUN-2003
 LOCUS AR292967
 DEFINITION Sequence 4702 from patent US 6537751.
 ACCESSION AR292967
 VERSION AR292967.1 GI:31680251
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 4702 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGGAGGACGAGGCTGAGG 202
 ||||| ||||| ||||| ||||| |||||
 Db 1 GGGGAGGAGGAGGATGAGG 19

RESULT 975
 AR294648 184730 19 bp DNA linear PAT 12-JUN-2003
 LOCUS AR294648
 DEFINITION Sequence 6383 from patent US 6537751.
 ACCESSION AR294648
 VERSION AR294648.1 GI:31681932
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 6383 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2770 GGTATTTCGGAAGACTAG 2788
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 Db 19 GGTATTTCGGAAGACTAG 1


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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3502 GATGTATTGTTGTAGACT 3520
Db 19 GTTGTGTTGTTGTAGTCT 1

RESULT 976
AX081351
LOCUS AX081351 19 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 30 from Patent WO0108707.
ACCESSION AX081351
VERSION AX081351.1 GI:13170193
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.
TITLE Conjugates and methods for the production thereof, and their use
for transporting molecules via biological membranes
JOURNAL Patent: WO 0108707-A 30 08-FEB-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source
1. .19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGAGGAGGCTGAGG 202
Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 977
AX128989/c
LOCUS AX128989 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 207 from Patent WO0130362.
ACCESSION AX128989
VERSION AX128989.1 GI:14135294
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 207 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1. .19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdk2 ribozyme binding site"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 655 AATGGCAGCAAGGTGGGCC 673
Db 1 TGGCTGACTTCGGCTGGC 19

RESULT 978
AX128990/c
LOCUS AX128990 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 208 from Patent WO0130362.
ACCESSION AX128990
VERSION AX128990.1 GI:14135295
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 208 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1. .19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdk2 ribozyme binding site"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 654 GAATGGCAGCAAGGTGGGC 672
Db 19 GAATGGCAGCAAGCTAGGC 1

RESULT 979
AX129129
LOCUS AX129129 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 347 from Patent WO0130362.
ACCESSION AX129129
VERSION AX129129.1 GI:14135434
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 347 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1. .19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdk3 ribozyme binding site"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1673 TGCAGACTTCGGCTGGC 1691
Db 1 TGGCTGACTTCGGCTGGC 19

RESULT 980
AX129366
LOCUS AX129366 19 bp DNA linear PAT 15-MAY-2001
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DEFINITION      Sequence 584 from Patent WO0130362.
ACCESSION       AX129366
VERSION         AX129366.1 GI:14135671
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS         Robbins,J.M. and Tritz,R.
TITLE           Ribozyme therapy for the treatment of proliferative skin and eye
                diseases
JOURNAL         Patent: WO 0130362-A 870 03-MAY-2001;
                IMMUSOL, INC. (US)
FEATURES        Location/Qualifiers
                source
                1..19
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="Cdk8 ribozyme binding site"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1673 TCGCAGACTTCGGCTGCC 1691
Db 1 TCGTGACTTCGGCCTTGC 19

RESULT 981
AX129367
LOCUS           AX129367 19 bp DNA linear PAT 15-MAY-2001
DEFINITION      Sequence 585 from Patent WO0130362.
ACCESSION       AX129367
VERSION         AX129367.1 GI:14135672
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS         Robbins,J.M. and Tritz,R.
TITLE           Ribozyme therapy for the treatment of proliferative skin and eye
                diseases
JOURNAL         Patent: WO 0130362-A 585 03-MAY-2001;
                IMMUSOL, INC. (US)
FEATURES        Location/Qualifiers
                source
                1..19
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="Cdk6 ribozyme binding site"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 CGCAGACTTCGGCTGCC 1692
Db 1 CGCTGACTTCGGCCTTGC 19

RESULT 982
AX129652
LOCUS           AX129652 19 bp DNA linear PAT 15-MAY-2001
DEFINITION      Sequence 870 from Patent WO0130362.
ACCESSION       AX129652
VERSION         AX129652.1 GI:14135957
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS         Robbins,J.M. and Tritz,R.
TITLE           Ribozyme therapy for the treatment of proliferative skin and eye
                diseases
JOURNAL         Patent: WO 0130362-A 2537 03-MAY-2001;
                IMMUSOL, INC. (US)

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REFERENCE
1
AUTHORS         Robbins,J.M. and Tritz,R.
TITLE           Ribozyme therapy for the treatment of proliferative skin and eye
                diseases
JOURNAL         Patent: WO 0130362-A 870 03-MAY-2001;
                IMMUSOL, INC. (US)
FEATURES        Location/Qualifiers
                source
                1..19
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="Cdk8 ribozyme binding site"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2001 GCAGCTGGTGGAGGACCTG 2019
Db 1 GGAGCGGGTCGAGGACCTG 19

RESULT 983
AX130617
LOCUS           AX130617 19 bp DNA linear PAT 15-MAY-2001
DEFINITION      Sequence 1835 from Patent WO0130362.
ACCESSION       AX130617
VERSION         AX130617.1 GI:14136922
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS         Robbins,J.M. and Tritz,R.
TITLE           Ribozyme therapy for the treatment of proliferative skin and eye
                diseases
JOURNAL         Patent: WO 0130362-A 1835 03-MAY-2001;
                IMMUSOL, INC. (US)
FEATURES        Location/Qualifiers
                source
                1..19
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="Cyclin D1 ribozyme binding site"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1875 GGAGGAGCTCTTCAAGCTG 1893
Db 1 GGAGGAGGTCTTCCGCTG 19

RESULT 984
AX131319
LOCUS           AX131319 19 bp DNA linear PAT 15-MAY-2001
DEFINITION      Sequence 2537 from Patent WO0130362.
ACCESSION       AX131319
VERSION         AX131319.1 GI:14137624
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS         Robbins,J.M. and Tritz,R.
TITLE           Ribozyme therapy for the treatment of proliferative skin and eye
                diseases
JOURNAL         Patent: WO 0130362-A 2537 03-MAY-2001;
                IMMUSOL, INC. (US)

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FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        /note="Cyclin F ribozyme binding site"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2120 CCTCAGGAGGACGACTCCGT 2138
  ||||| ||||| |||||
Db 1 CCTCAGGAGTCTCTCCGT 19

RESULT 985
AX132490
LOCUS AX132490 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3708 from Patent WO0130362.
ACCESSION AX132490
VERSION AX132490.1 GI:14138795
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
  diseases
JOURNAL Patent: WO 0130362-A 3708 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        /note="Cdc25 hs ribozyme binding site"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2745 GGGAGCCTTTACCTTTTAT 2763
  ||||| ||||| |||||
Db 1 GGGAGCCTTAACTTATAT 19

RESULT 986
AX204959/c
LOCUS AX204959 19 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 6 from Patent WO0155362.
ACCESSION AX204959
VERSION AX204959.1 GI:15394242
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE
  1 Zheng,C., O'Connell,B. and Baum,B.J.
  AUTHORS Hybrid adeno-retroviral vector for the transfection of cells
  TITLE Patent: WO 0155362-A 6 02-AUG-2001;
  JOURNAL THE SECRETARY, DEPARTMENT OF HEALTH AND SOCIAL SERVICES (US)
FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="PCR primer"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Beschreibung der kuenstlichen Sequenz:
        Oligonukleotide"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3061 TCTTGTTCACACCCCAA 3079
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Db 19 TATTGTTACACACCCCAA 1

RESULT 987
AX283181
LOCUS AX283181 19 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 19 from Patent WO0179216.
ACCESSION AX283181
VERSION AX283181.1 GI:17044062
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE
  1 Uhlmann,E., Breipohl,G. and Will,D.W.
  AUTHORS Polyamide nucleic acid derivatives, agents and methods for
  TITLE producing them
JOURNAL Patent: WO 0179216-A 19 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Beschreibung der kuenstlichen
        Sequenz:Oligonukleotide"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGAGGAGGCTGAGG 202
  ||||| ||||| |||||
Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 988
AX283247
LOCUS AX283247 19 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 11 from Patent WO0179249.
ACCESSION AX283247
VERSION AX283247.1 GI:17044128
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE
  1 Uhlmann,E., Breipohl,G. and Will,D.W.
  AUTHORS Polyamide nucleic acid derivatives, agents and methods for
  TITLE producing the same
JOURNAL Patent: WO 0179249-A 11 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
  source
    Location/Qualifiers
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Beschreibung der kuenstlichen Sequenz:
        Oligonukleotide"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGAGGAGGCTGAGG 202
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Db 1 GGGAGGAGGAGGATGAGG 19
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RESULT 989
AX384647
LOCUS AX384647 19 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 19 from Patent EP1182206.
ACCESSION AX384647
VERSION AX384647.1 GI:19577842
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Feymann,A., Uhlmann,E., Mag,M., Kretschmar,G., Helsberg,M. and
Winkler,I.
TITLE Stabilized oligonucleotids and the use thereof
JOURNAL Patent: EP 1182206-A 19 27-FEB-2002;
HOECHST AKTIENGESELLSCHAFT (DE)
FEATURES
source
1 /organism="synthetic construct"
/moi_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Antisense Oligonukleotid"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 184 GGGGAGGACGAGCTGAGG 202
| | | | | | | | | |
Db 1 GGGGAGGAGGAGGATGAGG 19

RESULT 990
AX474023/c
LOCUS AX474023 19 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 177 from Patent WO0246458.
ACCESSION AX474023
VERSION AX474023.1 GI:22208178
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Deneffe,P., Rosier-Montus,M.F., Prades,C., Arnould-Reguigne,I.,
Duverger,N., Allikmets,R. and Dean,M.
TITLE Nucleic acids of the human abca5, abca6, abca9, and abca10 genes,
vectors containing such nucleic acids and uses thereof
JOURNAL Patent: WO 0246458-A 177 13-JUN-2002;
Aventis Pharma S.A. (FR) ; The Secretary, Department of Health and
Human Services (US)
FEATURES
source
1 /organism="Homo sapiens"
/moi_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2485 GTGCAGAAATGTAAGTGGGC 2503
| | | | | | | | | |
Db 19 GTGAAGAATCCAAGTGGGC 1

RESULT 991
AX513754/c
LOCUS AX513754 19 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 19 from Patent WO0234947.
ACCESSION AX513754
VERSION AX513754.1 GI:23559900
KEYWORDS

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Khripin,Y.
JOURNAL Detecting specific nucleotide sequences
Patent: WO 0234947-A 19 02-MAY-2002;
Khripin, Yuri (US)
FEATURES
source
1 /organism="synthetic construct"
/moi_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1160 ACCCAATGGAGCTGTC 1178
| | | | | | | | | |
Db 19 ACTTCAATGGAGCTGTC 1

RESULT 992
AX644866/c
LOCUS AX644866 19 bp DNA linear PAT 27-FEB-2003
DEFINITION Sequence 14 from Patent WO02061104.
ACCESSION AX644866
VERSION AX644866.1 GI:28610842
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Zheng,C., Baum,B.J. and O'Connell,B.C.
JOURNAL Hybrid adenoviral vector
Patent: WO 02061104-A 14 08-AUG-2002;
The Secretary Department of Health and Human Services (US)
FEATURES
source
1 /organism="synthetic construct"
/moi_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide primer"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3061 TCCTGTTCACACCCCAA 3079
| | | | | | | | | |
Db 19 TATTGTTACACACCCCAA 1

RESULT 993
AX928387
LOCUS AX928387 19 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 22 from Patent WO03072822.
ACCESSION AX928387
VERSION AX928387.1 GI:40251950
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Hamelin,R. and Suraweera,N.
TITLE Mononucleotide repeats microsatellite markers for detecting
microsatellite instability
JOURNAL Patent: WO 03072822-A 22 04-SEP-2003;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE; (INSERM)
(PF)
FEATURES
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1 /organism="synthetic construct"
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/db_xref="taxon:32630"
/notes="Primer"

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            /db_xref="taxon:32630"
            /note="PCR primer"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1570 TACCAGGTGGCCCGGGCA 1588
Db      1 TACCAGGTGGCAAGGCGA 19

RESULT 994
AX956746
LOCUS      AX956746      19 bp      DNA      linear      PAT 08-JAN-2004
DEFINITION      Sequence 296 from Patent WO03097869.
ACCESSION      AX956746
VERSION      AX956746.1 GI:40785255
KEYWORDS
SOURCE      Rosa sp.
ORGANISM      Rosa sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.

REFERENCE      1
AUTHORS      Suess,K.H.
TITLES      Microsatellite markers for genetic analyses and the differentiation
            of roses
JOURNAL      Patent: WO 03097869-A 296 27-NOV-2003;
            Con/Cipio GmbH (DE)
FEATURES      Location/Qualifiers
source      1..19
            /organism="Rosa sp."
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            /db_xref="taxon:36598"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2104 ACCCCAGCTCCAGCTCCT 2122
Db      1 ACCTCAGCAGCAACTCCT 19

RESULT 995
BD002098/c
LOCUS      BD002098      19 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      Method and kit for detection of specific nucleotide sequence.
ACCESSION      BD002098
VERSION      BD002098.1 GI:18628838
KEYWORDS      JP 2000189198-A/19.
SOURCE      synthetic construct
ORGANISM      synthetic construct
            artificial sequences.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Ehrlich,H.A., Horne,G.T., Saiki,R.K. and Maris,C.B.
TITLES      Method and kit for detection of specific nucleotide sequence
JOURNAL      Patent: JP 2000189198-A 19 11-JUL-2000;
            F HOFFMANN LA ROCHE AG
COMMENT      OS Artificial Sequence
            PN JP 2000189198-A/19
            PD 11-JUL-2000
            PF 24-FEB-2000 JP 2000052306
            PR 13-MAR-1986 US 839331,22-AUG-1986 US 899344 PI
            HENRY ANTHONY EHRLICH,GLENN THOMAS HORNE,RANDALL KEICHI SAIKI, PI
            CURRY BANKS MARIS
            PC C12Q1/68//C12N15/09,C12N15/00
            CC
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Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 835 CTGCTGGGCTGCTGCCAGCG 853
Db      19 CTGCTGGGCTGCTGCCAGCG 1

RESULT 997
BD008057/c
LOCUS      BD008057      19 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      Method of detecting peritoneal thickening.
ACCESSION      BD008057
VERSION      BD008057.1 GI:18636430
KEYWORDS      JP 2001066306-A/16.
SOURCE      synthetic construct
ORGANISM      synthetic construct
            artificial sequences.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Hirahara,I. and Uneyama,K.
TITLES      Method of detecting peritoneal thickening
JOURNAL      Patent: JP 2001066306-A 16 16-MAR-2001;
            CURRY BANKS MARIS
            PC C12Q1/68//C12N15/09,C12N15/00
            CC
            FH Key      Location/Qualifiers

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            Location/Qualifiers
            1..19
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Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 835 CTGCTGGGCTGCTGCCAGCG 853
Db      19 CTGCTGGGCTGCTGCCAGCG 1

RESULT 996
BD002141/c
LOCUS      BD002141      19 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      Method and kit for detection of specific nucleotide sequence.
ACCESSION      BD002141
VERSION      BD002141.1 GI:18628881
KEYWORDS      JP 2000189199-A/19.
SOURCE      synthetic construct
ORGANISM      synthetic construct
            artificial sequences.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Ehrlich,H.A., Horne,G.T., Saiki,R.K. and Maris,C.B.
TITLES      Method and kit for detection of specific nucleotide sequence
JOURNAL      Patent: JP 2000189199-A 19 11-JUL-2000;
            F HOFFMANN LA ROCHE AG
COMMENT      OS Artificial Sequence
            PN JP 2000189199-A/19
            PD 11-JUL-2000
            PF 24-FEB-2000 JP 2000052307
            PR 13-MAR-1986 US 839331,22-AUG-1986 US 899344 PI
            HENRY ANTHONY EHRLICH,GLENN THOMAS HORNE,RANDALL KEICHI SAIKI, PI
            CURRY BANKS MARIS
            PC C12Q1/68//C12N15/09,C12N15/00
            CC
            FH Key      Location/Qualifiers

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            Location/Qualifiers
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            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 835 CTGCTGGGCTGCTGCCAGCG 853
Db      19 CTGCTGGGCTGCTGCCAGCG 1

RESULT 997
BD008057/c
LOCUS      BD008057      19 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      Method of detecting peritoneal thickening.
ACCESSION      BD008057
VERSION      BD008057.1 GI:18636430
KEYWORDS      JP 2001066306-A/16.
SOURCE      synthetic construct
ORGANISM      synthetic construct
            artificial sequences.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Hirahara,I. and Uneyama,K.
TITLES      Method of detecting peritoneal thickening
JOURNAL      Patent: JP 2001066306-A 16 16-MAR-2001;
            CURRY BANKS MARIS
            PC C12Q1/68//C12N15/09,C12N15/00
            CC
            FH Key      Location/Qualifiers

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COMMENT
OS Artificial Sequence
PN JP 2001066306-A/16
PD 16-MAR-2001
PF 30-AUG-1999 JP 1999244079
PR ICHIRO HIRAHARA, KAZUO UMEYAMA
PI G01N33/53, A61M1/28, C12N15/09, C12Q1/68, G01N33/50, G01N33/68, PC
PC G01N33/53, A61M1/28, C12N15/09, C12Q1/68, G01N33/50, G01N33/68, PC
C12N15/09
CC Key Location/Qualifiers
FH Key 1..19
FT Source /organism='Artificial Sequence'
FT Location/Qualifiers
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1..19
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2608 CAAGCTGAGCTGCAGGG 2626
Db 19 CAGAGCTGCCTGCAGAG 1
RESULT 998
AB067988/c
LOCUS 19 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, forward primer for human STS sts-190018T7
at 1p36.
ACCESSION AB067988
VERSION 1 GI:15128792
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morohashi, A., Ohtsuka, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.,
and Soeda, E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 19)
AUTHORS Horii, A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
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/note='forward primer for human STS sts-190018T7 at 1p36
sts-190018T7 obtained from clones B151P10, 170B16, B31617,
190018, ND, B37218, B372K8, B377E14, Human BAC library
RPCT-11'
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3652 TTGCTTGCCTGCAGGGCCA 3670
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Db 19 TTGCATGCTGCAGGTGCA 1
RESULT 999
A32748/c
LOCUS 20 bp DNA linear PAT 09-JUL-1996
DEFINITION Synthetic capture probe for E.coli beta-glucuronidase gene.
ACCESSION A32748
VERSION A32748.1 GI:1567596
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS
TITLE METHOD FOR DETECTING A NUCLEOTIDE SEQUENCE BY SANDWICH
HYBRIDIZATION
JOURNAL Patent: WO 9119812-A 48 26-DEC-1991;
FEATURES Location/Qualifiers
source
1..20
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1659 CAACGTGATGAGATCGCA 1677
|||||
Db 20 CAGCGTATATAGATCGCA 2
RESULT 1000
A47852/c
LOCUS 20 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 66 from Patent WO9533851.
ACCESSION A47852
VERSION A47852.1 GI:2301738
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS De, B. H., Portaeis, F., Machtelinckx, L., Jannes, G. and Rossau, R.
TITLE METHOD FOR THE DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF
MYCOBACTERIUM SPECIES
JOURNAL Patent: WO 9533851-A 66 14-DEC-1995;
COMMENT INNOGENETICS NV (BE)
FEATURES Other publication AU 2789695 960104.
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 355 GAGTTCGCGCGAGCACC 373
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Db 20 GAGTTCGCGCGAGTGCACC 2
RESULT 1001
A63042
LOCUS 20 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 13 from Patent WO9718308.
ACCESSION A63042
VERSION A63042.1 GI:3716906
KEYWORDS unidentified
SOURCE

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ORGANISM unidentified
REFERENCE 1
AUTHORS Ashcroft,F., Sakura,H., Ashfield,R. and Ashcroft,S.J.
TITLE K-ATP CHANNEL PROTEIN AND METHODS RELATING TO IT
JOURNAL Patent: WO 9718308-A 13 22-MAY-1997;
COMMENT WELLCOME TRUST LIMITED AS TRUS (GB)
FEATURES Other publication AU 7583296 19970605.
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/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1351 ATGGAGATGATGAAGATGA 1369
Db 1 AAGGACATGGTGAAGATGA 19

RESULT 1002
A97518
LOCUS 20 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 18 from Patent WO9915696.
ACCESSION A97518
VERSION A97518.1 GI:6780864
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Qiu,Y.
TITLE METHOD AND KIT FOR EARLY DIAGNOSIS OF AUTOIMMUNITY AND LYMPHOMA IN
JOURNAL CENTRAL NERVOUS SYSTEM
PATENT: WO 9915696-A 18 01-APR-1999;
QIN YUPEN (CA)
FEATURES Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 986 AAGGCTGGGCTCCGCCAC 1004
Db 1 ATGGCTGGGCTCCACTAC 19

RESULT 1003
AR012029
LOCUS 20 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 6 from patent US 5763186.
ACCESSION AR012029
VERSION AR012029.1 GI:3970019
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ludtke,D.N., Monahan,J.E. and Unger,J.T.
TITLE Use of antisense oligomers in a process for controlling
JOURNAL contamination in nucleic acid amplification reactions
PATENT: US 5763186-A 6 09-JUN-1998;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"

ORGANISM unidentified
REFERENCE 1
AUTHORS Ashcroft,F., Ashfield,R. and Ashcroft,S.J.
TITLE K-ATP CHANNEL PROTEIN AND METHODS RELATING TO IT
JOURNAL Patent: WO 9718308-A 13 22-MAY-1997;
COMMENT WELLCOME TRUST LIMITED AS TRUS (GB)
FEATURES Other publication AU 7583296 19970605.
source
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/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 812 GGTTCCTCATCTCTGC 830
Db 1 GGTTCCTCATCTCTCTAC 19

RESULT 1004
AR062662
LOCUS 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 62 from patent US 5843738.
ACCESSION AR062662
VERSION AR062662.1 GI:5990353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5843738-A 62 01-DEC-1998;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTGTCCTGGAGGG 3398
Db 2 CTGTGTGTCCTGGAGGG 20

RESULT 1005
AR062829/c
LOCUS 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5843757.
ACCESSION AR062829
VERSION AR062829.1 GI:5990520
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Vogelstein,B., Kinzler,K.W. and Nicolaides,N.C.
TITLE Human JTV1 gene overlaps PMS2 gene
JOURNAL Patent: US 5843757-A 16 01-DEC-1998;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACACTCACC 1795
Db 20 GACGAGTCTTCACTAACC 2

RESULT 1006
AR076718/c
LOCUS 20 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 83 from patent US 5959096.
ACCESSION AR076718
VERSION AR076718.1 GI:10003464
KEYWORDS

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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., and Dean,N.
TITLE Antisense oligonucleotides against human protein kinase C
JOURNAL Patent: US 5930936-A 83 28-SEP-1999;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1812 CTTTGGGTCCTGCTCTGG 1830
Db 19 CTGTGGTCCCTGCTCTGG 1

RESULT 1007
AR079558/c AR079558 20 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 2 from patent US 5965712.
DEFINITION AR079558
ACCESSION AR079558
VERSION AR079558.1 GI:10006302
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Conrad,D.H. and Kelly,A.E.
TITLE LZ-CD23 chimera for inhibition of IgE-mediated allergic disease
JOURNAL Patent: US 5965712-A 2 12-OCT-1999;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1294 GTGAAGATGCTGAAGACG 1312
Db 19 GTGAAGATGCTGAAGAG 1

RESULT 1008
AR104765 AR104765 20 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 62 from patent US 6093811.
DEFINITION AR104765
ACCESSION AR104765
VERSION AR104765.1 GI:12817473
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 6093811-A 62 25-JUL-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTGCCAGGACGG 3398

Db 2 CTGTGTGCTGGAGG 20

RESULT 1009
AR105587 AR105587 20 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 62 from patent US 6096722.
DEFINITION AR105587
ACCESSION AR105587
VERSION AR105587.1 GI:12819184
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Mirabelli,C.K. and Baker,B.
TITLE Antisense modulation of cell adhesion molecule expression and
treatment of cell adhesion molecule-associated diseases
JOURNAL Patent: US 6096722-A 62 01-AUG-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTGCCAGGACGG 3398
Db 2 CTGTGTGCTGGAGG 20

RESULT 1010
AR108646/c AR108646 20 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 10 from patent US 6111075.
DEFINITION AR108646
ACCESSION AR108646
VERSION AR108646.1 GI:12824133
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Xu,W.-f., Presnell,S.R., Yee,D.P. and Foster,D.C.
TITLE Protease-activated receptor PAR4 (ZCHEMR2)
JOURNAL Patent: US 6111075-A 10 29-AUG-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2415 CCCCCTGCTGTGCAACGG 2433
Db 20 CCATGCTGCTGTGCTACGG 2

RESULT 1011
AR116480 AR116480 20 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 61 from patent US 6133246.
DEFINITION AR116480
ACCESSION AR116480
VERSION AR116480.1 GI:14096802
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.


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TITLE      Antisense oligonucleotide compositions and methods for the
JOURNAL    modulation of JNK proteins
FEATURES   Patent: US 6133246-A 61 17-OCT-2000;
           Location/Qualifiers
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           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3379 GCTGTGTGTCCTCCAGGAGG 3397
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Db 2 GCTGGCTTTCGAGGCGG 20

RESULT 1012
AR122482/c
LOCUS      AR122482      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 36 from patent US 6165728.
ACCESSION AR122482
VERSION   AR122482.1 GI:14106799
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Ward,D.T. and Cowser,L.M.
TITLE     Antisense modulation of NCK-2 expression
JOURNAL   Patent: US 6165728-A 36 26-DEC-2000;
FEATURES   Location/Qualifiers
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           /organism="unknown"
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Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1293 CGTGAAGATGCTGAAGAC 1311
      |||||
Db 19 CGTGAAGACCTGAAGAC 1

RESULT 1013
AR122500/c
LOCUS      AR122500      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 54 from patent US 6165728.
ACCESSION AR122500
VERSION   AR122500.1 GI:14106817
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Ward,D.T. and Cowser,L.M.
TITLE     Antisense modulation of NCK-2 expression
JOURNAL   Patent: US 6165728-A 54 26-DEC-2000;
FEATURES   Location/Qualifiers
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           /organism="unknown"
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Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 865 GTGAGGCTGACGAGCGG 883
      |||||
Db 20 GAGGAGTGGACGAGCGG 2

TITLE      Antisense oligonucleotide compositions and methods for the
JOURNAL    modulation of JNK proteins
FEATURES   Patent: US 6133246-A 61 17-OCT-2000;
           Location/Qualifiers
           source
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3379 GCTGTGTGTCCTCCAGGAGG 3397
      |||||
Db 2 GCTGGCTTTCGAGGCGG 20

RESULT 1014
AR122507/c
LOCUS      AR122507      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 61 from patent US 6165728.
ACCESSION AR122507
VERSION   AR122507.1 GI:14106824
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Ward,D.T. and Cowser,L.M.
TITLE     Antisense modulation of NCK-2 expression
JOURNAL   Patent: US 6165728-A 61 26-DEC-2000;
FEATURES   Location/Qualifiers
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1533 GGAGCAGCTCACCTTCAAG 1551
      |||||
Db 20 GGAGGAGCTCAACTTCGAG 2

RESULT 1015
AR123249
LOCUS      AR123249      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 62 from patent US 6169079.
ACCESSION AR123249
VERSION   AR123249.1 GI:14108215
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Bennett,C.Frank. and Mirabelli,C.K.
TITLE     Oligonucleotide inhibition of cell adhesion
JOURNAL   Patent: US 6169079-A 62 02-JAN-2001;
FEATURES   Location/Qualifiers
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTGTCCCGAGGAGG 3398
      |||||
Db 2 CTGTGTGTCTGGGAGG 20

RESULT 1016
AR127702
LOCUS      AR127702      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 120 from patent US 6180774.
ACCESSION AR127702
VERSION   AR127702.1 GI:14114297
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Brown,S.Marie., Dean,D.Allen., Fromm,M.Ernest. and
           Sanders,P.Rigden.
TITLE     Synthetic DNA sequences having enhanced expression in
           monocotyledonous plants and method for preparation thereof
JOURNAL   Patent: US 6180774-A 120 30-JAN-2001;
FEATURES   Location/Qualifiers
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Thu Oct 28 12:48:19 2004

source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2617 GCTGCGAGGAGCCAC 2635
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GTCTGCAGAGTCCCCAC 20

RESULT 1017
ARI29756/c 20 bp DNA PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 160 from patent US 6187545.
ACCESSION ARI29756
VERSION ARI29756.1 GI:14117653
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay, R., Butler, M.M., Wyatt, J. and Cowsett, L.M.
TITLE Antisense modulation of pebok-cytosolic expression
JOURNAL Patent: US 6187545-A 160 13-FEB-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 42 GGGCCCCAGGGCTGCAG 60
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GAGGCCACAGTGTCTGCAG 2

RESULT 1018
ARI42705/c 20 bp DNA PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 3 from patent US 6203998.
ACCESSION ARI42705
VERSION ARI42705.1 GI:15103991
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Civelli, O. and Van Tol, H. Henri.-Marie.
TITLE Human dopamine receptor and its uses
JOURNAL Patent: US 6203998-A 3 20-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 98 GCTGCCGAGGGGCTCAC 116
| | | | | | | | | | | | | | | | | | | | | |
Db 19 GCGGCCGAGCGGCTCAC 1

RESULT 1019
ARI62412/c 20 bp DNA PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 92 from patent US 6258600.

ACCESSION ARI62412
VERSION ARI62412.1 GI:16229590
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Zhang, H. and Cowsett, L.M.
TITLE Antisense modulation of caspase 8 expression
JOURNAL Patent: US 6258600-A 92 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3260 GATATTTTATTGCTTGT 3278
| | | | | | | | | | | | | | | | | | | | | |
Db 19 GCTATTTTGTGTTTGT 1

RESULT 1020
ARI63862/c 20 bp DNA PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 60 from patent US 6271030.
ACCESSION ARI63862
VERSION ARI63862.1 GI:16234657
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P., Butler, M.M. and Wyatt, J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 60 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 243 CGAGCGGATGGACAGAG 261
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CGAGCGGCTGCAGAGAG 2

RESULT 1021
ARI63924 20 bp DNA PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 122 from patent US 6271030.
ACCESSION ARI63924
VERSION ARI63924.1 GI:16234757
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P., Butler, M.M. and Wyatt, J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 122 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 44 GGCCCGGAGCGGCTCCAGGT 62
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Db 1 GGCGGAGCGGCTCCAGGT 19

RESULT 1022
LOCUS AR164041/c 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 241 from patent US 6271030.
ACCESSION AR164041
VERSION AR164041.1 GI:16234953
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 241 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3250 TTCCAGTGAAGATATTTTA 3268
| | | | | | | | | | | | | | | |
Db 20 TTAAGTGAAGACATTTTA 2

RESULT 1023
LOCUS AR174372/c 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 32 from patent US 6306655.
ACCESSION AR174372
VERSION AR174372.1 GI:17914692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP alpha expression
JOURNAL Patent: US 6306655-A 32 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2041 TCACCGACGAGTACTGG 2059
| | | | | | | | | | | | | | | |
Db 19 TTCACGACGAGTCTCTGG 1

RESULT 1024
LOCUS AR177628/c 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 11 from patent US 6312939.
ACCESSION AR177628
VERSION AR177628.1 GI:17919983
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP alpha expression
JOURNAL Patent: US 6312939-A 11 06-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACACTCACC 1795
| | | | | | | | | | | | | | | |
Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1026
LOCUS BD181159/c 20 bp DNA linear PAT 15-MAY-2003
DEFINITION Human DNA mismatch repair proteins.
ACCESSION BD181159
VERSION BD181159.1 GI:30792077
KEYWORDS JP 2002325588-A/63.

REFERENCE 1 (bases 1 to 20)
AUTHORS Roberts,J., MacAllister,T.W., Sethuraman,N. and Freeman,A.G.
TITLE Genetically engineered glutaminase and its use in antiviral and anticancer therapy
JOURNAL Patent: US 6312939-A 11 06-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 845 TGCCAGCCGAGGAGGAGCT 863
| | | | | | | | | | | | | | | |
Db 19 TGCCAGCCCTGCAGGAGCT 1

RESULT 1025
LOCUS BD181148/c 20 bp DNA linear PAT 15-MAY-2003
DEFINITION Human DNA mismatch repair proteins.
ACCESSION BD181148
VERSION BD181148.1 GI:30792066
KEYWORDS JP 2002325588-A/52.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS Haseltine,W.A., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and Rosen,C.A.
TITLE Human DNA mismatch repair proteins
JOURNAL Patent: JP 2002325588-A 52 12-NOV-2002;
COMMENT HUMAN GENOME SCIENCES INC
OS Artificial Sequence
PN JP 2002325588-A/52
PD 12-NOV-2002
PF 25-JAN-2002 JP 2002016830 08/210143 PR
PR 27-JAN-1994 US 08/187757,16-MAR-1994 US 08/210143 PR
23-AUG-1994 US 08/294312
PI WILLIAM A HASELTINE,STEVEN M RUBEN,YING FEI WEI,MARK D ADAMS,
PI ROBERT D FLEISCHMANN,CLAIRE M FRASER,REBECCA A FULDNER,EWEN F
PI KIRKNESS,
PI CRAIG A ROSEN
PC C12N15/09,C07K14/47,C12P21/02,C12Q1/68// (C12P21/02,C12R1:19),
PC C12N15/00
CC hMLH3 primer
FH Key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACACTCACC 1795
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Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1026
LOCUS BD181159/c 20 bp DNA linear PAT 15-MAY-2003
DEFINITION Human DNA mismatch repair proteins.
ACCESSION BD181159
VERSION BD181159.1 GI:30792077
KEYWORDS JP 2002325588-A/63.

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SOURCE          synthetic construct
ORGANISM        /organism="synthetic construct"
REFERENCE       1 (bases 1 to 20)
AUTHORS         Haseltine,W.A., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D.,
                Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and Rosen,C.A.
TITLE           Human DNA mismatch repair proteins
JOURNAL         Patent: JP 2002325588-A 63 12-NOV-2002;
                HUMAN GENOME SCIENCES INC
COMMENT        OS Artificial Sequence
                PN JP 2002325588-A/63
                PD 12-NOV-2002
                PR 25-JAN-2002 JP 2002016830
                PR 27-JAN-1994 US 08/187757,16-MAR-1994 US 08/210143 PR
                PI WILLIAM A HASELTINE,STEVEN M RUBEN,YING FEI WEI,MARK D ADAMS,
                PI ROBERT D FLEISCHMANN,CLAIRE M FRASER,REBECCA A FULDNER,EVEN F
                PI KIRKNESS,
                PI CRAIG A ROSEN
                PC C12N15/09,C07K14/47,C12P21/02,C12Q1/68//(C12P21/02,C12R1:19),
                PC C12N15/00
                CC primer useful for amplifying codons 1 to 863 hMLH3 FH Key
                Location/Qualifiers
                FT source 1..20
                FT /organism='Artificial Sequence'.

FEATURES
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    Best Local Similarity 84.2%; Pred. No. 1.le+03;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 1777 GACCGAGCTCTACACTCACC 1795
  Db 20 GACAGAGCTCTCACTAACC 2

RESULT 1027
LOCUS          BD181162 20 bp DNA linear PAT 15-MAY-2003
DEFINITION    Human DNA mismatch repair proteins.
ACCESSION     BD181162
VERSION       BD181162.1 GI:30792080
KEYWORDS      JP 2002325588-A/66.
SOURCE        synthetic construct
ORGANISM      /organism="synthetic construct"
REFERENCE     1 (bases 1 to 20)
AUTHORS       Haseltine,W.A., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D.,
                Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and Rosen,C.A.
TITLE         Human DNA mismatch repair proteins
JOURNAL       Patent: JP 2002325588-A 66 12-NOV-2002;
                HUMAN GENOME SCIENCES INC
COMMENT        OS Artificial Sequence
                PN JP 2002325588-A/66
                PD 12-NOV-2002
                PR 25-JAN-2002 JP 2002016830
                PR 27-JAN-1994 US 08/187757,16-MAR-1994 US 08/210143 PR
                PI WILLIAM A HASELTINE,STEVEN M RUBEN,YING FEI WEI,MARK D ADAMS,
                PI ROBERT D FLEISCHMANN,CLAIRE M FRASER,REBECCA A FULDNER,EVEN F
                PI KIRKNESS,
                PI CRAIG A ROSEN
                PC C12N15/09,C07K14/47,C12P21/02,C12Q1/68//(C12P21/02,C12R1:19),
                PC C12N15/00
                CC primer useful for amplifying codons 415 to 863 of hMLH3 FH
                Location/Qualifiers
                FT source 1..20
                FT /organism='Artificial Sequence'.

FEATURES
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    Query Match 0.4%; Score 14.2; DB 1; Length 20;
    Best Local Similarity 84.2%; Pred. No. 1.le+03;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 1777 GACCGAGCTCTACACTCACC 1795
  Db 20 GACAGAGCTCTCACTAACC 2

RESULT 1027
LOCUS          BD181162 20 bp DNA linear PAT 15-MAY-2003
DEFINITION    Human DNA mismatch repair proteins.
ACCESSION     BD181162
VERSION       BD181162.1 GI:30792080
KEYWORDS      JP 2002325588-A/66.
SOURCE        synthetic construct
ORGANISM      /organism="synthetic construct"
REFERENCE     1 (bases 1 to 20)
AUTHORS       Haseltine,W.A., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D.,
                Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and Rosen,C.A.
TITLE         Human DNA mismatch repair proteins
JOURNAL       Patent: JP 2002325588-A 66 12-NOV-2002;
                HUMAN GENOME SCIENCES INC
COMMENT        OS Artificial Sequence
                PN JP 2002325588-A/66
                PD 12-NOV-2002
                PR 25-JAN-2002 JP 2002016830
                PR 27-JAN-1994 US 08/187757,16-MAR-1994 US 08/210143 PR
                PI WILLIAM A HASELTINE,STEVEN M RUBEN,YING FEI WEI,MARK D ADAMS,
                PI ROBERT D FLEISCHMANN,CLAIRE M FRASER,REBECCA A FULDNER,EVEN F
                PI KIRKNESS,
                PI CRAIG A ROSEN
                PC C12N15/09,C07K14/47,C12P21/02,C12Q1/68//(C12P21/02,C12R1:19),
                PC C12N15/00
                CC primer useful for amplifying codons 415 to 863 of hMLH3 FH
                Location/Qualifiers
                FT source 1..20
                FT /organism='Artificial Sequence'.

FEATURES
  source
    Query Match 0.4%; Score 14.2; DB 1; Length 20;
    Best Local Similarity 84.2%; Pred. No. 1.le+03;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 1777 GACCGAGCTCTACACTCACC 1795
  Db 20 GACAGAGCTCTCACTAACC 2

RESULT 1027
LOCUS          BD225060 20 bp DNA linear PAT 17-JUL-2003
DEFINITION    Antisense modulation of expression of tumor necrosis factor
                receptor-associated factor (TRAF).
ACCESSION     BD225060
VERSION       BD225060.1 GI:33034830
KEYWORDS      JP 2002526095-A/195.
SOURCE        synthetic construct
ORGANISM      /organism="synthetic construct"
REFERENCE     1 (bases 1 to 20)
AUTHORS       Baker,B.F., Cowsett,L.M., Monia,B.P. and Xu,X.S.
TITLE         Antisense modulation of expression of tumor necrosis factor
                receptor-associated factor (TRAF)

FEATURES
  source
    Query Match 0.4%; Score 14.2; DB 1; Length 20;
    Best Local Similarity 84.2%; Pred. No. 1.le+03;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 2004 GCTGGTGGAGGACCTGGAC 2022
  Db 19 GCTGGTGGAGGACGAGTGGAC 1

RESULT 1029
LOCUS          BD225060 20 bp DNA linear PAT 17-JUL-2003
DEFINITION    Antisense modulation of expression of tumor necrosis factor
                receptor-associated factor (TRAF).
ACCESSION     BD225060
VERSION       BD225060.1 GI:33034830
KEYWORDS      JP 2002526095-A/195.
SOURCE        synthetic construct
ORGANISM      /organism="synthetic construct"
REFERENCE     1 (bases 1 to 20)
AUTHORS       Baker,B.F., Cowsett,L.M., Monia,B.P. and Xu,X.S.
TITLE         Antisense modulation of expression of tumor necrosis factor
                receptor-associated factor (TRAF)

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JOURNAL Patent: JP 2002526095-A 195 20-AUG-2002;
COMMENT  ISIS PHARMACEUTICALS INC
          OS Artificial Sequence
          PN JP 2002526095-A/195
          PD 20-AUG-2002
          PP 05-OCT-1999 JP 2000574546
          PR 06-OCT-1998 US 09/167109
          PI BRENDA F BAKER, LEX M COWSERT, BRETT P MONIA, XIAOXING S XU PC
          C12N15/09, A61K31/7105, A61K48/00, A61P29/00, A61P35/00, A61P35/04, C12N15/00 CC
          antisense sequence
          FH Key Location/Qualifiers
          FT source 1..20
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1998 CAGGCGCTGGTAGGAC 2016
Db 2 CAGGCGCTGGTAGGAC 20

RESULT 1030
BD230252/c
LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Total genome radiation hybrid map of canine genome and its use for
          identification of interesting genes.
ACCESSION BD230252
VERSION BD230252.1 GI:33040022
KEYWORDS JP 2002530091-A/121.
SOURCE Canis familiaris
ORGANISM Canis familiaris
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 20)
AUTHORS Galibert, F. and Andre, C.
TITLE Total genome radiation hybrid map of canine genome and its use for
          identification of interesting genes
JOURNAL Patent: JP 2002530091-A 121 17-SEP-2002;
COMMENT CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
          OS Canis familiaris (dog)
          PN JP 2002530091-A/121
          PD 17-SEP-2002
          PP 15-NOV-1999 JP 2000582596
          PR 13-NOV-1998 US 60/108193
          PI FRANCIS GALIBERT, CATHERINE ANDRE
          PC C12N15/09, C12Q1/68, C12N15/00
          CC A0076
          FH Key Location/Qualifiers
          FT source 1..25
          FT /organism='Canis familiaris (dog)'.
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source
1..20
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 749 CCTTGACACGTCACCTT 767
Db 20 CCTTGACACGACCCCTT 2

RESULT 1031
JOURNAL Patent: JP 2002541784-A 138 10-DEC-2002;
COMMENT  ISIS PHARMACEUTICALS INC
          OS Artificial Sequence
          PN JP 2002541784-A/138
          PD 10-DEC-2002
          PP 06-APR-2000 JP 2000611544
          PR 08-APR-1999 US 09/488461
          PI JAMES G KARRAS
          PC C12N15/09, A61K31/711, A61K48/00, A61P29/00, A61P29/00, A61P35/00,
          PC A61P37/02,
          PC A61P43/00, C12N5/06, C12Q1/02, C12N15/00, C12N5/00 CC Antisense
          oligonucleotide
          FH Key Location/Qualifiers
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          FT /organism='Artificial Sequence'.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 GTGCACAGATCTCCGCT 1024
Db 1 GTGCTCAAGATGCCCGCT 19

RESULT 1032
CQ762181
LOCUS 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 799 from Patent WO2004003201.
ACCESSION CQ762181
VERSION CQ762181.1 GI:44905417
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kane, C.D.
TITLE Antisense modulation of lrlh expression
JOURNAL Patent: WO 2004003201-A 799 08-JAN-2004;
          Pharmacia Corporation (US)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Human LRLH antisense"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3558 CTGGACTGCTACCTTTCAA 3576
Db 2 CTGCACAGCTACCTTTAA 20
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AUTHORS	Kane,C.D.
TITLE	Antisense modulation of lrlh expression
JOURNAL	Patent: WO 2004003201-A 1498 08-JAN-2004;
Pharmacia Corporation (US)	
FEATURES	Location/Qualifiers
source	1..20
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="Human LRH1 antisense"
Query Match	0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity	84.2%; Pred.No.1.le+03;
Matches 16; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	2306 AGAGCTTTGGTGTGTTGT 2324
Db	19 AGAGCTTTGTCCCGTGTT 1
RESULT 1036	
LOCUS	CQ763511 20 bp DNA linear PAT 03-MAR-2004
DEFINITION	Sequence 2129 from Patent WO2004003201.
ACCESSION	CQ763511
VERSION	CQ763511.1 GI:44906747
KEYWORDS	. synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Kane,C.D.
TITLE	Antisense modulation of lrlh expression
JOURNAL	Patent: WO 2004003201-A 2129 08-JAN-2004;
Pharmacia Corporation (US)	
FEATURES	Location/Qualifiers
source	1..20
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	/db_xref="taxon:32630"
	/note="Human LRH1 antisense"
Query Match	0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity	84.2%; Pred.No.1.le+03;
Matches 16; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	319 CCCACTCCCCCATCTCCT 337
Db	1 CCCACTCCCCCAATCTCTT 19
RESULT 1037	
LOCUS	CQ764464 20 bp DNA linear PAT 03-MAR-2004
DEFINITION	Sequence 3082 from Patent WO2004003201.
ACCESSION	CQ764464
VERSION	CQ764464.1 GI:44907700
KEYWORDS	. synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Kane,C.D.
TITLE	Antisense modulation of lrlh expression
JOURNAL	Patent: WO 2004003201-A 3082 08-JAN-2004;
Pharmacia Corporation (US)	
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	/note="Human LRH1 antisense"

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Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3561 GACTGCTACTTTCAAAGC 3579
Db 20 GACTACAAACTTCAAAGC 2

RESULT 1038
LOCUS CQ764591/c 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 3209 from Patent WO2004003201.
ACCESSION CQ764591
VERSION CQ764591.1 GI:44907827
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kane, C.D.
TITLE Antisense modulation of lrlh expression
JOURNAL Patent: WO 2004003201-A 3209 08-JAN-2004;
Pharmacia Corporation (US)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Human LRH1 antisense"

Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3561 GACTGCTACTTTCAAAGC 3579
Db 19 GACTACAAACTTCAAAGC 1

RESULT 1039
CQ779747/c
LOCUS CQ779747 20 bp DNA linear PAT 17-MAR-2004
DEFINITION Sequence 27 from Patent WO2004016812.
ACCESSION CQ779747
VERSION CQ779747.1 GI:45535915
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Clinton, M.
TITLE Avian sex determination method
JOURNAL Patent: WO 2004016812-A 27 26-FEB-2004;
ROSLIN INSTITUTE (EDINBURGH) (GB)
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/notes="Primer"

Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2455 ACCGAGGGCGCTTTGTCT 2473
Db 19 ATCGAGGGCGCTTTATTCT 1

RESULT 1040
CQ779749/c
LOCUS CQ779749 20 bp DNA linear PAT 14-JUN-2004
DEFINITION Sequence 19 from Patent WO2004046381.
ACCESSION CQ819706
VERSION CQ819706.1 GI:48715186
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM

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LOCUS CQ779749 20 bp DNA linear PAT 17-MAR-2004
DEFINITION Sequence 29 from Patent WO2004016812.
ACCESSION CQ779749
VERSION CQ779749.1 GI:45535917
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Clinton, M.
TITLE Avian sex determination method
JOURNAL Patent: WO 2004016812-A 29 26-FEB-2004;
ROSLIN INSTITUTE (EDINBURGH) (GB)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2455 ACCGAGGGCGCTTTGTCT 2473
Db 19 ATCGAGGGCGCTTTATTCT 1

RESULT 1041
CQ786731
LOCUS CQ786731 20 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 7 from Patent WO2004018507.
ACCESSION CQ786731
VERSION CQ786731.1 GI:45721746
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Hanski, E., Moses, A. E. and Hidalgo-Grass, C.
TITLE Compositions and methods for treatment and prophylaxis of
infections caused by gram positive bacteria
JOURNAL Patent: WO 2004018507-A 7 04-MAR-2004;
YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW UNIVERS ITY OF
JERUSALEM (IL); HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT CO.
LTD. (IL)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence.Inverse PCR
primer from 5' of sila"

Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1995 CTTCAAGCAGCTGTGGAG 2013
Db 2 CTTCAAGCAGCTGTGGG 20

RESULT 1042
CQ819706
LOCUS CQ819706 20 bp DNA linear PAT 14-JUN-2004
DEFINITION Sequence 19 from Patent WO2004046381.
ACCESSION CQ819706
VERSION CQ819706.1 GI:48715186
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM

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artificial sequences.
1
REFERENCE
AUTHORS Ralston,S.
TITLE Polymorphisms in th clcn7 gene as genetic markers for bone mass
JOURNAL Patent: WO 2004046381-A 19 03-JUN-2004;
The University Court of The University of Aberdeen (GB)
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/db_xref="taxon:32630"
/note="Primer"
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Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1099 AGGCTGTCTCTCAGGGAGG 1117
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Db 1 AGGCTGTCTCTCAGATGGG 19
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RESULT 1043
LOCUS CO821690 20 bp DNA linear PAT 21-JUN-2004
DEFINITION Sequence 35 from Patent WO2004048606.
ACCESSION CO821690
VERSION CO821690.1 GI:49019968
KEYWORDS synthetic construct
synthetic construct
artificial sequences.
ORGANISM
REFERENCE
AUTHORS J Rgsensen,C.B., Cirera,S., Archibald,A., Andersson,L., Fredholm,M.
and Edfors-Lilja,I.
TITLE Porcine polymorphisms and methods for detecting them
JOURNAL Patent: WO 2004048606-A 35 10-JUN-2004;
Den KGL. Veterinaer- OG Landbohojskole (DK)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="lower primer related to gene RFC4"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 828 TGCCTGGCTGCTGCTGCTGCTG 846
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Db 1 TGCTTAGCTGATGCTGCTG 19
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RESULT 1044
E02948/c
LOCUS E02948 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer sequence for cloning of acylamino acid releasing enzyme by
PCR.
ACCESSION E02948
VERSION E02948.1 GI:2171170
KEYWORDS JP 1991147787-A/2.
synthetic construct
synthetic construct
artificial sequences.
ORGANISM
REFERENCE
AUTHORS Isekawa,Y., MuneKawa,Y., Oshima,A., Mukai,H. and Katou,I.
TITLE NEW METHOD FOR CLONING DNA
JOURNAL Patent: JP 1991147787-A 2 24-JUN-1991;
TAKARA SHUZO CO LTD
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1991147787-A/2

artificial sequences.
1
REFERENCE
AUTHORS PD 24-JUN-1991
PF 31-OCT-1989 JP 1989281811
PI ISEKAWA YUJI, MUNEKAWA YOSHIHIRO, OSHIMA ATSUSHI, PI MUKAI
HIROYUKI,
PI KATOU IKUNOSHIN
PC C12N15/10//C07H21/04;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2940 TGGAGGGAGGCCCCCAGGGG 2958
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Db 19 TGGATGGAGTCCACAGGGG 1
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RESULT 1045
E04077
LOCUS E04077 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for amplifying envelope region of type C hepatitis virus.
ACCESSION E04077
VERSION E04077.1 GI:2172287
KEYWORDS JP 1992349885-A/2.
synthetic construct
synthetic construct
artificial sequences.
ORGANISM
REFERENCE
AUTHORS Morinaga,T., Chayama,K., Kumada,H. and Ichikawa,Y.
TITLE NUCLEIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HEPATITIS C VIRUS
AND METHOD FOR DETECTING THE SAME
JOURNAL Patent: JP 1992349885-A 2 04-DEC-1992;
TEIJIN LTD
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1992349885-A/2
PD 04-DEC-1992
PF 23-MAY-1991 JP 1991152169
PI MORINAGA TSUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU, PI
ICHIKAWA YATARO
PC C12N15/10,C12Q1/68,C12Q1/70//C12N15/11;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No.
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3664 AGGGCCATGGCTCAGGGTG 3682
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Db 1 AGGGCCCTGGCGCATGGTG 19
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RESULT 1046
E11000/c
LOCUS E11000 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for detecting human cytochrome P4501A2 polymorphism(one
member of a couple).
ACCESSION E11000
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VERSION E11000.1 GI:22024641
KEYWORDS JP 1996070897-A/18.
SOURCE unidentifed
ORGANISM unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Fukui,T., Katsuragi,S., Kinoshita,M. and Shin,T.
TITLE DETECTION OF POLYMORPHISM OF HUMAN CYTOCHROME P4501A2 GENE
JOURNAL Patent: JP 1996070897-A 18 19-MAR-1996;
OTSUKA PHARMACEUT CO LTD
COMMENT OS None
OC Artificial sequences.
FN JP 1996070897-A/18
PD 19-MAR-1996
PF 06-JUL-1995 JP 1995170693
PR 06-JUL-1994 JP 94P 154571
PI FUKUI TAKASHI, KATSURAGI SHIYUKUTEN, KINOSHITA MORITOSHI, PI
SHIN TEIKIN
PC C12Q1/68,C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH key Location/Qualifiers
FH source 1..20 /organism='Artificial sequences'.
FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3426 TGTGTCAGGTTCCGATGT 3444
DB 19 TGTGTCAGGTTCCAGCAGT 1
RESULT 1047
E13769/c
LOCUS 20 bp DNA linear PAT 27-APR-1998
DEFINITION PCR primer for discriminating genotype 6a of HCV (Hepatitis C virus).
ACCESSION E13769
VERSION E13769.1 GI:3252537
KEYWORDS JP 1997234072-A/21.
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ono,T., Mukaide,M., Hikichi,K. and Mizogami,M.
TITLE NEW OLIGONUCLEOTIDE, PRIMER FOR DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS COMPRISING THE SAME AND DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS BY USING THE PRIMER
JOURNAL Patent: JP 1997234072-A 21 09-SEP-1997;
S R L-KK
COMMENT OS None
OC Artificial sequences.
FN JP 1997234072-A/21
PD 09-SEP-1997
PF 01-FEB-1996 JP 1996038875
PR 01-FEB-1995 JP 95P 35997, 30-DEC-1995 JP 95P 352511 PI
ONO TOMOYOSHI, MUKAIDE MASAKAZU, HIKICHI KAZUMASA, PI MIZOGAMI MASAFUMI
PC C12N15/09,C07H21/04,C12Q1/68,C12Q1/70,(C12N15/09,C12R1:92); CC
strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH key Location/Qualifiers
FH

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FT misc_feature 1..20 /note='Primer,OMM263'.
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Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3189 GCGTCGCCCGAGCTGGAG 3207
DB 19 GCGTCGCCCTGGGCTGGCG 1
RESULT 1048
E29869/c
LOCUS 20 bp DNA linear PAT 18-JUN-2001
DEFINITION HIV cofactor inhibitor.
ACCESSION E29869
VERSION E29869.1 GI:13021264
KEYWORDS JP 1999292795-A/23.
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hiroshi,T., Naoki,Y., Toru,K., Kazuyuki,T. and Akira,W.
TITLE HIV cofactor inhibitor
JOURNAL Patent: JP 1999292795-A 23 26-OCT-1999;
YAMANOUCHI PHARMACEUT CO LTD
COMMENT OS Unidentified
FN JP 1999292795-A/23
PD 26-OCT-1999
PF 02-APR-1998 JP 1998125452
PI HIROSHI TAKAHISA, NAOKI YAMAMOTO, TORU KIMURA, KAZUYUKI TAKAI, PI
AKIRA WADA
PC A61K48/00,A61K31/70,A61K31/70,C12N15/09,C12N15/00 CC
FH key Location/Qualifiers
FT source 1..20 /organism='Unidentified'.
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Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1615 ATCCACAGGACCTGGCTG 1633
DB 19 ATCGATAGTGCTACCTGGCTG 1
RESULT 1049
E30661/c
LOCUS 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Immortalized human external trichilemmal cell and method for evaluating hair growth stimulant by using the same.
ACCESSION E30661
VERSION E30661.1 GI:13017227
KEYWORDS JP 200000089-A/14.
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Jun.S., Eriko.T., Chika.H., Masahiro.T. and Hiroshi,H.


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      /organism="synthetic construct"
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  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3272 GCTTGTCTCTTTTCAGGA 3290
Db 1 GCTTTTCTCTTTGAGGA 19

RESULT 1053
LOCUS 120664 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Sequence 62 for purifying oligonucleotide.
ACCESSION E59332
VERSION E59332.1 GI:18622509
KEYWORDS JP 2000342265-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hirose,K. and Yoshida,T.
TITLE Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 13 12-DEC-2000;
TOAGOSEI CHEM IND CO LTD
COMMENT OS Artificial Sequence
PN JP 2000342265-A/13
PD 12-DEC-2000
PF 02-JUN-1999 JP 1999154974
PR KUNIHICO HIROSE,TADAO YOSHIDA
PC C12N15/09,B01D15/08,C12N15/00
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Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2924 GGGCGTGGGGGGGGCTGG 2942
Db 2 GGGCGGGGGGGGGGAGGG 20

RESULT 1054
LOCUS 112350 20 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 3 from patent US 542265.
ACCESSION 112350
VERSION 112350.1 GI:910373
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Civelli,O. and Van Tol,H.H.
TITLE DNA sequence for the human dopamine receptor D.sub.4 and expression thereof in mammalian cells
JOURNAL Patent: US 542265-A 3 06-JUN-1995;
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  Location/Qualifiers
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/organism="unknown"
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Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 98 GCTGCGGCGAGCGGCTCAC 116
Db 19 GCGGCGGAGCGGCTCAC 1

RESULT 1055
LOCUS 120664 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 62 from patent US 5514788.
ACCESSION 120664
VERSION 120664.1 GI:1601019
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5514788-A 62 07-MAY-1996;
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Query Match
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  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTGTCCAGGAGGG 3398
Db 2 CTGTGTGTCTGTGGAGGG 20

RESULT 1056
LOCUS 128186 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5569601.
ACCESSION 128186
VERSION 128186.1 GI:1818962
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Civelli,O.
TITLE Human dopamine receptor and its uses
JOURNAL Patent: US 5569601-A 3 29-OCT-1996;
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  Location/Qualifiers
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Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 98 GCTGCGGCGAGCGGCTCAC 116
Db 19 GCGGCGGAGCGGCTCAC 1

RESULT 1057
LOCUS 133357 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 62 from patent US 5591623.
ACCESSION 133357
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VERSION I3357.1 GI:1824148
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5591623-A 62 07-JAN-1997;
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTCCTCCAGGAGGG 3398
Db ||||||| ||||||| |||||||
2 CTGTGTCCTCCAGGAGGG 20

RESULT 1058
LOCUS I33959 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5594108.
ACCESSION I33959
VERSION I33959.1 GI:1824750
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 20)
AUTHORS Civelli,O. and Van Tol,H.H.
TITLE Human dopamine receptor and its uses
JOURNAL Patent: US 5594108-A 3 14-JAN-1997;
FEATURES
source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 98 GCTCGCGGACGGGCTCAC 116
Db ||||||| ||||||| |||||||
19 GCGGCGGACGGGCTCAC 1

RESULT 1059
LOCUS I75371 20 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 120 from patent US 5689052.
ACCESSION I75371
VERSION I75371.1 GI:3011512
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 20)
AUTHORS Brown,S.Marie., Dean,D.Allen., Fromm,M.Ernest. and Sanders,P.Rigden.
TITLE Synthetic DNA sequences having enhanced expression in monocotyledonous plants and method for preparation thereof
JOURNAL Patent: US 5689052-A 120 18-NOV-1997;
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2617 GCCTGCAGGAGAGCCAC 2635-
Db ||||||| ||||||| |||||||
2 GTCTGCAGAGATGCCAC 20

RESULT 1060
LOCUS I84306 20 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 77 from patent US 5695926.
ACCESSION I84306
VERSION I84306.1 GI:3021826
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cros,P., Allibert,P., Mallet,F., Mabilat,C. and Mandrand,B.
TITLE Sandwich hybridization assays using very short capture probes noncovalently bound to a hydrophobic support
JOURNAL Patent: US 5695926-A 77 09-DEC-1997;
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1659 CAACGTGATGAGATCGCA 1677
Db ||||||| ||||||| |||||||
20 CAGCGTGATAGATCGCA 2

RESULT 1061
LOCUS I88636 20 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 18 from patent US 5719026.
ACCESSION I88636
VERSION I88636.1 GI:3408576
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fukui,T., Katsuragi,K., Kinoshita,M. and Shin,S. deceased.
TITLE Method for detecting polymorphism of human cytochrome P4501A2 gene
JOURNAL Patent: US 5719026-A 18 17-FEB-1998;
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source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3426 TGTGTGCAGGTTCCGATGT 3444
Db ||||||| ||||||| |||||||
19 TGTGTGCAGGTTCCAGCACT 1

RESULT 1062
LOCUS ARI82775 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 83 from patent US 6339066.
ACCESSION ARI82775
VERSION ARI82775.1 GI:20225982
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides which have phosphorothioate linkages of
high chiral purity and which modulate beta.I., beta.II., gamma.,
delta., epsilon., zeta. and eta. isoforms of human protein
kinase C
JOURNAL Patent: US 6339066-A 83 15-JAN-2002;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1812 CTTTGGGTCCTGCTCTGG 1830
Db ||||| ||||| ||||| |||||

RESULT 1063
AR198529/c
LOCUS AR198529 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 37 from patent US 6352858.
ACCESSION AR198529
VERSION AR198529.1 GI:20248378
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cowsert,L.M. and Freier,S.M.
TITLE Antisense modulation of BTK expression
JOURNAL Patent: US 6352858-A 37 05-MAR-2002;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3498 ACAAGATGATTTTCTGTA 3516
Db ||||| ||||| ||||| |||||

RESULT 1064
AR207423
LOCUS AR207423 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 15 from patent US 6372900.
ACCESSION AR207423
VERSION AR207423.1 GI:21506333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Metallinos,D., Rine,J. and Bowling,A.
TITLE Horse endothelin-B receptor gene and gene products
JOURNAL Patent: US 6372900-A 15 16-APR-2002;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides which have phosphorothioate linkages of
high chiral purity and which modulate beta.I., beta.II., gamma.,
delta., epsilon., zeta. and eta. isoforms of human protein
kinase C
JOURNAL Patent: US 6339066-A 83 15-JAN-2002;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3427 GTGTGCAGTTCCGATGT 3445
Db ||||| ||||| ||||| |||||
1 GTGTGCAGTTCCGATGT 19

RESULT 1065
AR208741/c
LOCUS AR208741 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 40 from patent US 6383808.
ACCESSION AR208741
VERSION AR208741.1 GI:21509975
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 40 07-MAY-2002;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 491 AGACGTACAGCTGGACGT 509
Db ||||| ||||| ||||| |||||
20 AGACGCACATGCTGGATGT 2

RESULT 1066
AR211282
LOCUS AR211282 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 195 from patent US 6399297.
ACCESSION AR211282
VERSION AR211282.1 GI:21514563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
TITLE Antisense modulation of expression of tumor necrosis factor
receptor-associated factors (TRAFs)
JOURNAL Patent: US 6399297-A 195 04-JUN-2002;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1998 CAAGCAGCTGTTGGAGGAC 2016
Db ||||| ||||| ||||| |||||
2 CAAGCGCTGTGTAGAGGAC 20

RESULT 1067
AR217715/c
LOCUS AR217715 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 55 from patent US 6416984.
ACCESSION AR217715
VERSION AR217715.1 GI:23317586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
TITLE Antisense modulation of expression of tumor necrosis factor
receptor-associated factors (TRAFs)
JOURNAL Patent: US 6399297-A 195 04-JUN-2002;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

REFERENCE 1 (bases 1 to 20)
AUTHORS Haseltine,W.A., Ruben,S.M., Wei,Y.-F., Adams,M.D.,
Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and
Rosen,C.A.
TITLE Human DNA mismatch repair proteins
JOURNAL Patent: US 6416984-A 55 09-JUL-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1777 GACCGAGTCTACACTCACC 1795
Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1068
LOCUS AR217726/c 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 66 from patent US 6416984.
ACCESSION AR217726
VERSION AR217726.1 GI:23317597
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Haseltine,W.A., Ruben,S.M., Wei,Y.-F., Adams,M.D.,
Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and
Rosen,C.A.
TITLE Human DNA mismatch repair proteins
JOURNAL Patent: US 6416984-A 66 09-JUL-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1777 GACCGAGTCTACACTCACC 1795
Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1069
LOCUS AR217729/c 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 69 from patent US 6416984.
ACCESSION AR217729
VERSION AR217729.1 GI:23317600
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Haseltine,W.A., Ruben,S.M., Wei,Y.-F., Adams,M.D.,
Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and
Rosen,C.A.
TITLE Human DNA mismatch repair proteins
JOURNAL Patent: US 6416984-A 69 09-JUL-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1777 GACCGAGTCTACACTCACC 1795
Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1070
LOCUS AR221053/c 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 106 from patent US 6426188.
ACCESSION AR221053
VERSION AR221053.1 GI:23327938
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt,J.
TITLE Antisense modulation of phosphorylase kinase alpha 1 expression
JOURNAL Patent: US 6426188-A 106 30-JUL-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 858 GGAGCTGCTGGAGGCTGAC 876
Db 19 GCAGCCGGTGGAGGATGAC 1

RESULT 1071
LOCUS AR223313/c 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from patent US 6436393.
ACCESSION AR223313
VERSION AR223313.1 GI:23331464
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bilbao,G., Curjel,D.T. and Contreras,J.L.
TITLE Adenoviral vector encoding anti-apoptotic Bcl-2 gene and uses
JOURNAL Patent: US 6436393-A 1 20-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1013 AGATCTCCCGCTTCCGCT 1031
Db 19 ACATCTCCCGCATCCCACT 1

RESULT 1072
LOCUS AR223403/c 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 10 from patent US 6436400.
ACCESSION AR223403
VERSION AR223403.1 GI:23331588
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

```
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Xu, W.-f., Presnell, S.R., Yee, D.P. and Foster, D.C.
TITLE Protease-activated receptor PAR4 ZCHEMR2
JOURNAL Patent: US 6436400-A 10 20-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2415 CCCGCTGCTGTGCAACGG 2433
Db 20 CCATGCTGCTGTGCTACGG 2

RESULT 1073
LOCUS AR224513/c
DEFINITION Sequence 58 from patent US 6440737.
ACCESSION AR224513
VERSION AR224513.1 GI:23333353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Freier, S.M.
TITLE Antisense modulation of cellular apoptosis susceptibility gene
expression
JOURNAL Patent: US 6440737-A 58 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2235 AGCCACCTGCTGTGGT 2253
Db 19 AGCTAACCTGCTGTGT 1

RESULT 1074
LOCUS AR225072
DEFINITION Sequence 38 from patent US 6441156.
ACCESSION AR225072
VERSION AR225072.1 GI:23334207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lerman, M.I., Latif, F., Wei, M.-H., Duh, F.-M., Minna, J.D., Sekido, Y. and Gao, B.
TITLE Calcium channel compositions and methods of use thereof
JOURNAL Patent: US 6441156-A 38 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3706 TGGTGCCAGAGGTGTAC 3724
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Db 2 TGGTGCCACAGCTCAC 20

RESULT 1075
LOCUS AR231256/c
DEFINITION Sequence 30 from patent US 6451763.
ACCESSION AR231256
VERSION AR231256.1 GI:27272168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tombran-Tink, J., Chader, G.J., Becerra, S.P., Rodriguez, I.R., Steele, P.R. and Johnson, L.V.
TITLE Retinal pigmented epithelium derived neurotrophic factor and methods of use
JOURNAL Patent: US 6451763-A 30 17-SEP-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2585 GTGCGCTCGGCCCTCCCA 2603
Db 20 GTTCGCTCGTCGCTCCCA 2

RESULT 1076
LOCUS AR242698/c
DEFINITION Sequence 10 from patent US 6473765.
ACCESSION AR242698
VERSION AR242698.1 GI:27289188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fink, R.
TITLE Matching/merging two data warehouse physical data models
JOURNAL Patent: US 6473765-A 10 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2415 CCCGCTGCTGTGCAACGG 2433
Db 20 CCATGCTGCTGTGCTACGG 2

RESULT 1077
LOCUS AR243570/c
DEFINITION Sequence 20 from patent US 6475797.
ACCESSION AR243570
VERSION AR243570.1 GI:27290935
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
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AUTHORS Wyatt, J.
 TITLE Antisense modulation of SR-CYP expression
 JOURNAL Patent: US 6475797-A 20 05-NOV-2002;
 FEATURES Location/Qualifiers
 source 1. .20

Query Match	0.4%;	Score 14.2;	DB 1;	Length 20;
Best Local Similarity	84.2%;	Pred. No. 1.1e+03;		
Matches 16; Conservative	0;	Mismatches 3;	Indels	

QY 3242 GGAGGTGATTCAGTGAAG 3260
|||
pb 20 GGTGGTGACTTCAGTGAAG 2

RESULT 1078	AR255972	20 bp	DNA	linear	PAT 20-DEC-2002
AR255972/c	LOCUS	Sequence 31	from patent US 6482644.		
		DEFINITION			

ACCESSION	AR255972	
VERSION	AR255972.1	GI:27305231
KEYWORDS	.	
SOURCE	Unknown.	

ORGANISM: Unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS Cowsett, L.M.
TITLE Antisense modulation of dual specific phosphatase 8 expression
JOURNAL Patent: US 6482644-A 31 19-NOV-2002;
FEATURES Location/Qualifiers
1..20
source

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Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 258 GAAGCTGCTGCCGTGCCG 276
pb 19 GAAGCTGCTGCCGTGCCG 1

RESULT 1079	AR268291	20 bp	DNA	linear	PAT 10-APR-2003
AR268291/c	Sequence 83	from patent	US 6498035.		
LOCUS	DEFINITION				

ACCESSION	AR268291	
VERSION	AR268291.1	GI:29698566
KEYWORDS	.	
SOURCE	Unknown	

REFERENCE 1 (bases 1 to 20)
 AUTHORS Wyatt, J.
 TITLE Antisense modulation of MEK3 expression
 JOURNAL Patent: US 6498035-A 83 24-DEC-2002;
 FEATURES Location/Qualifiers
 source 1..20
 Unclassified.

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3377 TTGCTGTGTGTCCCAGGCA 3395
| | | | | | | | | |
nb 19 TTGCTGTCTCTCCCAGGCA 1

RESULT 1080	20 bp	DNA	linear	PAT 10-APR-2003
AR272010/c	AR272010	Sequence 80 from patent US 6503756.		
LOCUS	DEFINITION	AR272010		
ACCESSION	AR272010.1	GI:29703578		
VERSION	KEYWORDS			

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 20)
TITLE	Freier S.M. and Wyatt, J.
JOURNAL	Antisense modulation of syntaxin 4 interacting protein expression
	Patent: US 6503756-A 80 07-JAN-2003;

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FEATURES
source
1. .20
/organism="unknown"
/mol type="genomic DNA"
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Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 3026 GTATATTGTAAAGCTATT 3044
|||||
Db 19 GTATTTTGTAAACTTT 1

RESULT 1081					
AR279110	AR279110	Sequence 243 from patent US 6514694.	20 bp	DNA	
LOCUS	AR279110				linear
DEFINITION	AR279110				
ACCESSION	AR279110				
VERSION	AR279110.1	GI:29713753			
					PAT 10-APR-2003

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Milhausen, M.J.
TITLE Methods for the detection of encysted parasites
JOURNAL Patent: US 6514694-A 243 04-FEB-2003;
FEATURES Location/Qualifiers
1..20
/organism="genomic" /mol_type="genomic" DNA"

Query Match	0.4%;	Score 14.2;	DB 1;	Length 20;
Best Local Similarity	84.2%;	Pred. No. 1.1e+03;		
Matches 16;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0

QY 2850 TATGGAAGAGGAAAAGGCT 2868
| | | | | | | | | |
nb 1 TGTGGCAGAGGCAAAAGGCT 19

RESULT 1082			
AR299882	AR299882	20 bp	DNA
LOCUS	LOCUS	11617	from patent US 6537751.
			linear
			PAT 12-JUN-2003

AR299882
 AR299882.1 GI:31687166
 .
 Unknown.
 SOURCE
 ORGANISM
 Unclassified.
 Unclassified.
 1 (bases 1 to 20)
 Cohen,D., Chumakov,I. and Blumenfeld,M.
 Biallelic markers for use in constructing a high density
 disequilibrium map of the human genome
 Patent: US 6537751-A 11617 25-MAR-2003;
 Location/Qualifiers
 1..20
 source


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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2847 ATATATGGAAGAGAAAG 2865
| | | | | | | | | | | | | | | |
Db 2 AGATATGGAAGAGGAGAG 20

RESULT 1083
AR3100855/c
LOCUS AR3100855 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 83 from patent US 6537973.
ACCESSION AR3100855
VERSION AR3100855.1 GI:31688422
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.F., Dean,N.M., Holmlund,J.T. and Dorr,F.A.
TITLE Oligonucleotide inhibition of protein kinase C
JOURNAL Patent: US 6537973-A 83 25-MAR-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1812 CTTGGGTCCTGCTCTGG 1830
| | | | | | | | | | | | | | | |
Db 19 CTTGGGTCCTGCTCTGG 1

RESULT 1084
AR311304/c
LOCUS AR311304 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1841 from patent US 6559294.
ACCESSION AR311304
VERSION AR311304.1 GI:31704730
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 1841 06-MAY-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1208 TTGGGAGGCTCTCGG 1226
| | | | | | | | | | | | | | | |
Db 19 TTGAAGAGGCTCTCGG 1

RESULT 1085
AR312921
LOCUS AR312921 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3458 from patent US 6559294.

/organism="unknown"
/mol_type="genomic DNA"

ACCESSION AR312921 GI:31706347
VERSION AR312921.1
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 3458 06-MAY-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 50 AGCGGTCGAGTGCTGAA 68
| | | | | | | | | | | | | | | |
Db 1 AGCTGCTGGAGGTGTGAA 19

RESULT 1086
AR314131/c
LOCUS AR314131 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4668 from patent US 6559294.
ACCESSION AR314131
VERSION AR314131.1 GI:31707557
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 4668 06-MAY-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1303 CTGAAAGACGATGCCACTG 1321
| | | | | | | | | | | | | | | |
Db 19 CTAAAAGACGATGCCCGTG 1

RESULT 1087
AR314261/c
LOCUS AR314261 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4798 from patent US 6559294.
ACCESSION AR314261
VERSION AR314261.1 GI:31707687
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 4798 06-MAY-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 931 TTCATCCTGGTGGTGGCGG 949
 Db 19 TTTCATCGTGGTGAATTCGGG 1

RESULT 1088
 AR314448/c AR314448 20 bp DNA PAT 12-JUN-2003
 LOCUS Sequence 4985 from patent US 6559294.
 DEFINITION AR314448
 ACCESSION AR314448
 VERSION AR314448.1 GI:31707874
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
 TITLE Chlamydia pneumoniae polynucleotides and uses thereof
 JOURNAL Patent: US 6559294-A 4985 06-MAY-2003;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 GCTGTGACCGAGGACAAC 1662
 Db 19 GCTGTGTACCAAGACAAC 1

RESULT 1089
 AR315253 AR315253 20 bp DNA PAT 12-JUN-2003
 LOCUS Sequence 5790 from patent US 6559294.
 DEFINITION AR315253
 ACCESSION AR315253
 VERSION AR315253.1 GI:31708679
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
 TITLE Chlamydia pneumoniae polynucleotides and uses thereof
 JOURNAL Patent: US 6559294-A 5790 06-MAY-2003;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1708 CTCGACTACTACAGACA 1726
 Db 2 CTCGTCACTACAGACA 20

RESULT 1090
 AR316159 AR316159 20 bp DNA PAT 12-JUN-2003
 LOCUS Sequence 6696 from patent US 6559294.
 DEFINITION AR316159
 ACCESSION AR316159

VERSION AR316159.1 GI:31709585
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
 TITLE Chlamydia pneumoniae polynucleotides and uses thereof
 JOURNAL Patent: US 6559294-A 6696 06-MAY-2003;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2613 CTGAGCCTGCAGGAGCC 2631
 Db 2 CTGACCTTGCAGGAGATCC 20

RESULT 1091
 AR342815/c AR342815 20 bp DNA PAT 17-AUG-2003
 LOCUS Sequence 4 from patent US 6576468.
 DEFINITION AR342815
 ACCESSION AR342815
 VERSION AR342815.1 GI:33738019
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Nicolaides, N.C., Grasso, L. and Sass, P.M.
 TITLE Methods for obtaining microbe-resistant mammalian cells from hypermutable mammalian cells
 JOURNAL Patent: US 6576468-A 4 10-JUN-2003;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACCTCACC 1795
 Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1092
 AR361086/c AR361086 20 bp DNA PAT 17-AUG-2003
 LOCUS Sequence 3 from patent US 6599695.
 DEFINITION AR361086
 ACCESSION AR361086
 VERSION AR361086.1 GI:33768789
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Gage, F.H. and Ray, J.
 TITLE Method for assaying for early gene expression in neuroblasts
 JOURNAL Patent: US 6599695-A 3 29-JUL-2003;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;


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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACACTCACC 1795
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Db 20 GACAGAGTCTTCACTACCC 2

RESULT 1098
AR382950/c AR382950 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 190 from patent US 6610539.
ACCESSION AR382950
VERSION AR382950.1 GI:40091763
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wright, J.A., Young, A.H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences as inhibitors of microorganisms
JOURNAL Patent: US 6610539-A 190 26-AUG-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2004 GCTGGTGGAGGACCTGGAC 2022
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Db 19 GCTGGTGGAGGACGAGTGGAC 1

RESULT 1099
AR408461/c AR408461 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 66 from patent US 6632607.
ACCESSION AR408461
VERSION AR408461.1 GI:40158627
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS De Beenhouwer, H., Portaeels, F., Machtelinckx, L., Jannes, G. and
Rossau, R.
TITLE Mycobacterium antibiotic resistance detection
JOURNAL Patent: US 6632607-A 66 14-OCT-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 355 GAGTTCGCGCGGAGCACC 373
|||||
Db 20 GAGTTCGCGGAGCAGTGCACC 2

RESULT 1100
AR437052/c AR437052 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 104 from patent US 6656732.
ACCESSION AR437052
VERSION AR437052.1 GI:40200137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of src-c expression
JOURNAL Patent: US 6656732-A 104 02-DEC-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1533 GGAGCAGCTCACCTTCAAG 1551
|||||
Db 20 GGAGCGGCCACCTTCGAG 2

RESULT 1101
AR437053 AR437053 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 105 from patent US 6656732.
ACCESSION AR437053
VERSION AR437053.1 GI:40200137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of src-c expression
JOURNAL Patent: US 6656732-A 105 02-DEC-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 736 CTAGAGGTTCTCTCCTTGC 754
|||||
Db 1 CTAGAGGTTCTCTCCCGGC 19

RESULT 1102
AR437098/c AR437098 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 150 from patent US 6656732.
ACCESSION AR437098
VERSION AR437098.1 GI:40200182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of src-c expression
JOURNAL Patent: US 6656732-A 150 02-DEC-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1100 AR437052 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 104 from patent US 6656732.
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1214 AGGCTGCTTCGGCCAGGT 1232
|||||
Db 19 AGGTTGCTTCGGAGAGT 1

RESULT 1103
AR451291/c
LOCUS AR451291 20 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9 from patent US 6673913.
ACCESSION AR451291
VERSION AR451291.1 GI:42682269
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Sakaguchi, N. and Kuwahara, K.
TITLE GAMP proteins
JOURNAL Patent: US 6673913-A 9 06-JAN-2004;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 246 GCGATGGACAGAAGCTG 264
|||
Db 20 GCTTTGGACAGAAGCTG 2

RESULT 1104
AR488805
LOCUS AR488805 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 6 from patent US 6709817.
ACCESSION AR488805
VERSION AR488805.1 GI:47255003
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Zoghbi, H.Y., Van den Veyver, I.B., Amir, R. and Francke, U.
TITLE Method of screening Rett syndrome by detecting a mutation in MECP2
JOURNAL Patent: US 6709817-A 6 23-MAR-2004;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2154 GCTGCCCGCCGCCACCC 2172
|||
Db 1 GTTCCCGCCGCCACCC 19

RESULT 1105
AR492019/c
LOCUS AR492019 20 bp mRNA linear PAT 15-MAY-2004
DEFINITION Sequence 233 from patent US 6716600.
ACCESSION AR492019
VERSION AR492019.1 GI:47260384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Johnson, E.M., Milbrandt, J.D., Kotzbauer, P.T., Lampe, P.A., Klein, R. and DeSautage, F.
TITLE Persephin and related growth factors
JOURNAL Patent: US 6716600-A 233 06-APR-2004;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="mRNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3660 CTGCAGGCCATGGCTCAG 3678
|||||
Db 19 CTGCAGGCCAGGCCGAG 1

RESULT 1106
AR492377
LOCUS AR492377 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 76 from patent US 6716627.
ACCESSION AR492377
VERSION AR492377.1 GI:47260951
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dobie, K.W.
TITLE Antisense modulation of mucin 1, transmembrane expression
JOURNAL Patent: US 6716627-A 76 06-APR-2004;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2380 CATCTTGCTTCAGGTGCA 2398
|||||
Db 1 CATTTTGCTCTGGGTGCA 19

RESULT 1107
AR492685/c
LOCUS AR492685 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 55 from patent US 6716975.
ACCESSION AR492685
VERSION AR492685.1 GI:47262199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt, J.
TITLE Antisense modulation of EDG1 expression
JOURNAL Patent: US 6716975-A 55 06-APR-2004;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 933 CATCTTGCTGGCGGCT 951
|||
Db 19 CAGCCTGGTGTGCGGT 1

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RESULT 1108
AX080337
LOCUS AX080337 20 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 7 from Patent WO0107647.
ACCESSION AX080337
VERSION AX080337.1 GI:13159795
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Berlin, K.
TITLE Method for relative quantization of methylation of cytosin-type
bases in dna samples
JOURNAL Patent: WO 0107647-A 7 01-FEB-2001;
Epigenomics AG (DE)
FEATURES
source
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2447 GCTGCACGACGAGGGGCC 2465
DB 2 GCTGCACGACGAGGGGCC 20

RESULT 1109
AX080338/c
LOCUS AX080338 20 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 8 from Patent WO0107647.
ACCESSION AX080338
VERSION AX080338.1 GI:13159796
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Berlin, K.
TITLE Method for relative quantization of methylation of cytosin-type
bases in dna samples
JOURNAL Patent: WO 0107647-A 8 01-FEB-2001;
Epigenomics AG (DE)
FEATURES
source
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2447 GCTGCACGACGAGGGGCC 2465
DB 19 GCTGCACGACGAGGGGCC 1

RESULT 1110
AX148837/c
LOCUS AX148837 20 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 39 from Patent WO0136625.
ACCESSION AX148837
VERSION AX148837.1 GI:14347361
KEYWORDS

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Wright, J.A., Young, A.H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences derived from groel and groes as
inhibitors of microorganisms
JOURNAL Patent: WO 0136625-A 39 25-MAY-2001;
Genesense Technologies Inc. (CA)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1298 AGATGCTGAAGACGATGC 1316
DB 19 AGATGCTGAAGACGATGC 1

RESULT 1111
AX149220
LOCUS AX149220 20 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 422 from Patent WO0136625.
ACCESSION AX149220
VERSION AX149220.1 GI:14347744
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Wright, J.A., Young, A.H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences derived from groel and groes as
inhibitors of microorganisms
JOURNAL Patent: WO 0136625-A 422 25-MAY-2001;
Genesense Technologies Inc. (CA)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3120 ATTTTAACTTATGACAA 3138
DB 2 ATTTTCACTTTTGAGAA 20

RESULT 1112
AX167126
LOCUS AX167126 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 13 from Patent WO0144455.
ACCESSION AX167126
VERSION AX167126.1 GI:14596614
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Berri, R.
TITLE Antisense oligonucleotides
JOURNAL Patent: WO 0144455-A 13 21-JUN-2001;
Astrazeneca AB (SE)

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    Location/Qualifiers
      1..20
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        /note="Antisense oligonucleotide"

  Query Match
    Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 3652 TTGCTTGCTCGAGGCCA 3670
  Db 1 TTTCGCCAGCAGGCCA 19

RESULT 1113
AX224922
LOCUS AX224922 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 76 from Patent WO0161030.
ACCESSION AX224922
VERSION AX224922.1 GI:15554995
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gray,D.M. and Bollon,A.P.
TITLE Libraries of optimum subsequence regions of mrna and genomic dna
JOURNAL Patent: WO 0161030-A 76 23-AUG-2001; University of Texas at
Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

  Query Match
    Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 529 CGGCCCATCTCGAGCGG 547
  Db 1 CGGCCGAGCTGACGCGG 19

RESULT 1114
AX224927
LOCUS AX224927 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 81 from Patent WO0161030.
ACCESSION AX224927
VERSION AX224927.1 GI:15555000
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gray,D.M. and Bollon,A.P.
TITLE Libraries of optimum subsequence regions of mrna and genomic dna
JOURNAL Patent: WO 0161030-A 81 23-AUG-2001; University of Texas at
Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"

  Query Match
    Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 529 CGGCCCATCTCGAGCGG 547
  Db 1 CGGCCGAGCTGACGCGG 19

RESULT 1115
AX295702/c
LOCUS AX295702 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 7464 from Patent WO0179548.
ACCESSION AX295702
VERSION AX295702.1 GI:17057391
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
Patent: WO 0179548-A 7464 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Hypothetical Probe Sequence"

  Query Match
    Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 1053 GTCCAAACGGCTCCATGAGC 1071
  Db 20 GTCCAAACGGCTGATCCGC 2

RESULT 1116
AX296663
LOCUS AX296663 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 8425 from Patent WO0179548.
ACCESSION AX296663
VERSION AX296663.1 GI:17058352
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
Patent: WO 0179548-A 8425 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Hypothetical Probe Sequence"

  Query Match
    Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 2327 GTGTGTGCGTGTGTGTG 2345
  Db 1 GTGCGTGCAGTCTGTGTG 19
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RESULT 1117
AX296746
LOCUS AX296746 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 8508 from Patent WO0179548.
ACCESSION AX296746
VERSION AX296746.1 GI:17058435
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Barany,P., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 8508 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2958 GTCTCACCACGCAAGCAG 2976
Db 1 GTCTCAGCAGCAAGCAG 19

RESULT 1118
AX298596/c
LOCUS AX298596 20 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 230 from Patent WO0183749.
ACCESSION AX298596
VERSION AX298596.1 GI:17128586
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
TITLE Gene and sequence variation associated with sensing carbohydrate
compounds and other sweeteners
JOURNAL Patent: WO 0183749-A 230 08-NOV-2001;
WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
(US)
FEATURES
source
1..20
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 279 CGCCACACCTGTCGCTTC 297
Db 19 CTCCACACTGTCCTTC 1

RESULT 1119
AX298894
LOCUS AX298894 20 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 528 from Patent WO0183749.
ACCESSION AX298894

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VERSION AX298894.1 GI:17128884
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
TITLE Gene and sequence variation associated with sensing carbohydrate
compounds and other sweeteners
JOURNAL Patent: WO 0183749-A 528 08-NOV-2001;
WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
(US)
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QY 824 ACTCTGCGTGGCTGGTGT 842
Db 2 ACTGTACGTGGCTGGTGT 20

RESULT 1120
AX317742/c
LOCUS AX317742 20 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 3 from Patent WO0190313.
ACCESSION AX317742
VERSION AX317742.1 GI:17900627
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Feinberg,A.T., Strichman-Almashanu,L.T. and Jiang,S.C.
TITLE Methods for assaying gene imprinting and methylated cpg islands
JOURNAL Patent: WO 0190313-A 3 29-NOV-2001;
The Johns Hopkins University (US)
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
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QY 1346 CTGAGATGGAGATGATGAA 1364
Db 20 CTGAGATGGGATGAACAA 2

RESULT 1121
AX342778
LOCUS AX342778 20 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 45 from Patent WO0198474.
ACCESSION AX342778
VERSION AX342778.1 GI:18152134
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Delcours,J., Debyser,W., Gebruers,K., Goesaert,H., Fierens,K.,
Robben,J. and van Campenhout,S.

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Query Match	0.4%;	Score 14.2;	DB 1;	Length 20;	
Best Local Similarity	84.2%;	Pred. No. 1.1e+03;			
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QY	622	CCCACACATCCAGTGGCTCA	640		
DB	2	CCCACATACAGAGGCTAA	20		

RESULT 1124					
AX487048					
LOCUS	AX487048	20 bp	DNA	linear	PAT 16-AUG-2002
DEFINITION	Sequence 4348 from Patent WO02053728.				
ACCESSION	AX487048				
VERSION	AX487048.1	GI:22321196			
KEYWORDS					
SOURCE	Candida albicans				
ORGANISM	Candida albicans				

REFERENCE	1				
AUTHORS	Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.				
TITLE	Gene disruption methodologies for drug target discovery				
JOURNAL	Patent: WO 02053728-A 4348 11-JUL-2002;				
	Elitra Pharmaceuticals, Inc. (US)				

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QY	1638	CAATGTGCTGTCACCGAG	1656		
DB	1	CAATGAGCTCGTGACCGTG	19		

RESULT 1125					
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LOCUS	AX488257	20 bp	DNA	linear	PAT 16-AUG-2002
DEFINITION	Sequence 5557 from Patent WO02053728.				
ACCESSION	AX488257				
VERSION	AX488257.1	GI:22322337			
KEYWORDS					
SOURCE	Candida albicans				
ORGANISM	Candida albicans				

REFERENCE	1				
AUTHORS	Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.				
TITLE	Gene disruption methodologies for drug target discovery				
JOURNAL	Patent: WO 02053728-A 5557 11-JUL-2002;				
	Elitra Pharmaceuticals, Inc. (US)				

FEATURES	Location/Qualifiers				
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QY	829	GCCTGGCTGGTGGCTGC	847		
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RESULT 1126					
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AX589229
LOCUS AX589229 20 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 16 from Patent WO02084567.
ACCESSION AX589229
VERSION AX589229.1 GI:27900830
SOURCE Rattus rattus (black rat)
ORGANISM Rattus rattus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Soullou, J.P., Delsuc, M.A., Guillet, M., Sebille, F., Brouard, S.,
Gagne, K., Vanhove, B. and Pallier, A.
TITLE Method for analyzing T lymphocytes with the aid of T lymphocyte
receptors of an organism
JOURNAL Patent: WO 02084567-A 16 24-OCT-2002;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(FR)
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 326. CCTCCATCTCTCTGGCTGAA 344
Db 2 CATCCATCTCCAGCTGAA 20
RESULT 1127
AX658511/c
LOCUS AX658511 20 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 427 from Patent WO03000928.
ACCESSION AX658511
VERSION AX658511.1 GI:29160868
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Poulsen, H.S., Pedersen, N., Mortensen, S., Sorensen, S.B.,
Petersen, M.W. and Elisner, H.I.
TITLE Methods for identification of cancer cell surface molecules and
cancer specific promoters, and therapeutic uses thereof
JOURNAL Patent: WO 03000928-A 427 03-JAN-2003;
Odin Medical A/S (DK)
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 20 GGCATCAGCAGTGGAGCT 2
RESULT 1128
AX665329
LOCUS AX665329 20 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 87 from Patent WO03002765.
ACCESSION AX665329
VERSION AX665329.1 GI:29290452

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sellar, G.C. and Gabra, H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 87 09-JAN-2003;
Cancer Research Technology Limited (GB)
FEATURES
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QY 2101 GACACCCCGAGCTCCAGCT 2119
Db 2 GGCACCCCGAGCTCCAGCT 20
RESULT 1129
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LOCUS AX719302 20 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 17 from Patent WO03022298.
ACCESSION AX719302
VERSION AX719302.1 GI:29891742
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Giraudon, P., Belin, M.F., Malcus, C., Colas, P., Antoine, J.C. and
Honorat, J.
TITLE Utilisation d'une proteine de la famille des crmps pour le
traitement des maladies liees au systeme immunitaire
JOURNAL Patent: WO 03022298-A 17 20-MAR-2003;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(FR)
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/note="oligonucleotide"
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Best Local Similarity 84.2%; Pred. No. 1.1e+03;
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QY 1989 GCCACCTTCAAGCAGCTG 2007
Db 20 GTCCACCTTCCAGCAGATG 2
RESULT 1130
AX743793/c
LOCUS AX743793 20 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 10 from Patent WO03031985.
ACCESSION AX743793
VERSION AX743793.1 GI:30722545
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Akerblad, P. and Sigvardsson, M.
TITLE Method for identification of modulators of pre-adipocyte
differentiation

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JOURNAL Patent: WO 03031985-A 10 17-APR-2003;
FEATURES Astrazeneca AB (SE)
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
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QY 2041 TCCACGACGAGTACTGG 2059
Db 20 TTCAACGACGAGTCTCTGG 2

RESULT 1131
AX776233/c
LOCUS AX776233 20 bp DNA linear PAT 14-JUL-2003
DEFINITION Sequence 3 from Patent WO03048362.
ACCESSION AX776233
VERSION AX776233.1 GI:32693889
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Farrar,G.J., Humphries,P., Willington-Ward,S. and Kenna,P.F.
TITLE Suppression of polymorphic alleles
JOURNAL Patent: WO 03048362-A 3 12-JUN-2003;
College of the Holy and Undivided Trinity of Queen Elizabeth (IE)
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/db_xref="taxon:32630"
/note="3' human rhodopsin primer over BstEII site"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1897 AAGGAGGCCACCGCATGG 1915
Db 20 AAGGAGGTACCCGCATGG 2

RESULT 1132
AX804534/c
LOCUS AX804534 20 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 702 from Patent WO03060160.
ACCESSION AX804534
VERSION AX804534.1 GI:38521675
KEYWORDS Oreochromis niloticus (Nile tilapia)
SOURCE Oreochromis niloticus
ORGANISM Oreochromis niloticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
Labroidae; Cichlidae; Oreochromis.
REFERENCE 1
AUTHORS Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
TITLE Verification of food origin based on nucleic acid pattern
JOURNAL Patent: WO 03060160-A 702 24-JUL-2003;
Genomar ASA (NO)
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JOURNAL Patent: WO 03031985-A 10 17-APR-2003;
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QY 2676 TCCCGACCTCCAGGCTTTC 2694
Db 20 TCCACACCTCCTGCTCTTC 2

RESULT 1133
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LOCUS AX923443 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 20 from Patent WO03080816.
ACCESSION AX923443
VERSION AX923443.1 GI:40216492
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Andrews,P. and Draper,J.
TITLE Stem cell culture
JOURNAL Patent: WO 03080816-A 20 02-OCT-2003;
THE UNIVERSITY OF SHEFFIELD (GB)
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QY 174 TGACGAAGACGGGAGGAC 192
Db 2 TGACCAAGACTGAGAGGAC 20

RESULT 1134
AX938959
LOCUS AX938959 20 bp DNA linear PAT 07-JAN-2004
DEFINITION Sequence 14 from Patent EP1362914.
ACCESSION AX938959
VERSION AX938959.1 GI:40733318
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Nakanishi,O. and Tatamiya,T.
TITLE Histone deacetylase inhibitor and use thereof
JOURNAL Patent: EP 1362914-A 14 19-NOV-2003;
Schering AG (DE)
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2117 GCTCCTCAGGGGACGACTC 2135
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LOCUS AX958421 20 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 4 from Patent EP1369696.
ACCESSION AX958421
VERSION AX958421.1 GI:40879377
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Golz,S., Brueggemeier,U. and Geerts,A.
TITLE Diagnostics and therapeutics for diseases associated with
somatostatin receptor 3 (sstr3)
JOURNAL Patent: EP 1369696-A 4 10-DEC-2003;
Bayer HealthCare AG (DE)
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Db 19 CTCTACTTCTCGTGGTGG 1
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LOCUS AX962209/c 20 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 4 from Patent WO03104819.
ACCESSION AX962209
VERSION AX962209.1 GI:40881495
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Golz,S., Brueggemeier,U. and Geerts,A.
TITLE Diagnostics and therapeutics for diseases associated with
somatostatin receptor 3 (sstr3)
JOURNAL Patent: WO 03104819-A 4 18-DEC-2003;
Bayer HealthCare AG (DE)
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Db 19 CTCTACTTCTCGTGGTGG 1
RESULT 1137
LOCUS BD016082/c 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide modulation of protein kinase C-epsilon.
ACCESSION BD016082
VERSION BD016082.1 GI:22557220
KEYWORDS JP 2001224386-A/91.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE Oligonucleotide modulation of protein kinase C-zeta
JOURNAL Patent: JP 2001224387-A 91 21-AUG-2001;
ISIS PHARMACEUTICALS INC
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Qy 1812 CTTTGGGTCTGCTCTCG 1830
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AUTHORS Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE Oligonucleotide modulation of protein kinase C-epsilon
JOURNAL Patent: JP 2001224386-A 91 21-AUG-2001;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2001224386-A/91
PD 21-AUG-2001
PF 13-DEC-2000 JP 2000379218
PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
FRANK C BENNETT,RUSSELL T BOGGS,NICHOLAS M DEAN PC
C12N15/09,A61K48/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,PC
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Db 19 CTGTGGGTCTGCTCTCG 1
RESULT 1138
LOCUS BD016201/c 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide modulation of protein kinase C-zeta.
ACCESSION BD016201
VERSION BD016201.1 GI:22557339
KEYWORDS JP 2001224387-A/91.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE Oligonucleotide modulation of protein kinase C-zeta
JOURNAL Patent: JP 2001224387-A 91 21-AUG-2001;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2001224387-A/91
PD 21-AUG-2001
PF 13-DEC-2000 JP 2000379249
PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
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RESULT	1139		
LOCUS	BD017353/c		
DEFINITION	20 bp DNA linear PAT 27-AUG-2002		
ACCESSION	Oligonucleotide modulation of protein kinase C-eta.		
VERSION	BD017353.1	GI:22558529	
KEYWORDS	JP 2001231579-A/91.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Bennett, F.C., Boggs, R.T. and Dean, N.M.		
TITLE	Oligonucleotide modulation of protein kinase C-eta		
JOURNAL	Patent: JP 2001231579-A 91	28-AUG-2001;	
COMMENT	ISIS PHARMACEUTICALS INC		
	OS Artificial Sequence		
	PN JP 2001231579-A/91		
	PD 28-AUG-2001		
	PF 13-DEC-2000	JP 2000379234	
	PR 09-JUL-1993	US 08/089996, 22-FEB-1994	US 08/199779
	FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN	PC	
	C12N15/09, A61K31/711, A61K31/712, A61K31/712.5, A61K48/00, A61P29/00, A61P35/00,		
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	G01N33/50,		
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Best Local Similarity	84.2%;	Pred. No. 1.1e+03;	
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		Indels 0;	Gaps 0;
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DB	19	CTGTGGTCCCTGCTCTGG	1
RESULT	1140		
LOCUS	BD074637		
DEFINITION	20 bp DNA linear PAT 27-AUG-2002		
ACCESSION	Antisense oligonucleotide composition and modulation method of JNK		
VERSION	BD074637.1	GI:22620240	
KEYWORDS	JP 2001514905-A/61.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	McKay, R., Dean, N., Monia, B.P., Scott, P., Nero and Gaarde, W.A.		
TITLE	Antisense oligonucleotide composition and modulation method of JNK		
JOURNAL	Patent: JP 2001514905-A 61	18-SEP-2001;	
COMMENT	ISIS PHARMACEUTICALS INC		
	OS Artificial Sequence		
	PN JP 2001514905-A/61		
	PD 18-SEP-2001		
	PF 07-AUG-1998	JP 2000509875	
	PR 13-AUG-1997	US 08/910629	
	PI ROBERT MCKAY, NICHOLAS DEAN, BRETT P MONIA, PAMELA SCOTT	PI	

BD123453/c
LOCUS BD123453 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of incubating microplate.
ACCESSION BD123453
VERSION BD123453.1 GI:23218398
KEYWORDS JP 2002022749-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ando,K.
TITLE Method of incubating microplate.
JOURNAL Patent: JP 2002022749-A 3 23-JAN-2002;
FUJIREBIO INC
COMMENT OS Artificial Sequence
PN JP 2002022749-A/3
PD 23-JAN-2002
PF 07-JUL-2000 JP 2000206033
PI KEN ANDO
PC GOIN35/00,GOIN1/28,GOIN33/543//C12M1/00,C12N15/09,GOIN1/28, PC
C12N15/00
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/organism='synthetic construct'
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Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 20 CACCACCTTCTCCATCTCC 2
RESULT 1143
BD140699
LOCUS BD140699 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods for the simultaneous identification of novel biological
targets and lead structures for drug development.
ACCESSION BD140699
VERSION BD140699.1 GI:23235644
KEYWORDS JP 20020508507-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Heffner,D.L., Zepp,C.M., Gao,Y. and Jones,S.W.
TITLE Methods for the simultaneous identification of novel biological
targets and lead structures for drug development
JOURNAL Patent: JP 20020508507-A 1 19-MAR-2002;
SEPRACOR INC
COMMENT OS Artificial Sequence
PN JP 20020508507-A/1
PD 19-MAR-2002
PF 18-DEC-1998 JP 2000539165
PI 18-DEC-1997 US 60/068035
PI DONALD L HEEFNER, CHARLES M ZEPP, YUN GAO, STEVEN W JONES PC
GOIN33/542,C12Q1/04,C12Q1/68,C12Q1/70,GOIN21/00,GOIN21/76, PC
GOIN33/53
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3463 TATATATATCTATATATAT 3481
Db 2 TATATGATTCATATATAT 20
RESULT 1144
BD167962
LOCUS BD167962 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of constructing mutation DNA library and utilization
thereof.
ACCESSION BD167962
VERSION BD167962.1 GI:27873774
KEYWORDS WO 0226964-A/9.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tsuji,T. and Yanagawa,H.
TITLE Method of constructing mutation DNA library and utilization thereof
JOURNAL Patent: WO 0226964-A 9 04-APR-2002;
MITSUBISHI CHEMICAL CORP,TORU TSUJI,HIROSHI YANAGAWA
COMMENT OS Artificial Sequence
PN WO 0226964-A/9
PD 04-APR-2002
PF 26-SEP-2001 WO 2001JP008387
PR 27-SEP-2000 JP 00P 293692,06-FEB-2001 JP 01P 029138 PI
TORU TSUJI,HIROSHI YANAGAWA
PC C12N15/09,C12P21/02
CC Description of Artificial Sequence:Synthesized FH Key
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FT Location/Qualifiers
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/organism='synthetic construct'
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1679 ACTTCGGGCTGCGCCGGGA 1697
Db 2 ACTTCGGGATCGCCAGGA 20
RESULT 1145
BD271421/c
LOCUS BD271421 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Fab fragment libraries and method of using the same.
ACCESSION BD271421
VERSION BD271421.1 GI:33081189
KEYWORDS JP 2002543830-A/13.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hoogenboom,H.R.J.M.
TITLE Novel Fab fragment libraries and method of using the same
JOURNAL Patent: JP 2002543830-A 13 24-DEC-2002;
DVAX CORP
COMMENT OS Artificial Sequence
PN JP 2002543830-A/13
PD 24-DEC-2002
PF 18-MAY-2000 JP 2000618429

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PR 18-MAY-1999 EP 99201558.6
PI HENDRICUS RENERUS JACOBUS MATTHEUS HOOGENBOOM PC
C12N15/09,C07K16/34,G01N33/53,C12N15/00
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Db 23 CCRGWCTCCACGCTGCACCTC 1
RESULT 1146
LOCUS AR409907 23 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 20 from patent US 6635422.
ACCESSION AR409907
VERSION AR409907.1 GI:40161042
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 23)
AUTHORS Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
TITLE Methods for isolating and characterizing endogenous mRNA-protein
(mRNP) complexes
JOURNAL Patent: US 6635422-A 20 21-OCT-2003;
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Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 23;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3115 TTTTAAATTTTAACTTATT 3133
Db 2 TTTTAAATTTTAAATTTT 20
RESULT 1147
AR264929
LOCUS AR264929 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 13 from patent US 6492121.
ACCESSION AR264929
VERSION AR264929.1 GI:29693316
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 13 10-DEC-2002;
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PR 18-MAY-1999 EP 99201558.6
PI HENDRICUS RENERUS JACOBUS MATTHEUS HOOGENBOOM PC
C12N15/09,C07K16/34,G01N33/53,C12N15/00
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Query Match
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  Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3285
Db 3 ATATATTTTATTTTTCCTTTTCTTTT 29
RESULT 1148
AR478210
LOCUS AR478210 30 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 13 from patent US 6699661.
ACCESSION AR478210
VERSION AR478210.1 GI:47236858
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 13 02-MAR-2004;
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Query Match
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  Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3285
Db 3 ATATATTTTATTTTTCCTTTTCTTTT 29
RESULT 1149
BD072869
LOCUS BD072869 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072869
VERSION BD072869.1 GI:22618472
KEYWORDS JP 2001286300-A/7.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 7 16-OCT-2001;
JOURNAL JAPAN BIO INDUSTRY ASSOCIATION KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/7
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
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labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC CC
CC acid.
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Query Match 0.4%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTGCTTGTGCTTTT 3285
Db 3 ATATATTTTATTTTGTGCTTTT 29

RESULT 1151
BD072874 30 bp DNA linear PAT 27-AUG-2002
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION
ACCESSION BD072874
VERSION BD072874.1 GI:22618477
KEYWORDS JP 2001286300-A/12.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 5 08-JAN-2002; JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/5
PD 08-JAN-2002
PF 27-JUN-2000 JP 200193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PC KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12N15/34,C12Q1/68,C12N15/00 CC The base sequence was prepared synthetically on the aim of CC examining the decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target
CC CC
CC acid.
CC Key
FT source
FT Location/Qualifiers
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Query Match 0.4%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTGCTTGTGCTTTT 3285
Db 3 ATATATTTTATTTTGTGCTTTT 29

RESULT 1152
BD072874 30 bp DNA linear PAT 18-SEP-2002
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION
ACCESSION BD072874
VERSION BD072874.1 GI:23202319
KEYWORDS JP 2002000275-A/10.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 10 08-JAN-2002; JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/10
PD 18-SEP-2002
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PC KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,PC G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target
CC CC
CC acid.
CC Key
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Query Match 0.4%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/10
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/34,C12Q1/68,C12Q1/68,C12N15/00 CC The base
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examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
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Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3285
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Db 3 ATATATTTTATTTTTCCTTTTTCCTTTT 29
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RESULT 1154
BD145033
LOCUS
DEFINITION
BD145033 30 bp DNA linear PAT 17-JAN-2003
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION
BD145033
VERSION
BD145033.1 GI:27850791
KEYWORDS
JP 2002119291-A/14.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
Patent: JP 2002119291-A 14 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002119291-A/14
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
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PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
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examining the
CC decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..30
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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Query Match 0.4%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3259 AGATATTTTATTTGCTTTGTCCTTTT 3285
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Db 3 ATATATTTTATTTTTCCTTTTTCCTTTT 29
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RESULT 1155
BD145028
LOCUS
DEFINITION
BD145028 30 bp DNA linear PAT 17-JAN-2003
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION
BD145028
VERSION
BD145028.1 GI:27850786
KEYWORDS
JP 2002119291-A/9.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
Patent: JP 2002119291-A 9 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002119291-A/9
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
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PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers

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BD166033
LOCUS
DEFINITION Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method.

ACCESSION BD166033
VERSION BD166033.1 GI:27871845
KEYWORDS JP 2002191372-A/13.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method

JOURNAL Patent: JP 2002191372-A 13 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002191372-A/13
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI TORIMURA,
SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
decrease in fluorescence emission of a nucleic acid probe CC
examining the
labeled with
probe with a target
nucleic
acid.
CC
Key
FH
FT
FEATURES
source
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Location/Qualifiers
/organism='Artificial Sequence'.
Query Match 0.4%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTCCTTGTCTTTT 3285
Db 3 ATATATTTTCTTTTCTTTT 29

RESULT 1156
BD166129
LOCUS
DEFINITION Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method.

ACCESSION BD166129
VERSION BD166129.1 GI:27871941
KEYWORDS JP 2002191372-A/109.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method

JOURNAL Patent: JP 2002191372-A 109 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002191372-A/109
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI TORIMURA,
SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
decrease in fluorescence emission of a nucleic acid probe CC
examining the
labeled with
probe with a target
nucleic
acid.
CC
and the base sequence was used as that of the probe. FH Key
Location/Qualifiers
FT source 1. 30
Location/Qualifiers
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FEATURES
source
1. 30
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Query Match 0.4%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTCCTTGTCTTTT 3285
Db 3 ATATATTTTCTTTTCTTTT 29

RESULT 1157
AX248879/c
LOCUS
DEFINITION Sequence 958 from Patent WO0166800.
ACCESSION AX248879
VERSION AX248879.1 GI:15863502
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 958 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES
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Location/Qualifiers
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/mol_type='unassigned DNA'
/db_xref='taxon:9606'
Query Match 0.4%; Score 14.2; DB 1; Length 31;
Best Local Similarity 65.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 486 CCGGACAGCTACACGCTGGACGTCTGG 514
Db 30 CCGGACAGCCCGCCGCGAGGATGGGCGG 2

RESULT 1158
AR222444/c
LOCUS
DEFINITION Sequence 38 bp from Patent WO0166800.

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DEFINITION Sequence 2 from patent US 6429300.
ACCESSION AR222444
VERSION AR222444.1 GI:23329975
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 38)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 2 06-AUG-2002;
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    /mol_type="genomic DNA"
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  Best Local Similarity 62.9%; Pred. No. 1.6e+03;
  Matches 22; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 3307 GGATTTTCTTAGGAGATTATTTTGGACTTC 3341
Db 38 GGTTTTTTTTTTTTTTTTTTTTTTTTGCATCC 4
RESULT 1159
LOCUS I31428 42 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 340 from patent US 5582979.
ACCESSION I31428
VERSION I31428.1 GI:1822219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 42)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
  method of using the same
JOURNAL Patent: US 5582979-A 340 10-DEC-1996;
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  Best Local Similarity 62.9%; Pred. No. 1.6e+03;
  Matches 22; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 598 TGAAGGTGTACAGTCACGACACACACACACATCCA 632
Db 1 TGCCCGGCTACACACACACACACACACACACACA 35
RESULT 1160
LOCUS BD185612 14 bp DNA linear PAT 17-JUN-2003
DEFINITION Analysis of double stranded nucleic acid using scanning probe
  microscope.
ACCESSION BD185612
VERSION BD185612.1 GI:31877812
KEYWORDS JP 2002360300-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE
  1 (bases 1 to 14)
AUTHORS Takeuchi,M.
TITLE Analysis of double stranded nucleic acid using scanning probe
JOURNAL OLYMPUS OPTICAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002360300-A/1
PD 17-DEC-2002
PF 06-JUN-2001 JP 2001171590
PI MINORU TAKEUCHI
PC C12Q1/68,C12N15/09,G01N33/483,G01N33/50,C12N15/00 CC
  Analysis of double stranded nucleic acid using scanning probe CC
  microscope
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  FT /mol_type="genomic DNA"
  FT /db_xref="taxon:32630"
  Query Match 0.4%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 9.1e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2328 TGTGTGCGTGTGTG 2341
Db 14 TGTGTGCGTGTGTG 1
RESULT 1161
LOCUS BD185613 14 bp DNA linear PAT 17-JUN-2003
DEFINITION Analysis of double stranded nucleic acid using scanning probe
  microscope.
ACCESSION BD185613
VERSION BD185613.1 GI:31877813
KEYWORDS JP 2002360300-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE
  1 (bases 1 to 14)
AUTHORS Takeuchi,M.
TITLE Analysis of double stranded nucleic acid using scanning probe
JOURNAL OLYMPUS OPTICAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002360300-A/2
PD 17-DEC-2002
PF 06-JUN-2001 JP 2001171590
PI MINORU TAKEUCHI
PC C12Q1/68,C12N15/09,G01N33/483,G01N33/50,C12N15/00 CC
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  FT /mol_type="genomic DNA"
  FT /db_xref="taxon:32630"
  Query Match 0.4%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 9.1e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2328 TGTGTGCGTGTGTG 2341
Db 14 TGTGTGCGTGTGTG 1
RESULT 1162
LOCUS E32202 14 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION E32202
VERSION E32202.1 GI:13021735
KEYWORDS JP 2000060559-A/4.
SOURCE Hallotis discus discus
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ORGANISM  Haliotis discus discus
           Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
REFERENCE 1 (bases 1 to 14)
AUTHORS  Hidaeki,T. and Masashi,S.
TITLE    Method for isolating satellite sequence
JOURNAL  NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT  OS Haliotis discus discus
         PN JP 2000060559-A/4
         PD 29-FEB-2000
         PF 18-AUG-1998 JP 1998232153
         PR HIDEAKI TAKAHASHI,MASASHI SEKINO
         PC C12N15/09,C12Q1/68,C12N15/00
         CC Key Location/Qualifiers
         FH 1..14
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2318 TGTGTGTGTGTGTG 2331
Db  14 TGTGTGTGTGTGTG 1

RESULT 1163
I31524/c      14 bp      DNA      linear      PAT 06-FEB-1997
LOCUS      I31524
DEFINITION Sequence 436 from patent US 5582979.
ACCESSION  I31524
VERSION    I31524.1 GI:1822315
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS  Weber,J.L.
TITLE    Length polymorphisms in (dc-da).sub.n.(dG-dT).sub.n sequences and
         method of using the same
JOURNAL  Patent: US 5582979-A 436 10-DEC-1996;
FEATURES  Location/Qualifiers
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           /mol_type="unassigned DNA"
Query Match      0.4%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2319 GTGTGTGTGTGTG 2332
Db  14 GTGTGTGTGTGTG 1

RESULT 1164
AX175251
LOCUS      AX175251
DEFINITION Sequence 15 from Patent WO0144465.
ACCESSION  AX175251
VERSION    AX175251.1 GI:14598619
KEYWORDS  .
SOURCE    synthetic construct
ORGANISM  synthetic construct

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artificial sequences.
REFERENCE 1
AUTHORS  Phillips,N.C. and Filion,M.C.
TITLE    Therapeutically useful synthetic oligonucleotides
JOURNAL  Patent: WO 0144465-A 15 21-JUN-2001;
         Bioniche Life Sciences Inc. (CA)
FEATURES  Location/Qualifiers
           1..14
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           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
Query Match      0.4%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2318 TGTGTGTGTGTGTG 2331
Db  1 TGTGTGTGTGTGTG 14

RESULT 1165
AR241795
LOCUS      AR241795
DEFINITION Sequence 83 from patent US 6472154.
ACCESSION  AR241795
VERSION    AR241795.1 GI:27287607
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS  Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE    Polymorphic repeats in human genes
JOURNAL  Patent: US 6472154-A 83 29-OCT-2002;
FEATURES  Location/Qualifiers
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Query Match      0.4%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2832 ATATATATATATAA 2845
Db  1 ATATATATATATAA 14

RESULT 1166
BD234638
LOCUS      BD234638
DEFINITION Thymidine kinase mutants and fusion proteins having thymidine
         kinase and guanylate kinase activities.
ACCESSION  BD234638
VERSION    BD234638.1 GI:33044408
KEYWORDS  JP 2002516061-A/42.
SOURCE    unidentified
ORGANISM  unidentified.
REFERENCE  1 (bases 1 to 16)
AUTHORS  Black,M.E.
TITLE    Thymidine kinase mutants and fusion proteins having thymidine
         kinase and guanylate kinase activities
JOURNAL  Patent: JP 2002516061-A 42 04-JUN-2002;
         DARWIN MOLECULAR CORP
COMMENT  OS Unidentified
         PN JP 2002516061-A/42
         PD 04-JUN-2002
         PF 14-OCT-1998 JP 2000516019
         PR 14-OCT-1997 US 60/061812
         PI MARGARET E BLACK
         PC C12N15/09,A61K31/711,A61K35/76,A61K38/45,A61K48/00,A61K49/00,

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PC A61P31/00.
PC A61P35/00,C12N5/10,C12N9/12,C12N15/00,A61K37/52,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Thymidine kinase mutants and fusion proteins having thymidine
CC kinase and
CC guanylate kinase activities
FH Key Location/Qualifiers
FT source 1..16
/organism="Unidentified".
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2677 CCCACCTCCAGGC 2690
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Db 3 CCCACCTCCAGGC 16
RESULT 1167
AR230234
LOCUS 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 52 from patent US 6451571.
ACCESSION AR230234
VERSION AR230234.1 GI:27270289
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Loeb,I.A. and Black,M.E.
TITLE Thymidine kinase mutants
JOURNAL Patent: US 6451571-A 52 17-SEP-2002;
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/mol_type="genomic DNA"
Query Match 0.4%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2677 CCCACCTCCAGGC 2690
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Db 3 CCCACCTCCAGGC 16
RESULT 1168
AR328665
LOCUS 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6067 from patent US 6566127.
ACCESSION AR328665
VERSION AR328665.1 GI:33714473
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6067 20-MAY-2003;
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Query Match 0.4%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2317 CTGTGTGTGTGTGT 2330
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Db 3 CTGTGTGTGTGTGT 16
RESULT 1169
AR057463
LOCUS 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1667 from patent US 5837542.
ACCESSION AR057463
VERSION AR057463.1 GI:5983040
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1667 17-NOV-1998;
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Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1880 AGCTCTTCAAGCTG 1893
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Db 2 AGCTCTTCAAGCTG 15
RESULT 1170
AR115221
LOCUS 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1667 from patent US 6132967.
ACCESSION AR115221
VERSION AR115221.1 GI:14095543
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1667 17-OCT-2000;
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Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1880 AGCTCTTCAAGCTG 1893
|||||
Db 2 AGCTCTTCAAGCTG 15
RESULT 1171
BD241576
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241576

FT source
I. : I.
FT /organism='Homo sapiens (human)'.
I. : I.

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Db          2 AGCTCTTCAAGCTG 15
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RESULT 1175
AX687746    17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION  Sequence 478 from Patent EPI281758.
ACCESSION  AX687746
VERSION    AX687746.1 GI:29410442
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE   1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL    Patent: EP 1281758-A 478 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES   source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2006 TGGTGGAGGACCTG 2019
Db          4 TGGTGGAGGACCTG 17
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RESULT 1176
AX687747    17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION  Sequence 479 from Patent EPI281758.
ACCESSION  AX687747
VERSION    AX687747.1 GI:29410443
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE   1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL    Patent: EP 1281758-A 479 05-FEB-2003;
            Aeomica, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2006 TGGTGGAGGACCTG 2019
Db          3 TGGTGGAGGACCTG 16
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RESULT 1177
AX687748    17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION  Sequence 480 from Patent EPI281758.
ACCESSION  AX687748
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AX687748.1 GI:29410444
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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE   1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL    Patent: EP 1281758-A 480 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES   source
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Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2006 TGGTGGAGGACCTG 2019
Db          2 TGGTGGAGGACCTG 15
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RESULT 1178
AX687749    17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION  Sequence 481 from Patent EPI281758.
ACCESSION  AX687749
VERSION    AX687749.1 GI:29410445
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE   1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL    Patent: EP 1281758-A 481 05-FEB-2003;
            Aeomica, Inc. (US)
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Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2006 TGGTGGAGGACCTG 2019
Db          1 TGGTGGAGGACCTG 14
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RESULT 1179
AX687932    17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION  Sequence 664 from Patent EPI281758.
ACCESSION  AX687932
VERSION    AX687932.1 GI:29410630
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE   1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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RESULT 1184
AX688347/c 17 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 1079 from Patent EP1281758.
ACCESSION AX688347
VERSION AX688347.1 GI:29411047
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1079 05-FEB-2003;
Aeomica, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3657 TGCCTGCAGGGCCA 3670
Db 14 TGCCTGCAGGGCCA 1
RESULT 1185
AX728804 17 bp DNA linear PAT 08-MAY-2003
LOCUS
DEFINITION Sequence 438 from Patent WO03025175.
ACCESSION AX728804
VERSION AX728804.1 GI:30508147
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 438 27-MAR-2003;
Molecular Engines Laboratories (FR)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2566 CACCACGGGACATC 2579
Db 4 CACCACGGGACATC 17
RESULT 1186
AX759001/c 17 bp DNA linear PAT 25-JUN-2003
LOCUS
DEFINITION Sequence 2322 from Patent WO03040369.
ACCESSION AX759001
VERSION AX759001.1 GI:32253617
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 2322 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3388 CCCAGGCGGAGGA 3401
Db 16 CCCAGGCGGAGGA 3
RESULT 1187
A31423/c 18 bp DNA linear PAT 08-NOV-1995
LOCUS
DEFINITION oligonucleotide from patent DE3731874.
ACCESSION A31423
VERSION A31423.1 GI:1249355
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS
JOURNAL Patent: DE 3731874-A 1 30-MAR-1989;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3659 CCTGCAGGGCCATG 3672
Db 14 CCTGCAGGGCCATG 1
RESULT 1188
A57884 18 bp DNA linear PAT 05-MAR-1998
LOCUS
DEFINITION Sequence 7 from Patent EP0743367.
ACCESSION A57884
VERSION A57884.1 GI:3713655
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
AUTHORS Fischer,A.D.
TITLE Gene expression analysis
JOURNAL Patent: EP 0743367-A 7 20-NOV-1996;
COMMENT MAX PLANCK GESELLSCHAFT (DE)
Other publication JP 8308598 961126
Other publication DE 19518505 961121.
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Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GATGAAGATGATCGGAA 1376
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Db 1 GATGAAGMGATCGAGAA 18

RESULT 1189
CQ821210      18 bp DNA linear PAT 14-JUN-2004
LOCUS
DEFINITION Sequence 40 from Patent WO2004046377.
ACCESSION CQ821210
VERSION CQ821210.1 GI:48715894
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
1 Casari,G., de Fusco,M. and Marconi,R.
  Diagnostics and therapeutic means for pathologies associated with
  alpha 2 subunit of the na, k pump
  Patent: WO 2004046377-A 40 03-JUN-2004;
  FONDAZIONE CENTRO SAN ROMANELLO DEL MONTE TABOR (IT)
FEATURES
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  Location/Qualifiers
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    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 GGAGGAGCTGGTG 868
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Db 4 GGAGGAGCTGGTG 17

RESULT 1190
AX441362      18 bp DNA linear PAT 02-JUL-2002
LOCUS
DEFINITION Sequence 7 from Patent EP1209241.
ACCESSION AX441362
VERSION AX441362.1 GI:21690350
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
1 Fischer,A.
  Gene expression analysis
  Patent: EP 1209241-A 7 29-MAY-2002;
  Axaron Bioscience AG (DE)
FEATURES
  source
  Location/Qualifiers
    1..18
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Sequenz P041"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GATGAAGATGATCGGAA 1376
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Db 1 GATGAAGMGATCGAGAA 18

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2242 CCTGCTGCTGCTGTC 2255
|||||:|||||
Db 1 CCTGCTGCTGCTGTC 14

RESULT 1191
AX599908      18 bp DNA linear PAT 14-FEB-2003
LOCUS
DEFINITION Sequence 1248 from Patent WO02077272.
ACCESSION AX599908
VERSION AX599908.1 GI:28400058
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
1 Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
  Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
  Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
  Pelet,C. and Ziebarth,H.
  Methods and nucleic acids for the analysis of hematopoietic cell
  proliferative disorders
  Patent: WO 02077272-A 1248 03-OCT-2002;
  Epigenomics AG (DE)
FEATURES
  source
  Location/Qualifiers
    1..18
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Detection oligonucleotide for CDK 4"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2695 CCATTCCACCCCT 2708
|||||:|||||
Db 18 CCATTCCACCCCT 5

RESULT 1193
AX599910      18 bp DNA linear PAT 14-FEB-2003
LOCUS
DEFINITION Sequence 1250 from Patent WO02077272.

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ACCESSION AX599910
VERSION AX599910.1 GI:28400060
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Berlin,K., Braun,A., Disler,J., Guetig,D., Howe,A., Mueller,J.,
        Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
        Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
        Pellet.C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
        proliferative disorders
JOURNAL Patent: WO 02077272-A 1250 03-OCT-2002;
FEATURES Epigenomics AG (DS)
          Location/Qualifiers
          source
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              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Detection oligonucleotide for CDK 4"

Query Match 0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2695 CCACCTCCACCCCT 2708
Db 1 CCACCTCCACCCCT 14

RESULT 1194
A30762
LOCUS A30762 20 bp DNA linear PAT 24-JUL-1996
DEFINITION Artificial DNA for oligonucleotide (TB-1).
ACCESSION A30762
VERSION A30762.1 GI:1567062
KEYWORDS
SOURCE synthetic construct
          synthetic construct
          artificial sequences.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS
TITLE NUCLEOTIDIC SEQUENCES OF ACTINOMYCETALES, APPLICATIONS TO THE
        SYNTHESIS OR DETECTION OF NUCLEIC ACIDS, PRODUCTS OF EXPRESSION OF
        SUCH SEQUENCES AND APPLICATION AS IMMUNOGENIC COMPOSITIONS
JOURNAL Patent: WO 9012875-A 16 01-NOV-1990;
FEATURES Location/Qualifiers
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            1..20
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3199 GAGCTGGAGGATCC 3212
Db 7 GAGCTGGAGGATCC 20

RESULT 1195
A36727
LOCUS A36727 20 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 15 from Patent EP0586112.
ACCESSION A36727
VERSION A36727.1 GI:2293996
KEYWORDS
SOURCE Mycobacterium tuberculosis
          Mycobacterium tuberculosis
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

ACCESSION AX599910
VERSION AX599910.1 GI:28400060
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Berlin,K., Braun,A., Disler,J., Guetig,D., Howe,A., Mueller,J.,
        Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
        Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
        Pellet.C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
        proliferative disorders
JOURNAL Patent: WO 02077272-A 1250 03-OCT-2002;
FEATURES Epigenomics AG (DS)
          Location/Qualifiers
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            1..19
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Detection oligonucleotide for CDK 4"

Query Match 0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2695 CCACCTCCACCCCT 2708
Db 1 CCACCTCCACCCCT 14

RESULT 1194
A30762
LOCUS A30762 20 bp DNA linear PAT 24-JUL-1996
DEFINITION Artificial DNA for oligonucleotide (TB-1).
ACCESSION A30762
VERSION A30762.1 GI:1567062
KEYWORDS
SOURCE synthetic construct
          synthetic construct
          artificial sequences.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS
TITLE NUCLEOTIDIC SEQUENCES OF ACTINOMYCETALES, APPLICATIONS TO THE
        SYNTHESIS OR DETECTION OF NUCLEIC ACIDS, PRODUCTS OF EXPRESSION OF
        SUCH SEQUENCES AND APPLICATION AS IMMUNOGENIC COMPOSITIONS
JOURNAL Patent: WO 9012875-A 16 01-NOV-1990;
FEATURES Location/Qualifiers
          source
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Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3199 GAGCTGGAGGATCC 3212
Db 7 GAGCTGGAGGATCC 20

RESULT 1195
A36727
LOCUS A36727 20 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 15 from Patent EP0586112.
ACCESSION A36727
VERSION A36727.1 GI:2293996
KEYWORDS
SOURCE Mycobacterium tuberculosis
          Mycobacterium tuberculosis
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

tuberculosis complex.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tercero,J.C., Garcia,L.C., Ramos,J.A. and Alemany,J.C.
TITLE Control of PCR mediated detection of micro-organisms
JOURNAL Patent: EP 0586112-A 15 09-MAR-1994;
          PHARMA GEN S A (ES)
COMMENT Other publication JP 7087978 950404.
FEATURES Location/Qualifiers
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            1..20
              /organism="Mycobacterium tuberculosis"
              /mol_type="unassigned DNA"
              /db_xref="taxon:1773"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3199 GAGCTGGAGGATCC 3212
Db 7 GAGCTGGAGGATCC 20

RESULT 1196
AR126637/C
LOCUS AR126637 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 66 from patent US 6180353.
ACCESSION AR126637
VERSION AR126637.1 GI:14113230
KEYWORDS
SOURCE Unknown.
          ORGANISM Unclasseified.
          Dean,N.M. and Cowser,L.M.
          Antisense modulation of daxx expression
          Patent: US 6180353-A 66 30-JAN-2001;
          Location/Qualifiers
            1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 AGATGACGAGGACG 184
Db 16 AGATGACGAGGACG 3

RESULT 1197
BD270088
LOCUS BD270088 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Secreted proteins and polynucleotides encoding them.
ACCESSION BD270088
VERSION BD270088.1 GI:33079856
KEYWORDS JP 2002537757-A/50.
          synthetic construct
          synthetic construct
          artificial sequences.
          1 (bases 1 to 20)
          Valenzuela,D., Yuan,O., Hoffman,H., Hall,J. and Rapiejko,P.
          Secreted proteins and polynucleotides encoding them
          Patent: JP 2002537757-A 50 12-NOV-2002;
          ALPHAGEN INC
          OS Artificial Sequence
          PN JP 2002537757-A/50
          PD 12-NOV-2002
          PF 24-AUG-1998 JP 2000566287
          PR 24-AUG-1998 US 60/097638,24-AUG-1998 US 60/097659 PR
          09-SEP-1998 US 60/099618,28-SEP-1998 US 60/102092 PR
          25-NOV-1998 US 60/109978,23-DEC-1998 US 60/113645 PR
          23-DEC-1998 US 60/113646,23-AUG-1999 US 09/379246 PI DARIO
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VALENZUELA, OLIVE YUAN, HEIDI HOFFMAN, JEFF HALL, PETER PI RAPIEJKO
PC C12N15/09, A61K38/00, A61K48/00, A61P3/10, A61P11/06, A61P21/00, PC
A61P29/00,
PC A61P31/04, A61P31/10, A61P31/12, A61P31/18, A61P35/00, A61P37/00,
PC C07K14/47, C12N5/10, C12P21/02, G01N33/50, C12N15/00, A61K37/02, PC
C12N5/00
CC oligonucleotide Location/Qualifiers
FH Key 1..20
FT source /organism="synthetic construct"
FT source /mol_type="genomic DNA"
FT source /db_xref="taxon:32630"

FEATURES
source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2005 CTGTGTGGAGGACCT 2018
DB 6 CTGTGTGGAGGACCT 19
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RESULT 1198
CQ818366/c
LOCUS CQ818366 20 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 8 from Patent WO2004044581.
ACCESSION CQ818366
VERSION CQ818366.1 GI:48427039
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Mackenzie, I., Rees, C.M., Nikitenko, L.L., Bicknell, R. and Smith, D.M.
TITLE Transcriptional regulation of crlr and uses thereof
JOURNAL Patent: WO 2004044581-A 8 27-MAY-2004;
ISIS INNOVATION LIMITED (GB)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTG 2329
DB 14 TCTGTGTGTGTGTG 1
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RESULT 1199
CQ818386/c
LOCUS CQ818386 20 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 28 from Patent WO2004044581.
ACCESSION CQ818386
VERSION CQ818386.1 GI:48427059
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mackenzie, I., Rees, C.M., Nikitenko, L.L., Bicknell, R. and Smith, D.M.
TITLE Transcriptional regulation of crlr and uses thereof
JOURNAL Patent: WO 2004044581-A 28 27-MAY-2004;
ISIS INNOVATION LIMITED (GB)
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Location/Qualifiers

/organism="synthetic construct"
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Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTG 2329
DB 14 TCTGTGTGTGTGTG 1
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RESULT 1200
E30319
LOCUS E30319 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Gene participating in flower formation of plant.
ACCESSION E30319
VERSION E30319.1 GI:13017065
KEYWORDS JP 1999318462-A/6.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
AUTHORS Shinichiro, S. and Kiyotaka, O.
TITLE Gene participating in flower formation of plant
JOURNAL Patent: JP 1999318462-A 6 24-NOV-1999;
MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO
COMMENT
OS Unidentified
PN JP 1999318462-A/6
PD 24-NOV-1999
PF 15-MAY-1998 JP 1998134095
PR
PI SHINICHIRO SAWA, KIYOTAKA OKADA
PC C12N15/09, A01H5/00, C07K14/415, C07K16/16, C12N1/21, C12N5/10, PC
C12P21/02
PC C12P21/08, G01N33/53//C12N1/21, C12R1/19, (C12N5/10, C12R1/91),
PC (C12P21/02, C12R1/91), C12N15/00, C12N5/00, (C12N5/00, C12R1/91) CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
FT source /organism="Unidentified".
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1..20
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2108 CCAGCTCCAGCTCC 2121
DB 4 CCAGCTCCAGCTCC 17
|||||

RESULT 1201
AR266079/c
LOCUS AR266079 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 86 from patent US 6492171.
ACCESSION AR266079
VERSION AR266079.1 GI:29694925
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Monia, B.P., Gaarde, W.A., Freier, S.M. and Wanciewicz, E.
TITLE Antisense modulation of TERT expression
JOURNAL Patent: US 6492171-A 86 10-DEC-2002;
FEATURES
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Location/Qualifiers

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source      1. .20
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            /mol_type="genomic DNA"

Query Match      0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTG 2331
Db      20 TGTGTGTGTGTGTG 7

RESULT 1202
AX149325/c
LOCUS      AX149325      20 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION      Sequence 10 from Patent WO0136602.
ACCESSION      AX149325
VERSION      AX149325.1 GI:14347848
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1
AUTHORS      Dahlberg,M., Moll,J. and Galvani,A.
TITLE      Pak5 a member of the p21-activated kinase (pak) protein family,
            nucleic acids and methods related to the same
JOURNAL      Patent: WO 0136602-A 10 25-MAY-2001;
            PHARMACIA & UPJOHN S.P.A. (IT)
FEATURES
source      1. .20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer"

Query Match      0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 1.2e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1751 ACTGGATGGCGCTGAGG 1768
Db      19 AYTGGATGGCWCWGAGS 2

RESULT 1203
AX613800/c
LOCUS      AX613800      20 bp      DNA      linear      PAT 17-FEB-2003
DEFINITION      Sequence 4825 from Patent WO02072882.
ACCESSION      AX613800
VERSION      AX613800.1 GI:28409229
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Cullen,P. and Seedorf,U.
TITLE      Coronary chip
JOURNAL      Patent: WO 02072882-A 4825 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES
source      1. .20
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2098 CAGGACACCCCCAG 2111
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Db      20 CAGGACACCCCCAG 7

RESULT 1204
BD013149/c
LOCUS      BD013149      20 bp      DNA      linear      PAT 02-AUG-2002
DEFINITION      A gene encoding novel human secretory type phospholipase A2.
ACCESSION      BD013149
VERSION      BD013149.1 GI:22093338
KEYWORDS      WO 0121775-A/22.
SOURCE      synthetic construct
ORGANISM      synthetic construct
            artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Ishizaki,J., Suzuki,N. and Hanasaki,K.
TITLE      A gene encoding novel human secretory type phospholipase A2
JOURNAL      Patent: WO 0121775-A 22 29-MAR-2001;
            SHIONOGI & CO LTD JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI
COMMENT      OS Artificial Sequence
            PN WO 0121775-A/22
            PD 29-MAR-2001
            PF 18-SEP-2000 WO 2000JP006344
            PR 21-SEP-1999 JP 99P 266616
            PI JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI
            PC C12N9/20,C12N15/55,C12P21/02,C12P21/08,C07K16/40 CC
            FH Key Location/Qualifiers.
FEATURES
source      1. .20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2438 CTGACTGGTGCTGTC 2451
Db      16 CTGACTGGTGCTGTC 3

RESULT 1205
BD167763/c
LOCUS      BD167763      20 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION      Substance inhibiting binding of signal transducing molecule to
            KDR/Flk-1 phosphorylated at tyrosine at the 1175-position and
            method of using the same.
ACCESSION      BD167763
VERSION      BD167763.1 GI:27873575
KEYWORDS      WO 0229090-A/3.
SOURCE      synthetic construct
ORGANISM      synthetic construct
            artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Shibuya,M., Takahashi,T., Furuya,A. and Shitara,K.
TITLE      Substance inhibiting binding of signal transducing molecule to
            KDR/Flk-1 phosphorylated at tyrosine at the 1175-position and
            method of using the same
JOURNAL      Patent: WO 0229090-A 3 11-APR-2002;
            KYOWA HAKKO KOGYO CO LTD,MASABUMI SHIBUYA
COMMENT      OS Artificial Sequence
            PN WO 0229090-A/3
            PD 11-APR-2002
            PF 02-OCT-2001 WO 2001JP008684
            PR 03-OCT-2000 JP 00P 303694
            PI MASABUMI SHIBUYA,TOMOKO TAKAHASHI,AKIKO FURUYA,KENYA SHITARA
            PC C12Q1/02,C12Q1/48,C12N15/09,C07K16/18,C07K14/47,A61K39/395, PC
            A61P43/00,
            PC A61P35/00,A61P9/00,A61K45/00,G01N33/15,G01N33/50 CC a primer
            for replacing of human KDR/Flk-1 tyrosine residue at CC
            position 801
            CC tyrosine
            FH Key Location/Qualifiers

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FT	source	1..20	/organism='Artificial Sequence'
FT	Location/Qualifiers		
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	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
Query Match	0.4%; Score 14; DB 1; Length 20;		
Best Local Similarity	100.0%; Pred. No. 1.2e+03;		
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Qy	249 GATGGACAGAGC 262		
Db	19 GATGGACAGAGC 6		
RESULT 1206			
AX103869	AX103869	22 bp	DNA
LOCUS	Sequence 61 from Patent WO0122972.		
DEFINITION	Sequence 61 from Patent WO0122972.		
ACCESSION	AX103869		
VERSION	AX103869.1 GI:13920066		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Krieg,A.M., Schetter,C. and Vollmer,J.C.		
TITLE	Immunostimulatory nucleic acids		
JOURNAL	Patent: WO 0122972-A 61 05-APR-2001;		
	UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical		
	GmbH (DE)		
FEATURES	Location/Qualifiers		
source	1..22		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
Query Match	0.4%; Score 14; DB 1; Length 22;		
Best Local Similarity	77.3%; Pred. No. 1.3e+03;		
Matches 17; Conservative	0; Mismatches 5; Indels 0; Gaps 0;		
Qy	3264 TTTTATTGCTTTGTCCTTTT 3285		
Db	1 TTTTATTGCTTTTGTCTTTT 22		
RESULT 1207			
AX546922	AX546922	22 bp	DNA
LOCUS	Sequence 61 from Patent WO02053141.		
DEFINITION	Sequence 61 from Patent WO02053141.		
ACCESSION	AX546922		
VERSION	AX546922.1 GI:25812066		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Bratzler,R.L.		
TITLE	Inhibition of angiogenesis by nucleic acids		
JOURNAL	Patent: WO 02053141-A 61 11-JUL-2002;		
	Coley Pharmaceutical Group, Inc. (US)		
FEATURES	Location/Qualifiers		
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Query Match	0.4%; Score 14; DB 1; Length 22;		
Best Local Similarity	77.3%; Pred. No. 1.3e+03;		
Matches 17; Conservative	0; Mismatches 5; Indels 0; Gaps 0;		

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 44)
AUTHORS     Weber,J.L.
TITLE       Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
            method of using the same
JOURNAL     Patent: US 5582979-A 249 10-DEC-1996;
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 14; DB 1; Length 44;
Best Local Similarity 60.5%; Pred. No. 1.7e+03;
Matches 23; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 608 ACAGTCACGACAGCCCATCATCGTGGTCAAGCAC 645
Db 5 ACACACACACACACACACACACACACACACACAC 42

RESULT 1211
AR046263
LOCUS      AR046263
DEFINITION Sequence 1056 from patent US 5817796.
ACCESSION AR046263
VERSION    AR046263.1 GI:5967728
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL     Patent: US 5817796-A 1056 06-OCT-1998;
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3458 AAGTTTATATATCTA 3474
Db 1 AATTTTATATATATA 17

RESULT 1212
I53315
LOCUS      I53315
DEFINITION Sequence 1056 from patent US 5646042.
ACCESSION  I53315
VERSION     I53315.1 GI:2474518
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb targeted ribozymes
JOURNAL     Patent: US 5646042-A 1056 08-JUL-1997;
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 44)
AUTHORS     Weber,J.L.
TITLE       Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
            method of using the same
JOURNAL     Patent: US 5582979-A 249 10-DEC-1996;
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Query Match      0.4%; Score 14; DB 1; Length 44;
Best Local Similarity 60.5%; Pred. No. 1.7e+03;
Matches 23; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 608 ACAGTCACGACAGCCCATCATCGTGGTCAAGCAC 645
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RESULT 1211
AR046263
LOCUS      AR046263
DEFINITION Sequence 1056 from patent US 5817796.
ACCESSION AR046263
VERSION    AR046263.1 GI:5967728
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL     Patent: US 5817796-A 1056 06-OCT-1998;
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
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QY 3458 AAGTTTATATATCTA 3474
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RESULT 1212
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LOCUS      I53315
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ACCESSION  I53315
VERSION     I53315.1 GI:2474518
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb targeted ribozymes
JOURNAL     Patent: US 5646042-A 1056 08-JUL-1997;
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3458 AAGTTTATATATCTA 3474
Db 1 AATTTTATATATATA 17

RESULT 1213
A02372/c
LOCUS      A02372
DEFINITION Oligonucleotide Lys320-Ala.
ACCESSION  A02372
VERSION     A02372.1 GI:344633
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE   1 (bases 1 to 17)
AUTHORS
TITLE       ALTERED ANTIBODIES
JOURNAL     Patent: WO 8807089-A 14 22-SEP-1988;
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 588 GGAGTTCCACTGCAGG 604
Db 17 GGAGTTCCGCTGCAGG 1

RESULT 1214
A06173/c
LOCUS      A06173
DEFINITION Oligonucleotide probe.
ACCESSION  A06173
VERSION     A06173.1 GI:412792
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE   1 (bases 1 to 17)
AUTHORS
TITLE       GENE MODIFICATION
JOURNAL     Patent: WO 9001548-A 1 22-FEB-1990;
FEATURES    Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1515 CACCTGCAGCCGCCG 1531
Db 17 CACCTGCTAGCCGCCG 1

RESULT 1215
AR039211
LOCUS      AR039211
DEFINITION Sequence 59 from patent US 5807743.
ACCESSION  AR039211
VERSION     AR039211.1 GI:5958574
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
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Unclassified.
1 (bases 1 to 17)
REFERENCE
  Stinchcomb,D.T. and McSwiggen,J.A.
AUTHORS
  Interleukin-2 receptor gamma-chain ribozymes
TITLE
  Patent: US 5807743-A 59 15-SEP-1998;
JOURNAL
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Db 1 TTTCCACTGCCCCC 17

RESULT 1216
AR046566/c
LOCUS
  AR046566 17 bp DNA linear PAT 29-SEP-1999
DEFINITION
  Sequence 1359 from patent US 5817796.
ACCESSION
  AR046566
VERSION
  AR046566.1 GI:5968031
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unclassified.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE
  C-myb ribozymes having 2'-5'-linked adenylylate residues
JOURNAL
  Patent: US 5817796-A 1359 06-OCT-1998;
FEATURES
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    /mol_type="unassigned DNA"
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 17 CTGAGTCGAGTGAGG 1

RESULT 1217
AR047368/c
LOCUS
  AR047368 17 bp DNA linear PAT 29-SEP-1999
DEFINITION
  Sequence 2161 from patent US 5817796.
ACCESSION
  AR047368
VERSION
  AR047368.1 GI:5968833
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unclassified.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE
  C-myb ribozymes having 2'-5'-linked adenylylate residues
JOURNAL
  Patent: US 5817796-A 2161 06-OCT-1998;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2829 TACATATATATATAA 2845
Db 17 TACATATATATATAA 1

RESULT 1218
BD234970
LOCUS
  BD234970 17 bp DNA linear PAT 17-JUL-2003
DEFINITION
  A method for stimulating the immune system.
ACCESSION
  BD234970
VERSION
  BD234970.1 GI:33044740
KEYWORDS
  JP 2002517434-A/74.
SOURCE
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ORGANISM
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE
  A method for stimulating the immune system
JOURNAL
  Patent: JP 2002517434-A 74 18-JUN-2002;
COMMENT
  BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
  OS Homo sapiens (human)
  PN JP 2002517434-A/74
  PD 18-JUN-2002
  PF 10-JUN-1999 JP 200053044
  PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
  KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
  BRYSCH
  PC A61K45/06,A61K31/7089,A61K38/00,A61K39/395,A61K39/395,A61P31/
  PC 00,A61P35/00,
  PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
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Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2923 CGGGGGCGGGGGGGCGG 2939
Db 1 CGGGGGCGGGGGGGCGG 17

RESULT 1219
BD241250/c
LOCUS
  BD241250 17 bp DNA linear PAT 17-JUL-2003
DEFINITION
  Methods and products related to genotyping and DNA analysis.
ACCESSION
  BD241250
VERSION
  BD241250.1 GI:33051020
KEYWORDS
  JP 2002525127-A/197.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
TITLE
  Methods and products related to genotyping and DNA analysis
JOURNAL
  Patent: JP 2002525127-A 197 13-AUG-2002;
COMMENT
  MASSACHUSETTS INSTITUTE OF TECHNOLOGY
  OS Homo sapiens (human)
  PN JP 2002525127-A/197
  PD 13-AUG-2002
  PF 24-SEP-1999 JP 2000572407
  PR 25-SEP-1998 US 60/101757
  PI JOHN E LANDERS,BARBARA JORDAN,DAVID E HOUSMAN,ALAIN CHAREST PC
  C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/58,G01N37/00, PC
  G01N37/00,
  PC C12N15/00
  CC Methods and products related to genotyping and DNA analysis FH
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Key          Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1680 CTTGGGCTGCGCCGGG 1696
Db 17 CTTCTGGCTGCCCAGG 1

RESULT 1220
BD241618
LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Methods and products related to genotyping and DNA analysis.
ACCESSION    BD241618
VERSION      BD241618.1 GI:33051388
KEYWORDS     JP 2002525127-A/565.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
Methods and products related to genotyping and DNA analysis
Patent: JP 2002525127-A 565 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
OS Homo sapiens (human)
PN JP 2002525127-A/565
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572407
PR 25-SEP-1998 US 60/101757
PI JOHN E LANDERS,BARBARA JORDAN,DAVID E HOUSMAN,ALAIN CHAREST PC
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/58,G01N37/00, PC
G01N37/00,
PC C12N15/00
CC Methods and products related to genotyping and DNA analysis FH
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2326 TGTGTGTGCGTGTGTGT 2342
Db 1 TGTGTGTGCGCTGTCT 17

RESULT 1221
BD253988/c
LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Regulation of repressor genes using nucleic acid molecules.
ACCESSION    BD253988
VERSION      BD253988.1 GI:33063758
KEYWORDS     JP 2002541795-A/1781.
SOURCE       unidentified
ORGANISM     unidentified.
1 (bases 1 to 17)
REFERENCE
1 (bases 1 to 17)
AUTHORS      Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      Patent: JP 2002541795-A 1782 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/1782
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
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PC A61K37/02,
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CC Regulation of repressor genes using nucleic acid molecules FH
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2853 GGAAGAGGAAAAGCGCTG 2869
Db 17 GGGAGAGGATAGGCTG 1

RESULT 1222
BD253989/c
LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Regulation of repressor genes using nucleic acid molecules.
ACCESSION    BD253989
VERSION      BD253989.1 GI:33063759
KEYWORDS     JP 2002541795-A/1782.
SOURCE       unidentified
ORGANISM     unidentified.
1 (bases 1 to 17)
REFERENCE
1 (bases 1 to 17)
AUTHORS      Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      Patent: JP 2002541795-A 1782 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/1782
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
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C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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CC Regulation of repressor genes using nucleic acid molecules FH
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RIBOZYME PHARMACEUTICALS INC						
PATENT: JP 2002541795-A 2288 10-DEC-2002;						
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PD 10-DEC-2002						
PF 11-APR-2000 JP 2000611654						
PR 12-APR-1999 US 60/129390						
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC						
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C12P21/02,						
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Query Match 0.4%; Score 13.8; DB 1; Length 17;						
Best Local Similarity 88.2%; Pred. NO.1.le+03;						
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;						
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Db 17 TGGAGAGGAATAGGCT 1						
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LOCUS						
DEFINITION						
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AUTHORS						
TITLE						
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PD 10-DEC-2002						
PF 11-APR-2000 JP 2000611654						
PR 12-APR-1999 US 60/129390						
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC						
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Best Local Similarity 88.2%; Pred. NO.1.le+03;						
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;						
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ACCESSION						
VERSION						
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ORGANISM						
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AUTHORS						
TITLE						
JOURNAL						
COMMENT						
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PD 10-DEC-2002						
PF 11-APR-2000 JP 2000611654						
PR 12-APR-1999 US 60/129390						
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC						
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10,PC						
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PC A61K37/02,						
PC (C12N5/00,C12R1:91)						
CC Regulation of repressor genes using nucleic acid molecules FH						
Key source 1..17 Location/Qualifiers						
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Query Match 0.4%; Score 13.8; DB 1; Length 17;						
Best Local Similarity 88.2%; Pred. NO.1.le+03;						
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;						
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LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
COMMENT						
OS Eukaryote						
PN JP 2002541795-A/2288						
PD 10-DEC-2002						
PF 11-APR-2000 JP 2000611654						
PR 12-APR-1999 US 60/129390						
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC						
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10,PC						
C12P21/02,						
PC						
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C12R1:91),						
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,						
PC A61K37/02,						
PC (C12N5/00,C12R1:91)						
CC Regulation of repressor genes using nucleic acid molecules FH						
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Query Match 0.4%; Score 13.8; DB						

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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1563 CTGTGCTTACCAGTGG 1579
DB 1 CGGTGCTTACCAGCGG 17

RESULT 1226
CQ617474
LOCUS      CQ617474      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 2214 from Patent WO0192524.
ACCESSION  CQ617474
VERSION    CQ617474.1 GI:41667692
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2214 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 879 GCGGGCAGTGTGTATG 895
DB 1 GCGAGCAGTGTGTATG 17

RESULT 1227
CQ617930
LOCUS      CQ617930      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 2670 from Patent WO0192524.
ACCESSION  CQ617930
VERSION    CQ617930.1 GI:41668148
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2670 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2917 CCTGGGCGGGCGTGGG 2933
DB 1 CCTGGGCGGGCGGGGG 17

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1989 GCCCACCTTCAAGCAGC 2005
DB 1 GGCACACCTTCAAGCACC 17

RESULT 1230
CQ623102
LOCUS      CQ623102      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 7842 from Patent WO0192524.
ACCESSION  CQ623102
VERSION    CQ623102.1 GI:41673320
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
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RESULT 1228
CQ618036
LOCUS      CQ618036      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 2776 from Patent WO0192524.
ACCESSION  CQ618036
VERSION    CQ618036.1 GI:41668254
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2776 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1987 AGCCCCACCTTCAAGCA 2003
DB 1 ACGGCCACCTTCAAGCA 17

RESULT 1229
CQ618038
LOCUS      CQ618038      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 2778 from Patent WO0192524.
ACCESSION  CQ618038
VERSION    CQ618038.1 GI:41668256
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2778 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..17
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1989 GCCCACCTTCAAGCAGC 2005
DB 1 GGCACACCTTCAAGCACC 17

RESULT 1230
CQ623102
LOCUS      CQ623102      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 7842 from Patent WO0192524.
ACCESSION  CQ623102
VERSION    CQ623102.1 GI:41673320
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7842 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1997 TCAAGCAGCTGGTGGAG 2013
Db 1 TGAAGCAGCAGGTGGAG 17
RESULT 1231
LOCUS CQ623258 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 7998 from Patent WO0192524.
ACCESSION CQ623258
VERSION CQ623258.1 GI:41673476
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7998 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1994 CCTTCAAGCAGCTGGTG 2010
Db 1 CCATCAAGCAGCTGGAG 17
RESULT 1232
LOCUS CQ623261 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8001 from Patent WO0192524.
ACCESSION CQ623261
VERSION CQ623261.1 GI:41673479
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8001 06-DEC-2001;
Aeomica, Inc. (US)

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1997 TCAAGCAGCTGGTGGAG 2013
Db 1 TCAAGCAGCTGGAGCAG 17
RESULT 1233
LOCUS CQ623347 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8087 from Patent WO0192524.
ACCESSION CQ623347
VERSION CQ623347.1 GI:41673565
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8087 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGGTGA 869
Db 1 GAGGAGGAGCTGGAGGA 17
RESULT 1234
LOCUS CQ623985 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8725 from Patent WO0192524.
ACCESSION CQ623985
VERSION CQ623985.1 GI:41674203
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8725 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2049  CGAGTACCTGGACCTGT 2065
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          1  CGAGTACCTGGACAGT 17

RESULT 1235
LOCUS   CQ623986
DEFINITION
Sequence 8726 from Patent WO0192524.
ACCESSION CQ623986
VERSION   CQ623986.1 GI:41674204
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
          Shannon, M.E.
TITLE    Myosin-like gene expressed in human heart and muscle
JOURNAL  Patent: WO 0192524-A 8726 06-DEC-2001;
          Aeomica, Inc. (US)
FEATURES
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          /mol_type="unassigned DNA"
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2050  GAGTACTGGACCTGTC 2066
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RESULT 1236
LOCUS   CQ624607
DEFINITION
Sequence 9347 from Patent WO0192524.
ACCESSION CQ624607
VERSION   CQ624607.1 GI:41674825
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
          Shannon, M.E.
TITLE    Myosin-like gene expressed in human heart and muscle
JOURNAL  Patent: WO 0192524-A 9347 06-DEC-2001;
          Aeomica, Inc. (US)
FEATURES
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      190  GAGAGGCTGGAGAC 206
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          1  GAAGAGGCTGGGACAC 17

RESULT 1237
LOCUS   CQ624974
DEFINITION
Sequence 195 from Patent WO2004035803.
ACCESSION CQ806745
VERSION   CQ806745.1 GI:47112127
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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DEFINITION
Sequence 9714 from Patent WO0192524.
ACCESSION CQ624974
VERSION   CQ624974.1 GI:41675192
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
          Shannon, M.E.
TITLE    Myosin-like gene expressed in human heart and muscle
JOURNAL  Patent: WO 0192524-A 9714 06-DEC-2001;
          Aeomica, Inc. (US)
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2945  GGAGGCCCCAGGGTCT 2961
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          17 GGAGGCCCCAGTCGTCT 1

RESULT 1238
LOCUS   CQ625121
DEFINITION
Sequence 9861 from Patent WO0192524.
ACCESSION CQ625121
VERSION   CQ625121.1 GI:41675339
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
          Shannon, M.E.
TITLE    Myosin-like gene expressed in human heart and muscle
JOURNAL  Patent: WO 0192524-A 9861 06-DEC-2001;
          Aeomica, Inc. (US)
FEATURES
source   1..17
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          /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      277  GCCGCCAACACCGTCG 293
          |||||
          17 GCCGCCAACACCGTCGTG 1

RESULT 1239
LOCUS   CQ806745/c
DEFINITION
Sequence 195 from Patent WO2004035803.
ACCESSION CQ806745
VERSION   CQ806745.1 GI:47112127
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1

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AUTHORS Poekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F., Nimrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and Marx,A.

TITLE Method and nucleic acids for the improved treatment of breast cell proliferative disorders

JOURNAL Patent: WO 2004035803-A 195 29-APR-2004; Epigenomics AG (DE)

FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2004 GCTGGTGGAGGACTGG 2020
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Db 17 GCTGGTGGAGGACTGG 1

RESULT 1240
I53618/c 17 bp DNA linear PAT 07-OCT-1997
LOCUS I53618
DEFINITION Sequence 1359 from patent US 5646042.
ACCESSION I53618
VERSION I53618.1 GI:2474821
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1359 08-JUL-1997;
FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1346 CTGAGATGGAGATGATG 1362
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Db 17 CTGAGATGGAGGTGAGG 1

RESULT 1241
I54420/c 17 bp DNA linear PAT 07-OCT-1997
LOCUS I54420
DEFINITION Sequence 2161 from patent US 5646042.
ACCESSION I54420
VERSION I54420.1 GI:2475623
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 2161 08-JUL-1997;
FEATURES Location/Qualifiers
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 /organism="unknown"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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QY 2829 TACATATATATATAA 2845
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Db 17 TACATATATATAAAA 1

RESULT 1242
AR187317/c 17 bp DNA linear PAT 20-APR-2002
LOCUS AR187317
DEFINITION Sequence 2805 from patent US 6346398.
ACCESSION AR187317
VERSION AR187317.1 GI:20233282
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2805 12-FEB-2002;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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QY 3250 TTCCAGTGAAGATATTT 3266
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Db 17 TTCCATTGAAATATTT 1

RESULT 1243
AR187357 17 bp DNA linear PAT 20-APR-2002
LOCUS AR187357
DEFINITION Sequence 2845 from patent US 6346398.
ACCESSION AR187357
VERSION AR187357.1 GI:20233322
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2845 12-FEB-2002;
FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3251 TCCAGTGAAGATATTT 3267
 |||||
Db 1 TCCAGTGTAGATATAT 17

RESULT 1244
AR188717 17 bp DNA linear PAT 20-APR-2002
LOCUS AR188717
DEFINITION Sequence 4205 from patent US 6346398.
ACCESSION AR188717
VERSION AR188717.1 GI:20234682
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
source 1..17
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1587 CATGGAGTCTTGGCCT 1603
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Db 1 CATGGAGTCTTGGCAT 17
RESULT 1245
AR188718 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 4206 from patent US 6346398.
ACCESSION AR188718
VERSION AR188718.1 GI:20234693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1588 ATGGAGTCTTGGCCTC 1604
|||||
Db 1 ATGGAGTCTTGGCATC 17
RESULT 1246
AR188755 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 4243 from patent US 6346398.
ACCESSION AR188755
VERSION AR188755.1 GI:20234720
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1803 CGTCTGCTCTTTGGGG 1819

Db 1 CGTCTGCTCTTTGGTG 17
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RESULT 1247
AR190226 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 5714 from patent US 6346398.
ACCESSION AR190226
VERSION AR190226.1 GI:20236191
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1288 GTAGCGGTGAAGATGCT 1304
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Db 1 GTAGCGGTGAAGATGTT 17
RESULT 1248
AR190240 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 5728 from patent US 6346398.
ACCESSION AR190240
VERSION AR190240.1 GI:20236205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1393 AACCTGCTGGCGCCTG 1409
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Db 1 AACCTGCTAGGCGCCTG 17
RESULT 1249
AR190291 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 5779 from patent US 6346398.
ACCESSION AR190291
VERSION AR190291.1 GI:20236256
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5779 12-FEB-2002;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1587 CATGGAGTCTTGGCCT 1603
|||||
Db 1 CATGGAGTCTTGGCAT 17
RESULT 1250
AR190292 17 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 5780 from patent US 6346398.
DEFINITION AR190292
ACCESSION AR190292
VERSION AR190292.1 GI:20236257
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5780 12-FEB-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1588 ATGGAGTCTTGGCCTC 1604
|||||
Db 1 ATGGAGTCTTGGCATC 17
RESULT 1251
AR190307 17 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 5795 from patent US 6346398.
DEFINITION AR190307
ACCESSION AR190307
VERSION AR190307.1 GI:20236272
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5795 12-FEB-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1680 CTTGGGCTGGCCGG 1696
|||||

Db 1 CTTGGGCTTGGCCGG 17
RESULT 1252
AR192109 17 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 7597 from patent US 6346398.
DEFINITION AR192109
ACCESSION AR192109
VERSION AR192109.1 GI:20238074
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7597 12-FEB-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1296 GAAGATGCTGAAGACG 1312
|||||
Db 1 GAAGATGCTGAAGAGG 17
RESULT 1253
AR261711 17 bp DNA linear PAT 29-JAN-2003
LOCUS Sequence 195 from patent US 6322976.
DEFINITION AR261711
ACCESSION AR261711
VERSION AR261711.1 GI:28072789
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Altman, T. J., Scott, J. and Stanton, L. W.
TITLE Compositions and methods of disease diagnosis and therapy
JOURNAL Patent: US 6322976-A 195 27-NOV-2001;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2575 ACATCAGGGTGGCT 2591
|||||
Db 1 ACATCATAGGGTGTGCT 17
RESULT 1254
AR286089 17 bp RNA linear PAT 10-APR-2003
LOCUS Sequence 461 from patent US 6528640.
DEFINITION AR286089
ACCESSION AR286089
VERSION AR286089.1 GI:29723685
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.


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TITLE      Synthetic ribonucleic acids with RNase activity
JOURNAL    Patent: US 6528640-A 461 04-MAR-2003;
FEATURES   Location/Qualifiers
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           /organism="unknown"
           /mol_type="unassigned RNA"

Query Match
Best Local Similarity  0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      863  TGGTGGAGGCTGACGAG 879
Db      1    TGGTGGAGTGTGAGGAG 17

RESULT 1255
AR286406  AR286406  17 bp  RNA  linear  PAT 10-APR-2003
LOCUS
DEFINITION Sequence 778 from patent US 6528640.
ACCESSION AR286406
VERSION   AR286406.1 GI:29724002
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
           Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE     Synthetic ribonucleic acids with RNase activity
JOURNAL   Patent: US 6528640-A 778 04-MAR-2003;
FEATURES  Location/Qualifiers
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           /organism="unknown"
           /mol_type="unassigned RNA"

Query Match
Best Local Similarity  0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1744  CCGTGCAAGTGGATGGC 1760
Db      1    CCGATCAAGTGGATGGC 17

RESULT 1256
AR286407  AR286407  17 bp  RNA  linear  PAT 10-APR-2003
LOCUS
DEFINITION Sequence 779 from patent US 6528640.
ACCESSION AR286407
VERSION   AR286407.1 GI:29724003
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
           Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE     Synthetic ribonucleic acids with RNase activity
JOURNAL   Patent: US 6528640-A 779 04-MAR-2003;
FEATURES  Location/Qualifiers
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           /organism="unknown"
           /mol_type="unassigned RNA"

Query Match
Best Local Similarity  0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1751  AGTGGATGGCGCTGAG 1767
Db      1    AGTGGATGGCGCTGGAG 17

RESULT 1257
AR286445  AR286445  17 bp  RNA  linear  PAT 10-APR-2003
LOCUS
DEFINITION Sequence 817 from patent US 6528640.
ACCESSION AR286445
VERSION   AR286445.1 GI:29724041
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
           Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE     Synthetic ribonucleic acids with RNase activity
JOURNAL   Patent: US 6528640-A 817 04-MAR-2003;
FEATURES  Location/Qualifiers
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           /organism="unknown"
           /mol_type="unassigned RNA"

Query Match
Best Local Similarity  0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13    GGGCTGGTGGCCCTCGGA 29
Db      1    GGGCTGGAGCCCTCTGA 17

RESULT 1258
AR286463  AR286463  17 bp  RNA  linear  PAT 10-APR-2003
LOCUS
DEFINITION Sequence 835 from patent US 6528640.
ACCESSION AR286463
VERSION   AR286463.1 GI:29724059
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
           Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE     Synthetic ribonucleic acids with RNase activity
JOURNAL   Patent: US 6528640-A 835 04-MAR-2003;
FEATURES  Location/Qualifiers
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           /organism="unknown"
           /mol_type="unassigned RNA"

Query Match
Best Local Similarity  0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2149  GACCTGCTGCCCCCGGC 2165
Db      1    GACCTGCAGCCCCCGAC 17

RESULT 1259
AR317230  AR317230  17 bp  DNA  linear  PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 4 from patent US 6562624.
ACCESSION AR317230
VERSION   AR317230.1 GI:33696572
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Adachi,K., Hamer,J.E. and Hamer,L.
TITLE     Methods and materials for the rapid and high volume production of a
           gene knock-out library in an organism
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JOURNAL	Patent: US 6562624-A 4 13-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="genomic DNA"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.1e+03;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	2095 GGCCAGGACACCCCAG 2111
Db	1 GGCCAGGAACAATCCCAG 17
RESULT 1260	
AR323927/c	
LOCUS	17 bp RNA linear PAT 17-AUG-2003
DEFINITION	Sequence 1329 from patent US 6566127.
ACCESSION	AR323927
VERSION	AR323927.1 GI:33709735
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6566127-A 1329 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="unassigned RNA"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.1e+03;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	3250 TTCAGTGTGAATATT 3266
Db	17 TTCATTGAAATATT 1
RESULT 1261	
AR323967	
LOCUS	17 bp RNA linear PAT 17-AUG-2003
DEFINITION	Sequence 1369 from patent US 6566127.
ACCESSION	AR323967
VERSION	AR323967.1 GI:33709775
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6566127-A 1369 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="unassigned RNA"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.1e+03;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	3251 TCCAGTGTGAATATT 3267
Db	1 TCCAGTGTGAATATT 17

RESULT 1262	
AR324570	
LOCUS	17 bp RNA linear PAT 17-AUG-2003
DEFINITION	Sequence 1972 from patent US 6566127.
ACCESSION	AR324570
VERSION	AR324570.1 GI:33710378
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6566127-A 1972 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="unassigned RNA"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.1e+03;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1587 CATGGACTACTTGCGCT 1603
Db	1 CATGGAGTTCTTGGCAT 17
RESULT 1263	
AR324571	
LOCUS	17 bp RNA linear PAT 17-AUG-2003
DEFINITION	Sequence 1973 from patent US 6566127.
ACCESSION	AR324571
VERSION	AR324571.1 GI:33710379
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6566127-A 1973 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
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	/mol_type="unassigned RNA"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.1e+03;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1588 ATGGAGTACTTGCGCTC 1604
Db	1 ATGGAGTTCTTGGCATC 17
RESULT 1264	
AR324608	
LOCUS	17 bp RNA linear PAT 17-AUG-2003
DEFINITION	Sequence 2010 from patent US 6566127.
ACCESSION	AR324608
VERSION	AR324608.1 GI:33710416
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6566127-A 2010 20-MAY-2003;

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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1803 CGTCTGGTCTTTGGGG 1819
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Db 1 CGTCTGGTCTTTGGTG 17

RESULT 1265
LOCUS AR325195 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2597 from patent US 6566127.
ACCESSION AR325195
VERSION AR325195.1 GI:33711003
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2597 20-MAY-2003;
FEATURES Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1288 GTAGCGCTGAAGATGCT 1304
||||| ||||| |||||
Db 1 GTAGCGCTCAAGATGT 17

RESULT 1266
LOCUS AR325206 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2608 from patent US 6566127.
ACCESSION AR325206
VERSION AR325206.1 GI:33711014
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2608 20-MAY-2003;
FEATURES Location/Qualifiers
  source      1..17
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1393 AACCTGCTGGGCGCCTG 1409
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Db 1 AACCTCTAGGCGCCTG 17

RESULT 1267
LOCUS AR325259 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2661 from patent US 6566127.
ACCESSION AR325259
VERSION AR325259.1 GI:33711067
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2661 20-MAY-2003;
FEATURES Location/Qualifiers
  source      1..17
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1680 CTTGGGCTGGCCCGG 1696
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Db 1 CTTGGGCTTGGCCCGG 17

RESULT 1268
LOCUS AR325989 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3391 from patent US 6566127.
ACCESSION AR325989
VERSION AR325989.1 GI:33711797
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3391 20-MAY-2003;
FEATURES Location/Qualifiers
  source      1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GAAGATGCTGAAGACG 1312
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Db 1 GAAGATGTTGAAGAGG 17

RESULT 1269
LOCUS AR327329 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4731 from patent US 6566127.
ACCESSION AR327329
VERSION AR327329.1 GI:33713137
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4731 20-MAY-2003;
FEATURES Location/Qualifiers
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source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GAAGATGCTGAAGAGC 1312
||| ||||| ||||| |||||
Db 1 GAAATGCTGAAGAGG 17

RESULT 1270
AR327483 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 4885 from patent US 6566127.
ACCESSION AR327483
VERSION AR327483.1 GI:33713291
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4885 20-MAY-2003;
FEATURES
source
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1950 GATCATGCGGAGTGCT 1966
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Db 1 GATCATGCTGAGTGCT 17

RESULT 1271
AR328712 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 6114 from patent US 6566127.
ACCESSION AR328712
VERSION AR328712.1 GI:33714520
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6114 20-MAY-2003;
FEATURES
source
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 255 CAAGAGCTGCTGCCG 271
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Db 1 CAAGGTGCTGCTGCCG 17

RESULT 1272
AR329331 17 bp RNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 6733 from patent US 6566127.
ACCESSION AR329331
VERSION AR329331.1 GI:33715139
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6733 20-MAY-2003;
FEATURES
source
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1620 CAGGACCTGGTGGCC 1636
||| ||||| ||||| |||||
Db 1 CAGGACCTGGCGGCAC 17

RESULT 1273
AR329361 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 6763 from patent US 6566127.
ACCESSION AR329361
VERSION AR329361.1 GI:33715169
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6763 20-MAY-2003;
FEATURES
source
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1804 GTCTGTCCTTTGGGT 1820
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Db 1 GTCTGTCCTTTGGGT 17

RESULT 1274
AR398079 17 bp RNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 460 from patent US 6617438.
ACCESSION AR398079
VERSION AR398079.1 GI:40135600
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A.,
Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 460 09-SEP-2003;
FEATURES
source
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned RNA"
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Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 863 TGGTGGAGCTGACGAG 879
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Db 1 TGGTGGAGCTGACGAG 17

RESULT 1275
AR398396
LOCUS AR398396 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 777 from patent US 6617438.
ACCESSION AR398396
VERSION AR398396.1 GI:40136175
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 777 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1744 CCGTGAAGTGGATGCG 1760
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Db 1 CCGATCAAGTGGATGCG 17

RESULT 1276
AR398397
LOCUS AR398397 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 778 from patent US 6617438.
ACCESSION AR398397
VERSION AR398397.1 GI:40136177
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 778 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1751 AGTGGATGGCGCTGAG 1767
|||||
Db 1 AGTGGATGGCGCTGAG 17

RESULT 1277
AR398435
LOCUS AR398435 17 bp RNA linear PAT 18-DEC-2003

DEFINITION Sequence 816 from patent US 6617438.
ACCESSION AR398435
VERSION AR398435.1 GI:40136245
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 816 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GGGCTGGTGCCTCGGA 29
|||||
Db 1 GGGCTGGAGCCCTCTGA 17

RESULT 1278
AR398453
LOCUS AR398453 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 834 from patent US 6617438.
ACCESSION AR398453
VERSION AR398453.1 GI:40136278
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 834 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2149 GACCTGCTGCCCCCGC 2165
|||||
Db 1 GACCTGCAGCCCCCAGC 17

RESULT 1279
AR402298
LOCUS AR402298 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 638 from patent US 6623962.
ACCESSION AR402298
VERSION AR402298.1 GI:40149748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 638 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"

[illegible]

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QY 2324 TGTGTGTGTCGCGTGT 2340
Db 1 TGTGTTTGTGAGTGT 17

RESULT 1285
AR458537 AR458537 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 2214 from patent US 6686188.
DEFINITION AR458537
ACCESSION AR458537
VERSION AR458537.1 GI:42693594
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2214 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 879 GCGGGCAGTGTATG 895
Db 1 GCGAGGCAGTGTGATG 17

RESULT 1286
AR458993 AR458993 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 2670 from patent US 6686188.
DEFINITION AR458993
ACCESSION AR458993
VERSION AR458993.1 GI:42694050
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2670 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2917 CCTGGCGGGCGTGGG 2933
Db 1 CCTGGCGGGCGCGGGG 17

RESULT 1287
AR459099 AR459099 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 2776 from patent US 6686188.
DEFINITION AR459099
ACCESSION AR459099
VERSION AR459099.1 GI:42694156
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2776 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1989 GCCCACCCTTCAAGCAGC 2005
Db 1 GCCCACCCTTCAAGCACC 17

RESULT 1289
AR464165 AR464165 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 7842 from patent US 6686188.
DEFINITION AR464165
ACCESSION AR464165
VERSION AR464165.1 GI:42699222
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7842 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1987 AGCCCCACCTTCAAGCA 2003
Db 1 ACGGCCACCTTCAAGCA 17

RESULT 1288
AR459101 AR459101 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 2778 from patent US 6686188.
DEFINITION AR459101
ACCESSION AR459101
VERSION AR459101.1 GI:42694158
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2778 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1989 GCCCACCCTTCAAGCAGC 2005
Db 1 GCCCACCCTTCAAGCACC 17

RESULT 1289
AR464165 AR464165 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 7842 from patent US 6686188.
DEFINITION AR464165
ACCESSION AR464165
VERSION AR464165.1 GI:42699222
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7842 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1997 TCAAGCAGCTGGTGGAG 2013
Db 1 TGAAGCAGCAGTGGAG 17

RESULT 1290
AR464321 AR464321 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 7998 from patent US 6686188.
DEFINITION AR464321
ACCESSION AR464321
VERSION AR464321.1 GI:42699378
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7998 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1994 CCTTCAGCAGCTGGTG 2010
Db 1 CCATCAGCAGCTGGAG 17

RESULT 1291
AR464324 AR464324 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 8001 from patent US 6686188.
DEFINITION AR464324
ACCESSION AR464324
VERSION AR464324.1 GI:42699381
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 8001 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1997 TCAAGCAGCTGGTGGAG 2013
Db 1 TGAAGCAGCAGTGGAG 17

RESULT 1292
AR464410 AR464410 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 8087 from patent US 6686188.
DEFINITION

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ACCESSION AR464410
VERSION AR464410.1 GI:42699467
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 8087 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGGTGA 869
Db 1 GAGGAGGAAGCTGGAGGA 17

RESULT 1293
AR465048 AR465048 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 8725 from patent US 6686188.
DEFINITION AR465048
ACCESSION AR465048
VERSION AR465048.1 GI:42700105
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 8725 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2049 CGAGTACCTGGACCTGT 2065
Db 1 CGAGTACCTGGACACGT 17

RESULT 1294
AR465049 AR465049 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 8726 from patent US 6686188.
DEFINITION AR465049
ACCESSION AR465049
VERSION AR465049.1 GI:42700106
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 8726 03-FEB-2004;
FEATURES Location/Qualifiers

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2050 GAGTACCTGGACCTGTC 2066
Db 1 GAGTACCTGGACAGTC 17

RESULT 1295
AR465670
LOCUS AR465670 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9347 from patent US 6686188.
ACCESSION AR465670
VERSION AR465670.1 GI:42700727
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9347 03-FEB-2004;
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source Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 190 GACGAGGCTGGGACAC 206
Db 1 GAAGAGGCTGGGACAC 17

RESULT 1296
AR466037/c
LOCUS AR466037 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9714 from patent US 6686188.
ACCESSION AR466037
VERSION AR466037.1 GI:42701094
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9714 03-FEB-2004;
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source Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2945 GGAGGCCCGGAGGTCT 2961
Db 17 GGAGGCCCGGAGGTCT 1

RESULT 1297
AR466184/c
LOCUS AR466184 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9861 from patent US 6686188.
ACCESSION AR466184
VERSION AR466184.1 GI:42701241
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9861 03-FEB-2004;
FEATURES
source Location/Qualifiers
1. .17
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/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 277 GCGCCCAACACCGTCG 293
Db 17 GCGCCCAACACCGTCG 1

RESULT 1298
AR482439
LOCUS AR482439 17 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 3 from patent US 6703200.
ACCESSION AR482439
VERSION AR482439.1 GI:47244871
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hamer, J.E. and Hamer, L.
TITLE Methods and materials for the rapid and high volume production of a gene knock-out library in an organism
JOURNAL Patent: US 6703200-A 3 09-MAR-2004;
FEATURES
source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2095 GCGCAGGACACCCCGAG 2111
Db 1 GCGCAGGAACTCCCGAG 17

RESULT 1299
AR482751/c
LOCUS AR482751 17 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 197 from patent US 6703228.
ACCESSION AR482751
VERSION AR482751.1 GI:47245274
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Landers, J., Jordan, B., Housman, D.E. and Charest, A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: US 6703228-A 197 09-MAR-2004;
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/organism="genomic DNA"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1680 CTTGGGCTGGCCCGG 1696
Db 17 CTTCTGGCTGGCCCGG 1
RESULT 1300
AR483119 17 bp DNA linear PAT 14-MAY-2004
LOCUS
DEFINITION Sequence 565 from patent US 6703228.
ACCESSION AR483119
VERSION AR483119.1 GI:47245642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Landers,J., Jordan,B., Housman,D.E. and Charest,A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: US 6703228-A 565 09-MAR-2004;
FEATURES
source
1. .17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2326 TGTGTGCGGTGTGTGT 2342
Db 1 TGTGTGCGGTGTGTCT 17
RESULT 1301
AX009041 17 bp DNA linear PAT 06-SEP-2000
LOCUS
DEFINITION Sequence 74 from Patent WO963975.
ACCESSION AX009041
VERSION AX009041.1 GI:9996415
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 74 16-DEC-1999;
BIOGNOSTIK GBS (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2923 CGGGGCGTGGGGGGCG 2939
Db 1 CGGGGCGGGCGGGGGCG 17

RESULT 1302
AX216115 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 1557 from Patent WO0159103.
ACCESSION AX216115
VERSION AX216115.1 GI:15526158
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1557 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
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1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 502 CTGGACGTGCTGGAGCG 518
Db 1 CTGGAGGTGCTGGAGAG 17
RESULT 1303
AX216149/c 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 1591 from Patent WO0159103.
ACCESSION AX216149
VERSION AX216149.1 GI:15526192
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1591 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
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1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2932 GGGGGCGGTGGAGGGAG 2948
Db 17 GGGGGCGGGCGGGGAG 1
RESULT 1304
AX272795/c 17 bp RNA linear PAT 29-OCT-2001
LOCUS
DEFINITION Sequence 364 from Patent WO0162911.
ACCESSION AX272795
VERSION AX272795.1 GI:16545532

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 364 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 831 GTGGCTGGTGGTGTGC 847
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Db 17 GTGGCTGGTGGTGTGC 1

RESULT 1305
LOCUS AX272922 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 491 from Patent WO0162911.
ACCESSION AX272922
VERSION AX272922.1 GI:16545659
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 491 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATA 2840
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Db 1 ATATATACATATATATA 17

RESULT 1306
LOCUS AX273044 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 613 from Patent WO0162911.
ACCESSION AX273044
VERSION AX273044.1 GI:16545781
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid

JOURNAL Patent: WO 0162911-A 613 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

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QY 2003 AGCTGGTGGAGGACCTG 2019
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Db 1 AGCTGGTGGAGGACCTG 17

RESULT 1308
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DEFINITION Sequence 1455 from Patent WO0192512.
ACCESSION AX325317
VERSION AX325317.1 GI:18096073
KEYWORDS
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE 1
AUTHORS Knies, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1455 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)

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QY 3241 TGGAGTGATTCAGTG 3257
DB 17 TGGAGTTGTTCCAGTG 1

RESULT 1309
AX325318
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DEFINITION Sequence 1456 from Patent WO0192512.
ACCESSION AX325318
VERSION AX325318.1 GI:18096074
KEYWORDS Nicotiana tabacum (common tobacco)
SOURCE Nicotiana tabacum
ORGANISM Nicotiana tabacum
REFERENCE 1
AUTHORS Knier, E.B., Gampert, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
PATENT: WO 0192512-A 1456 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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QY 3241 TGGAGTGATTCAGTG 3257
DB 1 TGGAGTTGTTCCAGTG 17

RESULT 1310
AX422231/c
LOCUS AX422231 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 567 from Patent WO0188124.
ACCESSION AX422231
VERSION AX422231.1 GI:21525613
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 567 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1434 GCTGGTGAGTACGCGG 1450
DB 17 GCTGAGGAGGACGCGG 1

RESULT 1311
AX423119
LOCUS AX423119 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1455 from Patent WO0188124.
ACCESSION AX423119
VERSION AX423119.1 GI:21526501
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1455 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1568 CCTACCGAGTGCGCGG 1584
DB 1 CCGACGAGTGCGCGG 17

RESULT 1312
AX423120
LOCUS AX423120 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1456 from Patent WO0188124.
ACCESSION AX423120
VERSION AX423120.1 GI:21526502
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1456 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1571 ACCAGGTGCGCGCGG 1587
DB 1 ACGAGGTGCGCGCGG 17

RESULT 1313
AX475039/c
LOCUS AX475039 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 260 from Patent WO0224750.
ACCESSION AX475039
VERSION AX475039.1 GI:22214324
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 024750-A 260 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1527 GCCCGAGGAGCAGCTCA 1543
Db 17 GCCCGAGGTGCAGCTCA 1
RESULT 1314
AX530931
LOCUS AX530931 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 440 from Patent EP1239051.
ACCESSION AX530931
VERSION AX530931.1 GI:25253653
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 440 11-SEP-2002;
Aeomica, Inc. (US)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 544 GCGGGGCTGCCGCCCAA 560
Db 1 GAGGCGCTGCCGCCCAA 17
RESULT 1315
AX530944
LOCUS AX530944 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 453 from Patent EP1239051.
ACCESSION AX530944
VERSION AX530944.1 GI:25253678
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 453 11-SEP-2002;
Aeomica, Inc. (US)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 454 11-SEP-2002;
Aeomica, Inc. (US)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2239 CACCCCTGCTGCTGCTGC 2255
Db 1 CAACCTGCTGCTGCTGC 17
RESULT 1317
AX531999
LOCUS AX531999 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1508 from Patent EP1239051.
ACCESSION AX531999
VERSION AX531999.1 GI:25255764
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1508 11-SEP-2002;
Aeomica, Inc. (US)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
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Db 1 CAACCTGCTGCTGCTGC 17
RESULT 1317
AX531999
LOCUS AX531999 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1508 from Patent EP1239051.
ACCESSION AX531999
VERSION AX531999.1 GI:25255764
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1508 11-SEP-2002;
Aeomica, Inc. (US)
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QY 3671 TGGCTCAGGGTGTCTC 3687
Db 1 TGGCTCAGGGTGTCTC 17
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RESULT 1318
AX544529      AX544529      17 bp      DNA      linear      PAT 26-NOV-2002
LOCUS
DEFINITION    Sequence 42 from Patent EP1243660.
ACCESSION     AX544529
VERSION       AX544529.1 GI:25809740
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE
AUTHORS       Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE         Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL       Patent: EP 1243660-A 42 25-SEP-2002;
              Aeomica, Inc. (US)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3697 CCCAGTGCATGGTGCC 3713
Db 1 CCCAGTCTGGTGGAC 17

RESULT 1319
AX544984/c    AX544984      17 bp      DNA      linear      PAT 26-NOV-2002
LOCUS
DEFINITION    Sequence 497 from Patent EP1243660.
ACCESSION     AX544984
VERSION       AX544984.1 GI:25810195
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE
AUTHORS       Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE         Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL       Patent: EP 1243660-A 497 25-SEP-2002;
              Aeomica, Inc. (US)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3697 CCCAGTGCATGGTGCC 3713
Db 1 CCCAGTCTGGTGGAC 17

RESULT 1320
AX578222      AX578222      17 bp      RNA      linear      PAT 10-JAN-2003
LOCUS
DEFINITION    Sequence 60 from Patent WO0211674.
ACCESSION     AX578222
VERSION       AX578222.1 GI:27647424
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE
AUTHORS       Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.
TITLE         Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL       Patent: WO 0211674-A 60 14-FEB-2002;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
              Thompson, James (US)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3468 ATATCTATATATATAT 3484
Db 1 ATCTGTATATATATAT 17

RESULT 1321
AX578223      AX578223      17 bp      RNA      linear      PAT 10-JAN-2003
LOCUS
DEFINITION    Sequence 61 from Patent WO0211674.
ACCESSION     AX578223
VERSION       AX578223.1 GI:27647425
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE
AUTHORS       Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.
TITLE         Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL       Patent: WO 0211674-A 61 14-FEB-2002;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3466 ATATCTATATATATATA 3482
Db 1 ATATCTGTATATATATA 17

RESULT 1322
AX649233      AX649233      17 bp      DNA      linear      PAT 22-MAR-2003
LOCUS
DEFINITION    Sequence 1073 from Patent EP1273660.
ACCESSION     AX649233
VERSION       AX649233.1 GI:29152051
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE
AUTHORS       Gu, Y.
TITLE         Human sodium-hydrogen exchanger like protein 1
JOURNAL       Patent: EP 1273660-A 1073 08-JAN-2003;
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Query Match
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  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 548 GGCTGCGCGCCACACAG 564
Db 1 GGCTGCGCGCCTAACAG 17

RESULT 1323
AX671977/c
LOCUS AX671977 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 422 from Patent WO03004526.
ACCESSION AX671977
VERSION AX671977.1 GI:293330325
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens (human)
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or resistance to viruses and their use as
  medicines
JOURNAL Patent: WO 03004526-A 422 16-JAN-2003;
  Molecular Engines Laboratories (FR)
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QY 807 TATTGGCTTTTCATC 823
Db 17 TATTGGCTTTTCATC 1

RESULT 1324
AX676121/c
LOCUS AX676121 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 74 from Patent WO02059381.
ACCESSION AX676121
VERSION AX676121.1 GI:29333805
KEYWORDS
SOURCE
  ORGANISM
    Mus sp.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1
AUTHORS Slaugenhaupt,S. and Gusella,J.F.
TITLE Gene for identifying individuals with familial dysautonomia
JOURNAL Patent: WO 02059381-A 74 01-AUG-2002;
  The General Hospital Corporation (US)
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QY 1530 CGAGGACGAGCTCACCT 1546
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RESULT 1325
AX687732
LOCUS AX687732 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 464 from Patent EPI281758.
ACCESSION AX687732
VERSION AX687732.1 GI:29410428
KEYWORDS
SOURCE
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    Homo sapiens (human)
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
JOURNAL Patent: EP 1281758-A 464 05-FEB-2003;
  Aeomica, Inc. (US)
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QY 1260 CAAGGACCGCGCGCCA 1276
Db 1 CAAGGCCCTGGCGGCCA 17

RESULT 1326
AX687796
LOCUS AX687796 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 528 from Patent EPI281758.
ACCESSION AX687796
VERSION AX687796.1 GI:29410492
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens (human)
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
JOURNAL Patent: EP 1281758-A 528 05-FEB-2003;
  Aeomica, Inc. (US)
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QY 3385 TGTCACGAGCGAGGAGA 3401
Db 1 TGCCACAGCGAGGAGA 17

RESULT 1327
AX687852
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LOCUS AX687852 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 584 from Patent EP1281758.
ACCESSION AX687852
VERSION AX687852.1 GI:29410550
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL
PATENT: EP 1281758-A 584 05-FEB-2003;
Aeomica, Inc. (US)
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QY 381 AGGCATCAAGCTGGGC 397
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Db 1 AGGCATCCAGCTGGGC 17
RESULT 1328
AX688383/c
LOCUS AX688383 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1115 from Patent EP1281758.
ACCESSION AX688383
VERSION AX688383.1 GI:29411083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL
PATENT: EP 1281758-A 1115 05-FEB-2003;
Aeomica, Inc. (US)
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QY 3 CGATGGCACAGGCTGG 19
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Db 17 GGATGGCACCGTGGTGG 1
RESULT 1329
AX688727/c
LOCUS AX688727 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1459 from Patent EP1281758.
ACCESSION AX688727
VERSION AX688727.1 GI:29411431
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL
PATENT: EP 1281758-A 1459 05-FEB-2003;
Aeomica, Inc. (US)
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QY 3 CGATGGCACAGGCTGG 19
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Db 17 GGATGGCACCGTGGTGG 1
RESULT 1330
AX690707/c
LOCUS AX690707 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3439 from Patent EP1281758.
ACCESSION AX690707
VERSION AX690707.1 GI:29413614
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL
PATENT: EP 1281758-A 3439 05-FEB-2003;
Aeomica, Inc. (US)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
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QY 55 CTGCAGGTGCTGAATGC 71
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Db 17 CTGCAGGTGCTGCCTGC 1
RESULT 1331
AX722945/c
LOCUS AX722945 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 632 from Patent WO03025176.
ACCESSION AX722945
VERSION AX722945.1 GI:30423446
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS Teclerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL
PATENT: WO 03025176-A 632 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Location/Qualifiers

REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL
PATENT: EP 1281758-A 1459 05-FEB-2003;
Aeomica, Inc. (US)
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/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 17 CTGCAGGTGCTGCCTGC 1
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DEFINITION Sequence 3439 from Patent EP1281758.
ACCESSION AX690707
VERSION AX690707.1 GI:29413614
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL
PATENT: EP 1281758-A 3439 05-FEB-2003;
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3378 TGCTGTGTGTCGCCAGGC 3394
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Db 17 TGCTGTGTGTCGCCAGGC 1
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LOCUS AX722945 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 632 from Patent WO03025176.
ACCESSION AX722945
VERSION AX722945.1 GI:30423446
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS Teclerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL
PATENT: WO 03025176-A 632 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Location/Qualifiers


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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 249 GATGGACAAGAGCTGC 265
Db 1 GATGCACAAGACCTGC 17

RESULT 1332
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LOCUS AX722971 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 658 from Patent WO03025176.
ACCESSION AX722971
VERSION AX722971.1 GI:30423472
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 658 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2589 GCTCGGCCCTCCACAC 2605
Db 1 GATCGTCCCTCCACAC 17

RESULT 1333
AX724318
LOCUS AX724318 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2005 from Patent WO03025176.
ACCESSION AX724318
VERSION AX724318.1 GI:30503661
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 2005 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2944 GGGAGGCCCCAGGGGTC 2960
Db 17 GGGAGGCCCCAGGGGATC 1

RESULT 1336
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QY 2111 GTCCAGCTCCTCAGG 2127
Db 1 GATCCAGCTTCTCAGG 17

RESULT 1334
AX727665/c
LOCUS AX727665 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5352 from Patent WO03025176.
ACCESSION AX727665
VERSION AX727665.1 GI:30507008
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5352 27-MAR-2003;
Molecular Engines Laboratories (FR)
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"

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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2341 GTGTGTGTGTGCACATC 2357
Db 17 GTGTGTGTGTGAAGATC 1

RESULT 1335
AX729266/c
LOCUS AX729266 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 900 from Patent WO03025175.
ACCESSION AX729266
VERSION AX729266.1 GI:30508609
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 900 27-MAR-2003;
Molecular Engines Laboratories (FR)
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QY 2944 GGGAGGCCCCAGGGGTC 2960
Db 17 GGGAGGCCCCAGGGATC 1

RESULT 1336
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AX734014
LOCUS AX734014 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5648 from Patent WO03025175.
ACCESSION AX734014
VERSION AX734014.1 GI:30513357
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 5648 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2206 GGTCCCAACAATGTGA 2222
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Db 1 GATCCCAACAATGTCA 17

RESULT 1337
AX734582
LOCUS AX734582 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 172 from Patent WO03025177.
ACCESSION AX734582
VERSION AX734582.1 GI:30513859
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 172 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3065 GTTCCCAACCCCAACA 3081
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Db 1 GATCCCAACCCCAACA 17

RESULT 1338
AX735982
LOCUS AX735982 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1572 from Patent WO03025177.
ACCESSION AX735982
VERSION AX735982.1 GI:30515259
KEYWORDS Homo sapiens (human)
SOURCE

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ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 1572 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Qy 3741 GATTTTGTAAACCCAGC 3757
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Db 1 GATCTTGTAAACCCATC 17

RESULT 1339
AX736612
LOCUS AX736612 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2202 from Patent WO03025177.
ACCESSION AX736612
VERSION AX736612.1 GI:30515900
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2202 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2314 GGTCTGTGTGTGTGTGT 2330
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Db 1 GATCTGTGTGTGTGTGT 17

RESULT 1340
AX737215/c
LOCUS AX737215 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2805 from Patent WO03025177.
ACCESSION AX737215
VERSION AX737215.1 GI:30516503
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use

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Patent: WO 03025177-A 2805 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1314 TGCCACTGCAAGGACC 1330
Db 17 TGCCACGGACAAGGATC 1

RESULT 1341
AX737594/c
LOCUS AX737594 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3184 from Patent WO03025177.
ACCESSION AX737594
VERSION AX737594.1 GI:30516882
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03025177-A 3184 27-MAR-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
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Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 501 GCTGGACGTGCTGGAC 517
Db 17 GCTGGACCTGCTGGATC 1

RESULT 1342
AX733829/c
LOCUS AX733829 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 176 from Patent WO03037931.
ACCESSION AX733829
VERSION AX733829.1 GI:32166526
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 176 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
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            /db_xref="taxon:9606"

thereof as medicaments
Patent: WO 03025177-A 2805 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2239 CACCCTGCTGCTGGTGC 2255
Db 17 CCCCCCTGCTGCTGTTC 1

RESULT 1343
AX753876/c
LOCUS AX753876 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 223 from Patent WO03037931.
ACCESSION AX753876
VERSION AX753876.1 GI:32166573
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 223 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
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Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2432 GGTCTCTCTGACTGGTGC 2448
Db 17 GGACTTCTGACTGGTGC 1

RESULT 1344
AX759942
LOCUS AX759942 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3263 from Patent WO03040369.
ACCESSION AX759942
VERSION AX759942.1 GI:32254558
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3263 15-MAY-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2747 GAGCCTTTTACCTTTTAT 2763
Db 1 GATCCCTTGGCTTTTAT 17
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RESULT 1345
AX760079
LOCUS AX760079 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3400 from Patent WO03040369.
ACCESSION AX760079
VERSION AX760079.1 GI:32254695
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
JOURNAL medicines
Molecular Engines Laboratories (FR)
FEATURES Patent: WO 03040369-A 3400 15-MAY-2003;
source Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2206 GGTCCCCCAACAATGTGA 2222
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Db 1 GATCCCCCAACAATGTCA 17

RESULT 1346
AX761940
LOCUS AX761940 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5261 from Patent WO03040369.
ACCESSION AX761940
VERSION AX761940.1 GI:32256556
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
1
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
JOURNAL medicines
Molecular Engines Laboratories (FR)
FEATURES Patent: WO 03040369-A 5261 15-MAY-2003;
source Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1068 GAGCTCCACACACACAC 1084
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Db 1 GATCCCCCAACAATGTCA 17

RESULT 1347
AX782224/c
LOCUS AX782224 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 555 from Patent WO03050284.
ACCESSION AX782224
VERSION AX782224.1 GI:32950073
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
1
REFERENCE Guo,J.
AUTHORS Human prostate cancer candidate protein 1
TITLE Patent: WO 03050284-A 555 19-JUN-2003;
JOURNAL Amersham Biosciences (SV) Corp. (US)
FEATURES Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3280 CTTTTCAGGAGAAATTA 3296
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Db 17 CTTTTCAGGAGGCAATTA 1

RESULT 1348
AX783664
LOCUS AX783664 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 1995 from Patent WO03050284.
ACCESSION AX783664
VERSION AX783664.1 GI:32951513
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
1
REFERENCE Guo,J.
AUTHORS Human prostate cancer candidate protein 1
TITLE Patent: WO 03050284-A 1995 19-JUN-2003;
JOURNAL Amersham Biosciences (SV) Corp. (US)
FEATURES Location/Qualifiers
1. .17
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1222 TTCGCCAGGTGTCAT 1238
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Db 1 TTCGCCAGGAGTCAT 17

RESULT 1349
AX783665
LOCUS AX783665 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 1996 from Patent WO03050284.
ACCESSION AX783665
VERSION AX783665.1 GI:32951514
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
1
REFERENCE Guo,J.
AUTHORS Human prostate cancer candidate protein 1
TITLE Patent: WO 03050284-A 1996 19-JUN-2003;
JOURNAL Amersham Biosciences (SV) Corp. (US)
FEATURES Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 TCGGCCAGGTGGTCATG 1239
Db 1 TCAGCCAGGAGGTCATG 17

RESULT 1350
BD002054
LOCUS 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Agent for retarding the conversion of hormone-dependent cancer into
hormone-independent cancer.
ACCESSION BD002054
VERSION JP 200178202-A/5.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
Matsutani,T. and Naito,K.
AUTHORS Agent for retarding the conversion of hormone-dependent cancer into
TITLE hormone-independent cancer
JOURNAL Patent: JP 2000178202-A 5 27-JUN-2000;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Artificial Sequence
PN JP 2000178202-A/5
PD 27-JUN-2000
PR TOSHIYA MATSUTANI, KENICHIRO NAITO
PC A61K38/04,A61K38/22,A61K45/00,A61P13/08,A61P35/00//C07K7/23 CC
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.

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/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1618 CACAGGAGCTGGCTGC 1634
Db 1 CAYMGRGACTGGCGC 17

RESULT 1351
BD067798
LOCUS 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067798
VERSION BD067798.1 GI:22613401
KEYWORDS JP 2001511003-A/638.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
Akhtar,S., Fell,P. and McSwiggen,J.A.
AUTHORS Enzymatic nucleic acid treatment of diseases or conditions related
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
JOURNAL Patent: JP 2001511003-A 638 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1803 CCGTCGGTCCTTTGGGG 1819
Db 1 CATCAGGTCCTTTGGGG 17

RESULT 1352
BD104450
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104450
VERSION BD104450.1 GI:22650024
KEYWORDS WO 0192572-A/554.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
Nishida,M.
AUTHORS Kit and method for determining HLA type
TITLE Patent: WO 0192572-A 554 06-DEC-2001;
JOURNAL NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/554
PD 06-DEC-2001
PR 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
MATSUMURA,
PI SHOGO MORIYA,MICHIO NISHIDA
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
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FT /organism='Artificial Sequence'.

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/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GCTCGAGTCGCTGGCG 1159
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Db      1  GCTGGGGTGCCTGCCG 17

RESULT 1353
DOGP36202/c
LOCUS   18 bp      DNA      linear      MAM 11-MAR-1996
DEFINITION
DOGP36202
ACCESSION
L24249.1  GI:401916
VERSION
PCR identification; PCR primer; STS.
SEGMENT
2 of 2
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1  (bases 1 to 18)
Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
One hundred and one new simple sequence repeat-based markers for
the canine genome
Mamm. Genome 6 (3), 192-195 (1995)
JOURNAL
MEDLINE
95268214
PUBMED
7749226
COMMENT
Original source text: Canis familiaris (library: E. Ostrander, in
pBluescript+) adult spleen DNA.
Submitted by:
Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
e-mail: EOostrander@hl.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
PCR Cycles: 33
Final Extension: 74 degrees C for 5.00 minutes.
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/mol_type="genomic DNA"
/db_xref="taxon:9615"
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primer_bind
complement(1..18)

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1948  ATGATCATGCGGGAGTG 1964
Db      17  ATGCTCATGGGGAGTG 1

RESULT 1354
A88187/c
LOCUS   18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION
Sequence 335 from Patent WO9833904.
ACCESSION
A88187
VERSION
A88187.1  GI:6736757
KEYWORDS
SOURCE
unidentified
ORGANISM
unidentified
REFERENCE
1  (bases 1 to 18)
Brysch,W. and Schlingensiepen,K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
PATENT: WO 9833904-A 335 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
JOURNAL
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Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1948  ATGATCATGCGGGAGTG 1964
Db      17  ATGCTCATGGGGAGTG 1

RESULT 1355
A90154/c
LOCUS   18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION
Sequence 335 from Patent EP0856579.
ACCESSION
A90154
VERSION
A90154.1  GI:6738668
KEYWORDS
SOURCE
unidentified
ORGANISM
unidentified
REFERENCE
1  (bases 1 to 18)
Brysch,W.D. and Schlingensiepen,K.D.
An antisense oligonucleotide preparation method
PATENT: EP 0856579-A 335 05-AUG-1998;
BIOGNOSTIK GES (DE)
JOURNAL
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1792  CACCAGAGTGACGTCTG 1808
Db      17  CACCAGAGTGATGTGTG 1

RESULT 1356
A90829/c
LOCUS   18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION
Sequence 8 from Patent WO9830687.
ACCESSION
A90829
VERSION
A90829.1  GI:6739239
KEYWORDS
SOURCE
unidentified
ORGANISM
unidentified
REFERENCE
1  (bases 1 to 18)
Poustka,A. and Mollenhauer,J.
PROTEIN CONTAINING AN SRCR DOMAIN
PATENT: WO 9830687-A 8 16-JUL-1998;
DEUTSCHES KREBSFORSCH (DE); POUSTKA ANNEMARIE (DE)
JOURNAL
FEATURES
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Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1792  CACCAGAGTGACGTCTG 1808
Db      17  CACCAGAGTGATGTGTG 1

RESULT 1357
A90829/c
LOCUS   18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION
Sequence 8 from Patent WO9830687.
ACCESSION
A90829
VERSION
A90829.1  GI:6739239
KEYWORDS
SOURCE
unidentified
ORGANISM
unidentified
REFERENCE
1  (bases 1 to 18)
Poustka,A. and Mollenhauer,J.
PROTEIN CONTAINING AN SRCR DOMAIN
PATENT: WO 9830687-A 8 16-JUL-1998;
DEUTSCHES KREBSFORSCH (DE); POUSTKA ANNEMARIE (DE)
JOURNAL
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Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1148  AGCTGCTGCCGACCCC 1164
Db      17  AGCTGCTGCAGACCAC 1

RESULT 1357

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A91171/c
LOCUS A91171 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 5 from Patent WO9827206.
ACCESSION A91171
VERSION A91171.1 GI:6740207
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Icard-Liepkalns, C., Mallet, J. and Corresponding, N.A.
JOURNAL Patent: WO 9827206-A 5 25-JUN-1998;
ICARD LIEPKALNS CHRISTINE (FR); MALLET JACQUES (FR)
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/db_xref="taxon:32644"
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Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2092 GGTGGCCAGACACCCC 2108
Db 18 GGTGGCCAGACACCGC 2
RESULT 1358
AR036682/c
LOCUS AR036682 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 21 from patent US 5800811.
ACCESSION AR036682
VERSION AR036682.1 GI:5954538
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hall, F.L., Nimni, M.E., Tuan, T.-L., Wu, L. and Cheung, D.T.
TITLE Artificial skin prepared from collagen matrix containing transforming growth factor-beta, having a collagen binding site
JOURNAL Patent: US 5800811-A 21 01-SEP-1998;
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1354 GAGATGATGATGATGAT 1370
Db 18 GTGATGATGATGATGAT 2
RESULT 1359
AR062605/c
LOCUS AR062605 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5843738.
ACCESSION AR062605
VERSION AR062605.1 GI:5990296
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C.Frank, and Mirabelli, C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5843738-A 5 01-DEC-1998;
FEATURES
source
1..18
Location/Qualifiers

A91171/c
LOCUS A91171 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 5 from Patent WO9827206.
ACCESSION A91171
VERSION A91171.1 GI:6740207
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Icard-Liepkalns, C., Mallet, J. and Corresponding, N.A.
JOURNAL Patent: WO 9827206-A 5 25-JUN-1998;
ICARD LIEPKALNS CHRISTINE (FR); MALLET JACQUES (FR)
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/mol_type="unassigned DNA"
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Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2092 GGTGGCCAGACACCCC 2108
Db 18 GGTGGCCAGACACCGC 2
RESULT 1358
AR036682/c
LOCUS AR036682 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 21 from patent US 5800811.
ACCESSION AR036682
VERSION AR036682.1 GI:5954538
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hall, F.L., Nimni, M.E., Tuan, T.-L., Wu, L. and Cheung, D.T.
TITLE Artificial skin prepared from collagen matrix containing transforming growth factor-beta, having a collagen binding site
JOURNAL Patent: US 5800811-A 21 01-SEP-1998;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1354 GAGATGATGATGATGAT 1370
Db 18 GTGATGATGATGATGAT 2
RESULT 1359
AR062605/c
LOCUS AR062605 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5843738.
ACCESSION AR062605
VERSION AR062605.1 GI:5990296
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C.Frank, and Mirabelli, C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5843738-A 5 01-DEC-1998;
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source
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Location/Qualifiers

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Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2690 CTTTCCCACTTCCACC 2706
Db 18 CTTTCCCACTGCCCATC 2
RESULT 1360
AR078582/c
LOCUS AR078582 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 8 from patent US 5962672.
ACCESSION AR078582
VERSION AR078582.1 GI:10005328
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Coswert, L.M.
TITLE Antisense modulation of RhoB expression
JOURNAL Patent: US 5962672-A 8 05-OCT-1999;
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1998 CAAGCAGCTGTGGAGG 2014
Db 17 CAAGCAGCTGTGGTGG 1
RESULT 1361
AR080699
LOCUS AR080699 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 4 from patent US 5968826.
ACCESSION AR080699
VERSION AR080699.1 GI:10007429
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C.Frank., Condon, T.P. and Coswert, L.M.
TITLE Antisense inhibition of integrin.alpha.4 expression
JOURNAL Patent: US 5968826-A 4 19-OCT-1999;
FEATURES
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1965 CTGGCATGCCGCCCT 1981
Db 2 CTGGCATGCCGCCACT 18
RESULT 1362
AR082993
LOCUS AR082993 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 19 from patent US 5976798.
ACCESSION AR082993

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide inhibition of cell adhesion
JOURNAL Patent: US 6169079-A 5 02-JAN-2001;
FEATURES Location/Qualifiers
source 1..18
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2690 CTTTCCACATCCACC 2706
Db 18 CTTTCCACTGCCATC 2

RESULT 1368
ARI138072
LOCUS ARI138072 18 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 82 from patent US 6197584.
ACCESSION ARI138072
VERSION ARI138072.1 GI:14479581
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank. and Cowsert,L.M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: US 6197584-A 82 06-MAR-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
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Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2132 ACTCCGTGTTGCCAC 2148
Db 2 ACTCCGTGTTGCCAC 18

RESULT 1369
ARI145511
LOCUS ARI145511 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 10 from patent US 6217658.
ACCESSION ARI145511
VERSION ARI145511.1 GI:15108700
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Galun,E., Nahor,O. and Blum,H.E.
TITLE Pharmaceutical composition for treating hepatitis B virus (HBV) infection
JOURNAL Patent: US 6217658-A 10 17-APR-2001;
FEATURES Location/Qualifiers
source 1..18
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 588 GGAGTTCCTCACTGCAAG 604
Db 1 GGAATTCCTCACTGCAAG 17

RESULT 1370
ARI162682
LOCUS ARI162682 18 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 4 from patent US 6258790.
ACCESSION ARI162682
VERSION ARI162682.1 GI:16229996
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank., Condon,T.P. and Cowsert,L.M.
TITLE Antisense modulation of integrin.alpha.4 expression
JOURNAL Patent: US 6258790-A 4 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..18
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1965 CTGGCATCGCGGCCT 1981
Db 2 CTGGCATCGCGGCCT 18

RESULT 1371
BD178738/c
LOCUS BD178738 18 bp DNA linear PAT 16-APR-2003
DEFINITION Gene panel for genes involving liver regeneration.
ACCESSION BD178738
VERSION BD178738.1 GI:30016005
KEYWORDS WO 02077222-A/76.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Yokoya,F., Okutsu,T., Mori,M., Yoshiyuki, Takahara, Fukuda,H., Aburatani,H. and Sonaka,I.
TITLE Gene panel for genes involving liver regeneration
JOURNAL Patent: WO 02077222-A 76 03-OCT-2002;
COMMENT AJINOMOTO CO INC,FUMIHIKO YOKOYA,TOMOHISA OKUTSU,MAIKO MORI,YOSHIYUKI TAKAHARA,HISAO FUKUDA,HIROYUKI ABURATANI,ICHIRO SONAKA
OS Artificial Sequence
PN WO 02077222-A/76
PD 03-OCT-2002
PF 13-MAR-2002 WO 2002JP002372
PR 13-MAR-2001 JP 01P 070940
PI FUMIHIKO YOKOYA,TOMOHISA OKUTSU,MAIKO MORI,YOSHIYUKI PI
TAKAHARA,HISAO FUKUDA,
PI HIROYUKI ABURATANI,ICHIRO SONAKA
PC C12N15/09,C12Q1/68,G01N33/15,G01N33/50,G01N37/00 CC
Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..18
/organism='Artificial Sequence'.
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1339 CTGGTCTCTGAGATGGA 1355
 DB 18 CTGGTGGCTGGGATGGA 2

RESULT 1372
 BD226623 18 bp DNA linear PAT 17-JUL-2003
 LOCUS Antisense modulation of CD40 expression.
 DEFINITION BD226623
 ACCESSION BD226623
 VERSION BD226623.1 GI:33036393
 KEYWORDS JP 2002513593-A/82.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Bennett,C.F. and Cowsert,L.M.
 TITLE Antisense modulation of CD40 expression
 JOURNAL Patent: JP 2002513593-A 82 14-MAY-2002;
 ISIS PHARMACEUTICALS INC
 COMMENT OS Unidentified
 PN JP 2002513593-A/82
 PD 14-MAY-2002
 PF 22-APR-1999 JP 2000547271
 PR 01-MAY-1998 US 09/071433
 PI C FRANK BENNETT, LEX M COWSERT
 PC C12N15/09,A61K9/10,A61K45/00,A61K48/00,A61P1/00,A61P11/06, PC
 A61P17/06,
 PC A61P29/00,A61P35/00,A61P37/02,A61P43/00,C12P19/34,
 PC C12Q1/68,
 PC C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Antisense modulation of CD40 expression
 FH Key Location/Qualifiers
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 FT /organism='Unidentified'.
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 /mol_type='genomic DNA'
 /db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2132 ACTCCGTGTTGCCAC 2148
 DB 2 ACTGCTGTTGCCAC 18

RESULT 1373
 BD227742 18 bp DNA linear PAT 17-JUL-2003
 LOCUS Antisense modulation of integrin alph 4 expression.
 DEFINITION BD227742
 ACCESSION BD227742
 VERSION BD227742.1 GI:33037512
 KEYWORDS JP 2002526555-A/4.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Bennett,F.C., Condon,T.P. and Cowsert,L.M.
 TITLE Antisense modulation of integrin alph 4 expression
 JOURNAL Patent: JP 2002526555-A 4 20-AUG-2002;
 ISIS PHARMACEUTICALS INC
 COMMENT OS Artificial Sequence
 PN JP 2002526555-A/4
 PD 20-AUG-2002
 PF 19-AUG-1999 JP 2000574727
 PR 05-OCT-1998 US 09/166203
 PI FRANK C BENNETT, THOMAS P CONDON, LEX M COWSERT PC

QY 1339 CTGGTCTCTGAGATGGA 1355
 DB 18 CTGGTGGCTGGGATGGA 2

RESULT 1372
 BD226623 18 bp DNA linear PAT 17-JUL-2003
 LOCUS Antisense modulation of CD40 expression.
 DEFINITION BD226623
 ACCESSION BD226623
 VERSION BD226623.1 GI:33036393
 KEYWORDS JP 2002513593-A/82.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Bennett,C.F. and Cowsert,L.M.
 TITLE Antisense modulation of CD40 expression
 JOURNAL Patent: JP 2002513593-A 82 14-MAY-2002;
 ISIS PHARMACEUTICALS INC
 COMMENT OS Unidentified
 PN JP 2002513593-A/82
 PD 14-MAY-2002
 PF 22-APR-1999 JP 2000547271
 PR 01-MAY-1998 US 09/071433
 PI C FRANK BENNETT, LEX M COWSERT
 PC C12N15/09,A61K9/10,A61K45/00,A61K48/00,A61P1/00,A61P11/06, PC
 A61P17/06,
 PC A61P29/00,A61P35/00,A61P37/02,A61P43/00,C12P19/34,
 PC C12Q1/68,
 PC C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Antisense modulation of CD40 expression
 FH Key Location/Qualifiers
 FT source 1..18
 FT /organism='Unidentified'.
 FEATURES source
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 /mol_type='genomic DNA'
 /db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2132 ACTCCGTGTTGCCAC 2148
 DB 2 ACTGCTGTTGCCAC 18

RESULT 1373
 BD227742 18 bp DNA linear PAT 17-JUL-2003
 LOCUS Antisense modulation of integrin alph 4 expression.
 DEFINITION BD227742
 ACCESSION BD227742
 VERSION BD227742.1 GI:33037512
 KEYWORDS JP 2002526555-A/4.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Bennett,F.C., Condon,T.P. and Cowsert,L.M.
 TITLE Antisense modulation of integrin alph 4 expression
 JOURNAL Patent: JP 2002526555-A 4 20-AUG-2002;
 ISIS PHARMACEUTICALS INC
 COMMENT OS Artificial Sequence
 PN JP 2002526555-A/4
 PD 20-AUG-2002
 PF 19-AUG-1999 JP 2000574727
 PR 05-OCT-1998 US 09/166203
 PI FRANK C BENNETT, THOMAS P CONDON, LEX M COWSERT PC

C07H21/04,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/ PC
 00,A61P11/16,
 PC A61P3/00,A61P11/06,A61P25/28,A61P29/00,A61P29/00,A61P35/00, PC
 A61P35/04,
 PC A61P37/06,A61P43/00,C12N15/09,C12Q1/02,C12Q1/68,C12N15/00 CC
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 FH Key 1..18
 FT source /organism='Artificial Sequence'.
 FT Location/Qualifiers
 1..18
 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1965 CTGGCATCGCGCCCT 1981
 DB 2 CTGGCATCGCGCCACT 18

RESULT 1374
 BD250528 18 bp DNA linear PAT 17-JUL-2003
 LOCUS Identification of genetic targets for modulation by
 DEFINITION oligonucleotides and generation of oligonucleotides for gene
 modulation.
 ACCESSION BD250528
 VERSION BD250528.1 GI:33060298
 KEYWORDS JP 2002511276-A/82.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M.,
 Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
 TITLE Identification of genetic targets for modulation by
 oligonucleotides and generation of oligonucleotides for gene
 modulation
 JOURNAL Patent: JP 2002511276-A 82 16-APR-2002;
 ISIS PHARMACEUTICALS INC
 COMMENT OS Artificial Sequence
 PN JP 2002511276-A/82
 PD 16-APR-2002
 PF 13-APR-1999 JP 2000543647
 PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
 LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
 M SASNOR,
 PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
 BORCHERS,
 PI TIMOTHY A VIKKARS
 PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
 C12N15/00
 CC Antisense Oligonucleotide
 FH Key Location/Qualifiers
 FT source 1..18
 FT /organism='Artificial Sequence'.
 FT Location/Qualifiers
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 /mol_type='genomic DNA'
 /db_xref='taxon:32630'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2132 ACTCCGTGTTGCCAC 2148
 DB 2 ACTGCTGTTGCCAC 18

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RESULT 1375
CQ788499/c
LOCUS          CQ788499          18 bp      DNA          linear          PAT 24-MAR-2004
DEFINITION     Sequence 76 from Patent WO2004020619.
ACCESSION      CQ788499
VERSION        CQ788499.1  GI:45723264
SOURCE         synthetic construct
ORGANISM       artificial construct
REFERENCE      1
AUTHORS        Constien,R., Mudde,G., Schroeder,A., Yu,P. and Hanke,P.
TITLE          Modified phospholipase C-gamma-2, expression products, and
non-human animal models comprising said genes, and therapeutic uses
JOURNAL        Patent: WO 2004020619-A 76 11-MAR-2004;
Ingenium Pharmaceuticals AG (DE)
FEATURES       source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer p1cg2-60"

Query Match          0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2305 CAGAGCTTTCGTCTGTG 2321
Db 18 CAGTCTTCGTCTGTG 2

RESULT 1376
E05446/c
LOCUS          E05446          18 bp      DNA          linear          PAT 29-SEP-1997
DEFINITION     DNA sequence of synthetic terminator.
ACCESSION      E05446
VERSION        E05446.1  GI:2173635
KEYWORDS       JP 1993244940-A/6.
SOURCE         synthetic construct
ORGANISM       artificial construct
REFERENCE      1 (bases 1 to 18)
AUTHORS        Yamaguchi,T., Fukushi,H., Hirai,K., Aoyama,S., Yamaguchi,T.,
Iritani,K., Hayashi,K., Yoneda,Y., Okawa,S. and Kamogawa,K.
TITLE          RECOMBINANT AVIPOX VIRUS AND VACCINE COMPOSED THEREOF
JOURNAL        Patent: JP 1993244940-A 6 24-SEP-1993;
NIPPON ZEON CO LTD, SHIONOGI & CO LTD
COMMENT        OS Artificial Gene
OC Artificial sequence; Genes.
PN JP 1993244940-A/6
PD 24-SEP-1993
PF 04-MAR-1992 JP 1992082800
PR 09-AUG-1991 JP 91P 224868
PI YAMAGUCHI TAKESHI, FUKUSHI HIDEOTO, HIRAI KATSUYA, PI Aoyama
SHIGEMI,
PI YAMAGUCHI TAKESHI, IIRITANI KOICHI, HAYASHI KOJI, PI YONEDA
YASUHIRO,
PI OKAWA SETSUKO, KAMOGAWA KOICHI
PC C12N7/01,A61K39/275,C12N15/40,C12N15/86//C12P21/02,(C12P21/02,
PC C12R1/92);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
LOCATION/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

RESULT 1377
E39158/c
LOCUS          E39158          18 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     DNA encoding novel fused protein and process for producing useful
protein mediating the expression thereof.
ACCESSION      E39158
VERSION        E39158.1  GI:13019232
KEYWORDS       JP 1999341991-A/4.
SOURCE         synthetic construct
ORGANISM       artificial construct
REFERENCE      1 (bases 1 to 18)
AUTHORS        Seiji,S., Masahiko,H., Toshiyuki,K. and Masaaki,K.
TITLE          DNA encoding novel fused protein and process for producing useful
protein mediating the expression thereof
JOURNAL        Patent: JP 1999341991-A 3 14-DEC-1999;
ITO HAM KK, JUZO UDAKA
COMMENT        OS Artificial Sequence
PN JP 1999341991-A/3
PD 14-DEC-1999
PF 30-MAR-1999 JP 1999089488
PR
PI SEIJI SATO,MASAHIKO HIGASHIKUJI,TOSHIYUKI KUDO,MASAOKI KONDO
PC C12N15/09,C12N1/21,C12P21/02,C12P21/02//C07K14/605,C07K14/62,
PC C07K14/655,
PC C07K19/00,(C12N15/09,C12R1/08),(C12N1/21,C12R1/08),(C12P21/02,
PC C12R1/08),
PC C12N15/00,(C12N15/00,C12R1/08)
CC
CC Key Location/Qualifiers
FT source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match          0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGAGATGAT 1370
Db 18 GTGATGATGATGATGAT 2

RESULT 1378
E39158/c
LOCUS          E39158          18 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     DNA encoding novel fused protein and process for producing useful
protein mediating the expression thereof.
ACCESSION      E39158
VERSION        E39158.1  GI:13019232
KEYWORDS       JP 1999341991-A/4.
SOURCE         synthetic construct
ORGANISM       artificial construct
REFERENCE      1 (bases 1 to 18)
AUTHORS        Seiji,S., Masahiko,H., Toshiyuki,K. and Masaaki,K.
TITLE          DNA encoding novel fused protein and process for producing useful
protein mediating the expression thereof
JOURNAL        Patent: JP 1999341991-A 4 14-DEC-1999;
ITO HAM KK, JUZO UDAKA

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COMMENT      OS      Artificial Sequence
PD           JP 1999341991-A/4
PF           14-DEC-1999
PR           30-MAR-1999 JP 1999089488
PI           SEIJI SATO,MASAHKO HIGASHIKUJI,TOSHIYUKI KUDO,MASAAKI KONDO
PC           C12N15/09,C12N1/21,C12P21/02,C12P21/02//C07K14/605,C07K14/62,
PC           C07K14/655
PC           C07K19/00,(C12N15/09,C12R1:08),(C12N1/21,C12R1:08),(C12P21/02,
PC           C12R1:08),
PC           C12R1:08),
PC           C12N15/00,(C12N15/00,C12R1:08)
FH           Key      Location/Qualifiers
FT           source   1..18
FT           Location/Qualifiers
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source           1..18
                  /organism="synthetic construct"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32630"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1354 GAGATGATGAAGATGAT 1370
Db      1 GTGATGATGATGAT 17

RESULT 1379
I18339
LOCUS      18 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION      Sequence 12 from patent US 5495009.
ACCESSION      I18339
VERSION      I18339.1 GI:1598694
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS      Matteucci,M., Jones,B. and Lin,X.-Y.
TITLE      Oligonucleotide analogs containing thioformacetal linkages
JOURNAL      Patent: US 5495009-A 12 27-FEB-1996;
FEATURES
source           1..18
                  /organism="unknown"
                  /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3269 TTGCTTTGTCCTTTT 3285
Db      1 TTTTCTTCTCCTTTT 17

RESULT 1380
I20607/c
LOCUS      18 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION      Sequence 5 from patent US 5514788.
ACCESSION      I20607
VERSION      I20607.1 GI:1600962
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS      Bennett,C.Frank. and Mirabelli,C.K.
TITLE      Oligonucleotide modulation of cell adhesion
JOURNAL      Patent: US 5514788-A 5 07-MAY-1996;
FEATURES
source           1..18
                  /organism="unknown"
                  /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3269 CTTTCCCACTTCCACC 2706
Db      18 CTTTCCCACTGCCATC 2

RESULT 1381
I33300/c
LOCUS      18 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION      Sequence 5 from patent US 5591623.
ACCESSION      I33300
VERSION      I33300.1 GI:1824091
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS      Bennett,C.Frank. and Mirabelli,C.K.
TITLE      Oligonucleotide modulation of cell adhesion
JOURNAL      Patent: US 5591623-A 5 07-JAN-1997;
FEATURES
source           1..18
                  /organism="unknown"
                  /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2690 CTTTCCCACTTCCACC 2706
Db      18 CTTTCCCACTGCCATC 2

RESULT 1382
I57038/c
LOCUS      18 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION      Sequence 39 from patent US 5650553.
ACCESSION      I57038
VERSION      I57038.1 GI:2477451
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS      Ecker,J., Rothenberg,M., Lehman,A. and Roman,G.
TITLE      Plant genes for sensitivity to ethylene and pathogens
JOURNAL      Patent: US 5650553-A 39 22-JUL-1997;
FEATURES
source           1..18
                  /organism="unknown"
                  /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      543 GCGGGGCTGCCGCCA 559
Db      18 GCGTGGCTGCCAGCA 2

RESULT 1383
I92477
LOCUS      18 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION      Sequence 7 from patent US 5728523.

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ACCESSION 192477
VERSION 192477.1 GI:3936947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Vogelstein,B. and Kinzler,K.W.
TITLE Polymerase delta mutations in colorectal tumors with replication errors
JOURNAL Patent: US 5728523-A 7 17-MAR-1998;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 657 TGGCAGCAAGGTGGGCC 673
Db 1 TGTGAGCATGGTGGGCC 17

RESULT 1384
AR193175/c
LOCUS AR193175 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 9 from patent US 6346606.
ACCESSION AR193175
VERSION AR193175.1 GI:20239140
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Mollenhauer,J. and Poustka,A.
TITLE Protein containing a scavenger receptor cysteine rich domain
JOURNAL Patent: US 6346606-A 9 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
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Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1148 AGCTGCTCGCAGCC 1164
Db 17 AGCTGCTCGCAGCCAC 1

RESULT 1385
AR198571/c
LOCUS AR198571 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 21 from patent US 6352972.
ACCESSION AR198571
VERSION AR198571.1 GI:20248420
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Nimni,M.E., Hall,F.L., Wu,L., Han,B. and Shors,E.C.
TITLE Bone morphogenetic proteins and their use in bone growth
JOURNAL Patent: US 6352972-A 21 05-MAR-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1148 AGCTGCTCGCAGCC 1164
Db 17 AGCTGCTCGCAGCCAC 1

RESULT 1386
AR198571/c
LOCUS AR198571 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 21 from patent US 6352972.
ACCESSION AR198571
VERSION AR198571.1 GI:20248420
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Nimni,M.E., Hall,F.L., Wu,L., Han,B. and Shors,E.C.
TITLE Bone morphogenetic proteins and their use in bone growth
JOURNAL Patent: US 6352972-A 21 05-MAR-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1148 AGCTGCTCGCAGCC 1164
Db 17 AGCTGCTCGCAGCCAC 1

RESULT 1387
AR214545/c
LOCUS AR214545 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 10 from patent US 6410009.
ACCESSION AR214545
VERSION AR214545.1 GI:23312417
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Galun,E., Nahor,O. and Blum,H.E.
TITLE Pharmaceutical composition for treating hepatitis B virus (HBV) infection
JOURNAL Patent: US 6410009-A 10 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 543 GCGGGGCTGCCGCCA 559
Db 18 GCGGTGGCTGCCGCCA 2

RESULT 1387
AR214545/c
LOCUS AR214545 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 10 from patent US 6410009.
ACCESSION AR214545
VERSION AR214545.1 GI:23312417
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Galun,E., Nahor,O. and Blum,H.E.
TITLE Pharmaceutical composition for treating hepatitis B virus (HBV) infection
JOURNAL Patent: US 6410009-A 10 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 543 GCGGGGCTGCCGCCA 559
Db 18 GCGGTGGCTGCCGCCA 2

RESULT 1388
AR215521/c
LOCUS AR215521 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 69 from patent US 6410323.
ACCESSION AR215521
VERSION AR215521.1 GI:23313777
KEYWORDS
SOURCE Unknown.
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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Roberts,M.L. and Cowser,L.M.
TITLE Antisense modulation of human Rho family gene expression
JOURNAL Patent: US 6410323-A 69 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1998 CAAGACGCTGGTGAGG 2014
Db 17 CAAGACGCTGGTGAGG 1

RESULT 1389
AR274624/c
LOCUS AR274624 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 8 from patent US 6506595.
ACCESSION AR274624
VERSION AR274624.1 GI:29707158
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sato,S., Higashikuni,N., Kudo,T. and Kondo,M.
TITLE DNAs encoding new fusion proteins and processes for preparing useful polypeptides through expression of the DNAs
JOURNAL Patent: US 6506595-A 8 14-JAN-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGAAGATGAT 1370
Db 1 GTGATGATGATGATGAT 17

RESULT 1390
LOCUS AR274625 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 9 from patent US 6506595.
ACCESSION AR274625
VERSION AR274625.1 GI:29707159
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sato,S., Higashikuni,N., Kudo,T. and Kondo,M.
TITLE DNAs encoding new fusion proteins and processes for preparing useful polypeptides through expression of the DNAs
JOURNAL Patent: US 6506595-A 9 14-JAN-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGAAGATGAT 1370
Db 1 GTGATGATGATGATGAT 17

RESULT 1391
LOCUS AR293143 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4878 from patent US 6537751.
ACCESSION AR293143
VERSION AR293143.1 GI:31680427
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4878 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1535 AGCAGCTCACCTTCAAG 1551
Db 17 AGCAGCTCAAGTTCAAG 1

RESULT 1392
LOCUS AR294845 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6580 from patent US 6537751.
ACCESSION AR294845
VERSION AR294845.1 GI:31682129
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 6580 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2016 CCTGACCGCTGCTTCA 2032
Db 18 CCTGTACCTTGCTTCA 2

RESULT 1393
LOCUS AR295340 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7075 from patent US 6537751.
ACCESSION AR295340
VERSION AR295340.1 GI:31682624
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7075 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7075 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2996 GCACCCGAGTTTGTGTT 3012
||||| |||||
Db 1 GCACCGCATTTTGTTAT 17
||||| |||||
RESULT 1394
AR296057
LOCUS AR296057 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7792 from patent US 6537751.
ACCESSION AR296057
VERSION AR296057.1 GI:31683341
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7792 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 53 GGCTCAGGTCGCTGAAT 69
||||| ||||| |||||
Db 1 GGCTTCAGGTCGCTAAAT 17
||||| ||||| |||||
RESULT 1395
AR370530/c
LOCUS AR370530 18 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 5 from patent US 6300491.
ACCESSION AR370530
VERSION AR370530.1 GI:34607283
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C.F. and Mirabelli, C.K.
TITLE Oligonucleotide inhibition of cell adhesion
JOURNAL Patent: US 6300491-A 5 09-OCT-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2690 CTTTCCCACTTCCACC 2706
||||| ||||| |||||

Db 18 CTTTCCCACTGCCCATC 2
RESULT 1396
AR390575
LOCUS AR390575 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 445 from patent US 6610839.
ACCESSION AR390575
VERSION AR390575.1 GI:40112501
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Morin, G.B. and Andrews, W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 445 26-AUG-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 458 GCGTCGTGGAGACAAAG 474
||||| ||||| |||||
Db 1 GCGACATGGAGACAAAG 17
||||| ||||| |||||
RESULT 1397
AR393189
LOCUS AR393189 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 445 from patent US 6617110.
ACCESSION AR393189
VERSION AR393189.1 GI:40118483
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B., Harley, C.B. and Andrews, W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in drug screening
JOURNAL Patent: US 6617110-A 445 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 458 GCGTCGTGGAGACAAAG 474
||||| ||||| |||||
Db 1 GCGACATGGAGACAAAG 17
||||| ||||| |||||
RESULT 1398
AX060284
LOCUS AX060284 18 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 8 from Patent WO0100831.
ACCESSION AX060284
VERSION AX060284.1 GI:12405773
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Conklin, D.C. and Gao, Z.

TITLE Helical polypeptide zalpha29
JOURNAL Patent: WO 010831-A 8 04-JAN-2001;
ZymoGenetics, Inc. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide primer ZC21,720"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1857 GTACCCCGGATCCCTG 1873
Db 2 GTACCCCGGATCACAG 18

RESULT 1399
AX060757
LOCUS AX060757 18 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 45 from Patent WO0078972.
ACCESSION AX060757
VERSION AX060757.1 GI:12406144
KEYWORDS
synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 45 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ABC1 sequencing primer"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2100 GGACACCCCGAGTCCA 2116
Db 2 GGACACCCCGAGCTTCA 18

RESULT 1400
AX060936
LOCUS AX060936 18 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 45 from Patent WO0078971.
ACCESSION AX060936
VERSION AX060936.1 GI:12406311
KEYWORDS
synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE Atp binding cassette transporter protein abc1 polypeptides
JOURNAL Patent: WO 0078971-A 45 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ABC1 sequencing primer"

Query Match 0.4%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2100 GGACACCCCGAGTCCA 2116
Db 2 GGACACCCCGAGCTTCA 18

RESULT 1401
AX082556
LOCUS AX082556 18 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 7 from Patent WO0111047.
ACCESSION AX082556
VERSION AX082556.1 GI:13184666
KEYWORDS
Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Bowman,B.M. and Wang,K.
TITLE Dna sequences isolated from human colonic epithelial cells
JOURNAL Patent: WO 0111047-A 7 15-FEB-2001;
Bayer Corporation (US)
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3411 GGGAGGGCGGCCCTG 3427
Db 1 GGGAGGAGCCAGCCCTG 17

RESULT 1402
AX082560
LOCUS AX082560 18 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 11 from Patent WO0111047.
ACCESSION AX082560
VERSION AX082560.1 GI:13184670
KEYWORDS
Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Bowman,B.M. and Wang,K.
TITLE Dna sequences isolated from human colonic epithelial cells
JOURNAL Patent: WO 0111047-A 11 15-FEB-2001;
Bayer Corporation (US)
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3411 GGGAGGGCGGCCCTG 3427
Db 1 GGGAGGAGCCAGCCCTG 17

RESULT 1403
AX082562
LOCUS AX082562 18 bp DNA linear PAT 28-FEB-2001

DEFINITION Sequence 13 from Patent WO0111047.
ACCESSION AX082562
VERSION AX082562.1 GI:13184672
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Bowman, B.M. and Wang, K.
TITLE Dna sequences isolated from human colonic epithelial cells
JOURNAL Patent: WO 0111047-A 13 15-FEB-2001;
Bayer Corporation (US)
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3411 GGGAGGGCGCCGCTG 3427
|||||
Db 1 GGGAGGAGCCGACGCTG 17
RESULT 1404
AX101276
LOCUS AX101276 18 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 17 from Patent WO0121791.
ACCESSION AX101276
VERSION AX101276.1 GI:13620066
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Clare, J.J., Plumpton, M., Moss, F.J. and Sansau, P.
TITLE Starazin-like neuronal ca2+-channel gamma subunit polypeptides
JOURNAL Patent: WO 0121791-A 17 29-MAR-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 428 TGGTGGCCTCGACCGC 444
|||||
Db 2 TGGTGGCATCGACCGC 18
RESULT 1405
AX110441
LOCUS AX110441 18 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1174 from Patent WO0123604.
ACCESSION AX110441
VERSION AX110441.1 GI:13926733
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J. and Roy, P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL Patent: WO 0123604-A 2167 05-APR-2001;
Infecio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 297 CCGCTGCCCGCCGCTG 313
|||||
Db 17 CCGCGCCCGCCGCTG 1
RESULT 1407
AX233412
LOCUS AX233412 18 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 55 from Patent WO0162788.
ACCESSION AX233412
VERSION AX233412.1 GI:15592750
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Olaveson, M., Lench, N., Allen, M. and Tazi-Ahmini, R.U.
TITLE Corneodesmosin based test and model for inflammatory disease
JOURNAL Patent: WO 0162788-A 55 30-AUG-2001;
Oxagen Limited (GB)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

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Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 319 CCCACTCCCTCCATCTC 335
DB 1 CCCACCCCTCCACCTC 17

RESULT 1408
LOCUS AX599395/c 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 735 from Patent WO02077272.
ACCESSION AX599395
VERSION AX599395.1 GI:28399539
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
Pellet,C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL Patent: WO 02077272-A 735 03-OCT-2002;
Epigenomics AG (DE)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3762 AACTTCCGAAATAA 3778
DB 17 AAATTTCCGAAACAA 1

RESULT 1409
AX599440/c
LOCUS AX599440 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 780 from Patent WO02077272.
ACCESSION AX599440
VERSION AX599440.1 GI:28399584
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
Pellet,C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL Patent: WO 02077272-A 780 03-OCT-2002;
Epigenomics AG (DE)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for MLH1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;

QY 3481 TAATTTATGAGTTT 3497
DB 1 TAATTTTGGAGTTT 17

RESULT 1411
AX659428/c
LOCUS AX659428 18 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 30 from Patent WO02102824.
ACCESSION AX659428
VERSION AX659428.1 GI:29161658
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Beinfuhr,C. and Snaidr,J.
TITLE Method for specific fast detection of relevant bacteria in drinking
water
JOURNAL Patent: WO 02102824-A 30 27-DEC-2002;
Vermicon AG (DE)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1222 TTCGGCCAGGTGGTCAT 1238
DB 17 TTCGGCTAGGGGTGTCAT 1
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RESULT 1412
AX695098/c
LOCUS AX695098 18 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 725 from Patent WO03008583.
ACCESSION AX695098
VERSION AX695098.1 GI:29418216
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryotka; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Morris, D.W. and Engelhard, E.K.
JOURNAL Novel compositions and methods for cancer
Patent: WO 03008583-A 725 30-JAN-2003;
Sagres Discovery (US)
FEATURES
source Location/Qualifiers
1.18
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2334 CGTGTGTGTGTGTGTGT 2350
Db 18 CATGTGTGTGTGTGTGT 2

RESULT 1413
AX705489/c
LOCUS AX705489 18 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 158 from Patent WO03014388.
ACCESSION AX705489
VERSION AX705489.1 GI:29562154
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Distler, J., Model, F. and Taubert, H.
TITLE Method and nucleic acids for the analysis of colon cancer
JOURNAL Patent: WO 03014388-A 158 20-FEB-2003;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for p21"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1705 AACCTCGACTACTACAA 1721
Db 17 AACCTCGCTACTACAA 1

RESULT 1414
AX705491
LOCUS AX705491 18 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 160 from Patent WO03014388.
ACCESSION AX705491
VERSION AX705491.1 GI:29562156
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Burger, M., Caldwell, C., Genc, B., Becker, E., Maier, S. and
Nimmrich, I.
TITLE Method and nucleic acids for the analysis of a lymphoid cell
JOURNAL Patent: WO 03044226-A 458 30-MAY-2003;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for p21"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1705 AACCTCGACTACTACAA 1721
Db 17 AACCTCGCTACTACAA 1

RESULT 1416
AX767810/c
LOCUS AX767810 18 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 458 from Patent WO03044226.
ACCESSION AX767810
VERSION AX767810.1 GI:32436496
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Burger, M., Caldwell, C., Genc, B., Becker, E., Maier, S. and
Nimmrich, I.
TITLE Method and nucleic acids for the analysis of a lymphoid cell
JOURNAL Patent: WO 03044226-A 458 30-MAY-2003;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for CDKN1A"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1705 AACCTCGACTACTACAA 1721
Db 17 AACCTCGCTACTACAA 1

RESULT 1415
AX767755/c
LOCUS AX767755 18 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 403 from Patent WO03044226.
ACCESSION AX767755
VERSION AX767755.1 GI:32436360
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Burger, M., Caldwell, C., Genc, B., Becker, E., Maier, S. and
Nimmrich, I.
TITLE Method and nucleic acids for the analysis of a lymphoid cell
JOURNAL Patent: WO 03044226-A 403 30-MAY-2003;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for CDKN1A"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1705 AACCTCGACTACTACAA 1721
Db 2 AACCTCGCTACTACAA 18

RESULT 1416
AX767810/c
LOCUS AX767810 18 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 458 from Patent WO03044226.
ACCESSION AX767810
VERSION AX767810.1 GI:32436496
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Burger, M., Caldwell, C., Genc, B., Becker, E., Maier, S. and
Nimmrich, I.
TITLE Method and nucleic acids for the analysis of a lymphoid cell
JOURNAL Patent: WO 03044226-A 458 30-MAY-2003;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for CDKN1A"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1705 AACCTCGACTACTACAA 1721
Db 17 AACCTCGCTACTACAA 1
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for MLH1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1417
AX796279/c 18 bp DNA linear PAT 04-OCT-2003
LOCUS
DEFINITION Sequence 622 from Patent WO03052135.
ACCESSION AX796279
VERSION AX796279.1 GI:37516945
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
and Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lung cell
JOURNAL proliferative disorder
Patent: WO 03052135-A 622 26-JUN-2003;
Epigenomics AG (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3762 AACTTTCGAAAAATAA 3778
Db 17 AAATTCGAAAAACAA 1

RESULT 1418
AX796334/c 18 bp DNA linear PAT 04-OCT-2003
LOCUS
DEFINITION Sequence 677 from Patent WO03052135.
ACCESSION AX796334
VERSION AX796334.1 GI:37517000
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
and Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lung cell
JOURNAL proliferative disorder
Patent: WO 03052135-A 677 26-JUN-2003;
Epigenomics AG (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for MLH1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;

/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1419
AX822802/c 18 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION Sequence 694 from Patent EP1340818.
ACCESSION AX822802
VERSION AX822802.1 GI:39749438
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: EP 1340818-A 694 03-SEP-2003;
Epigenomics AG (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for MLH1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1420
AX823043/c 18 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION Sequence 935 from Patent EP1340818.
ACCESSION AX823043
VERSION AX823043.1 GI:39749679
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: EP 1340818-A 935 03-SEP-2003;
Epigenomics AG (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3762 AACTTTCGAAAAATAA 3778
Db 17 AAATTCGAAAAACAA 1

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RESULT 1421
AX826442/c
LOCUS AX826442 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 694 from Patent WO03072821.
ACCESSION AX826442
VERSION AX826442.1 GI:39751956
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: WO 03072821-A 694 04-SEP-2003;
Epigenomics AG (DE)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for MLH1"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1422
AX826683/c
LOCUS AX826683 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 935 from Patent WO03072821.
ACCESSION AX826683
VERSION AX826683.1 GI:39752197
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: WO 03072821-A 935 04-SEP-2003;
Epigenomics AG (DE)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3762 AACTTTCGAAATAA 3778
Db 17 AAATTCGAAATAA 1

RESULT 1423
BD023630/c
LOCUS BD023630 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Polypeptide belonging to the family of basic helix-loop-helix
(bHLH) family and nucleic acid sequence corresponding thereto.
ACCESSION BD023630
VERSION BD023630.1 GI:22564853

KEYWORDS JP 2001510464-A/5.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 18)
AUTHORS Liepkalns, C.I., Mallet, J. and Ravassard, P.
TITLE Polypeptide belonging to the family of basic helix-loop-helix
(bHLH) family and nucleic acid sequence corresponding thereto
JOURNAL Patent: JP 2001510464-A 5 31-JUL-2001;
COMMENT RHONE-POULENC RORER SA
PN JP 2001510464-A/5
PD 31-JUL-2001
PF 19-DEC-1997 JP 1998527415
PI 19-DEC-1996 FR 96/15651
PI CHRISTINE ICARD LIEPKALNS, JACQUES MALLET, PHILIPPE RAVASSARD PC
C07K14/47, A61K31/711, A61K35/76, A61K38/00, A61P25/00, PC
C12N15/09,
PC C12N15/00, A61K37/02
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source
1. .18
/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2092 GGTGGCCAGGACACCCC 2108
Db 18 GGTGGCCAGGACACCCG 2

RESULT 1424
BD064969/c
LOCUS BD064969 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Protein containing an SRCR domain.
ACCESSION BD064969
VERSION BD064969.1 GI:22610572
KEYWORDS JP 2001509667-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Mollenhauer, J. and Poustka, A.
TITLE Protein containing an SRCR domain
JOURNAL Patent: JP 2001509667-A 7 24-JUL-2001;
COMMENT DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS
OS Artificial Sequence
PN JP 2001509667-A/7
PD 24-JUL-2001
PF 09-JAN-1998 JP 1998530469
PI 09-JAN-1997 DE 197 00 519.5, 18-JUL-1997 DE 197 30 997.6 PI
JAN MOLLENHAUER, ANNEMARIE POUSTKA
PC C12N15/12, C12N15/70, C12N1/21, C12Q1/68, C07K14/47, C07K16/18, PC
A61K38/17,
PC A61K48/00, G01N33/50
CC Description of Artificial Sequence: primer sequence for CC
amplifying a DNA
encoding a protein containing SRCR domain.
FH Key Location/Qualifiers
FT source
1. .18
/organism="Artificial Sequence".
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1148 AGCTGCTGCGGACCC 1164
Db 17 AGCTGCTGCGGACCC 1

RESULT 1425
BD065700/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS An antisense oligonucleotide preparation method.

ACCESSION BD065700
VERSION BD065700.1 GI:22611303
KEYWORDS JP 2001511000-A/335.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingsiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 335 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Unknown
PN JP 2001511000-A/335
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key

FT source 1. .18
Location/Qualifiers
/organism='Unknown'.
FEATURES source
1. .18
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1792 CACCAGGTGACGTCTG 1808
Db 17 CACCAGGTGATGTGTG 1

RESULT 1426
BD070462 18 bp DNA linear PAT 27-AUG-2002
LOCUS Methods for detecting mitochondrial mutations diagnostic for
DEFINITION Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid.

ACCESSION BD070462
VERSION BD070462.1 GI:22616065
KEYWORDS JP 2001514500-A/19.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 18)
AUTHORS Parker,W.D., Herrnstadt,C., Ghosh,S. and Fahy,E.D.
TITLE Methods for detecting mitochondrial mutations diagnostic for
JOURNAL Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid
Patent: JP 2001514500-A 19 11-SEP-2001;

COMMENT MITOKOR
OS Unidentified
PN JP 2001514500-A/19
PD 11-SEP-2001

PF 27-FEB-1998 JP 1998537738
PR 28-FEB-1997 US 08/810599
PI WILLIAM DAVIS PARKER,CORINNA HERRNSTADT,SOUMITRA GHOSH,ROIN D
PI FAHY
PC C12Q1/68,C07H21/04
CC Strandedness: Double;
CC Topology: Linear;
CC Methods for detecting mitochondrial mutations diagnostic for
CC Alzheimer's
CC disease and methods for determining heteroplasmy of CC
mitochondrial nucleic

CC acid
FH Key Location/Qualifiers
FT source 1. .18
/organism='Unidentified'.
FEATURES source
1. .18
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2075 TCGAGCAGTACTCCCG 2091
Db 2 TCGAGTAGTACTCCCG 18

RESULT 1427
BD089937 18 bp DNA linear PAT 27-AUG-2002
LOCUS A method of arraying genome clone.
DEFINITION
ACCESSION BD089937
VERSION BD089937.1 GI:22635547
KEYWORDS JP 2001321190-A/2181.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 18)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 2181 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS

COMMENT OS Artificial Sequence
PN JP 2001321190-A/2181
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,C01N33/53,C01N33/566, PC
C12N15/00,

PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
CC Location/Qualifiers
FT source 1. .18
Location/Qualifiers
/organism='Artificial Sequence'.
FEATURES source
1. .18
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2101 GACACCCCGCTCCAG 2117
Db 2 GACACCCCGCTCCAG 18

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RESULT 1428
SSAJ787/c
LOCUS          SSAJ787          19 bp  mRNA  linear  MAM 29-JUL-1997
DEFINITION    Sus scrofa EST 3'UTR SSC1G2 forward primer.
ACCESSION     AJ000787
VERSION       AJ000787.1  GI:2286010
KEYWORDS      PCR primer.
SOURCE        Sus scrofa (pig)
ORGANISM      Sus scrofa
REFERENCE     1 (bases 1 to 19)
AUTHORS       Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
TITLE         Fridolfsson,A.K., Hori,T., Wintero,A.K., Fredholm,M., Yerle,M.,
              Robic,A., Andersson,L. and Ellegren,H.
              Expansion of the pig comparative map by expressed sequence tags
              (EST) mapping
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 19)
AUTHORS       Fridolfsson,A.K.
TITLE         Direct Submission
JOURNAL       Submitted (27-JUL-1997) Fridolfsson A.K., Animal Breeding and
              Genetics, Swedish University of Agricultural Sciences, Biomedical
              Center, Box 597, S-751 24 Uppsala, SWEDEN
FEATURES      Location/Qualifiers
             source
              1..19
                /organism="Sus scrofa"
                /mol_type="mRNA"
                /db_xref="taxon:9823"
                /chromosome="1"
                /map="1q"

Query Match          0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1565  GTGCTTACGAGTGGCC 1581
Db  17  GTGCTTCCGAGTGGCC 1

RESULT 1429
A36743/c
LOCUS          A36743          19 bp  DNA  linear  PAT 05-MAR-1997
DEFINITION    Sequence 9 from Patent EP0584023.
ACCESSION     A36743
VERSION       A36743.1  GI:2294010
KEYWORDS      unidentified
SOURCE        unidentified
ORGANISM      unidentified
REFERENCE     1 (bases 1 to 19)
AUTHORS       Mabilat,C. and Pechere,J.
TITLE         Mycobacteria DNA fragments, amplification primers, hybridization
              probes, reagents and detection process of mycobacteria
JOURNAL       Patent: EP 0584023-A 9 23-FEB-1994;
              BIO MERIEUX (FR)
COMMENT       Other publication CA 2103933 940213
              Other publication FR 2694754 940218.
FEATURES      Location/Qualifiers
             source
              1..19
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match          0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  242  CCGAGCGGATGGACAAG 258
Db  19  CCGAGCGGATGGACAAG 3

RESULT 1430
A36744
LOCUS          A36744          19 bp  DNA  linear  PAT 05-MAR-1997
DEFINITION    Sequence 10 from Patent EP0584023.
ACCESSION     A36744
VERSION       A36744.1  GI:2294011
KEYWORDS      unidentified
SOURCE        unidentified
ORGANISM      unidentified
REFERENCE     1 (bases 1 to 19)
AUTHORS       Mabilat,C. and Pechere,J.
TITLE         Mycobacteria DNA fragments, amplification primers, hybridization
              probes, reagents and detection process of mycobacteria
JOURNAL       Patent: EP 0584023-A 10 23-FEB-1994;
              BIO MERIEUX (FR)
COMMENT       Other publication CA 2103933 940213
              Other publication FR 2694754 940218.
FEATURES      Location/Qualifiers
             source
              1..19
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match          0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  242  CCGAGCGGATGGACAAG 258
Db  1  CCGAGCGGATGGACAAG 17

RESULT 1431
AR030969
LOCUS          AR030969          19 bp  DNA  linear  PAT 29-SEP-1999
DEFINITION    Sequence 1 from patent US 5861501.
ACCESSION     AR030969
VERSION       AR030969.1  GI:5944183
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE         Capped synthetic RNA, analogs, and aptamers
JOURNAL       Patent: US 5861501-A 1 19-JAN-1999;
              Location/Qualifiers
FEATURES      source
              1..19
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match          0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3114  GTTTTAATTTTAACTT 3130
Db  1  GTTTTAATTTTAACTT 17

RESULT 1432
AR030972
LOCUS          AR030972          19 bp  DNA  linear  PAT 29-SEP-1999
DEFINITION    Sequence 4 from patent US 5861501.
ACCESSION     AR030972
VERSION       AR030972.1  GI:5944186
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.

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TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 4 19-JAN-1999;
FEATURES   Location/Qualifiers
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           1..19
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1433
AR030974
LOCUS      AR030974      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5861501.
ACCESSION  AR030974
VERSION     AR030974.1 GI:5944188
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseiler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 6 19-JAN-1999;
FEATURES   Location/Qualifiers
           source
           1..19
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1434
AR030975
LOCUS      AR030975      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5861501.
ACCESSION  AR030975
VERSION     AR030975.1 GI:5944189
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseiler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 7 19-JAN-1999;
FEATURES   Location/Qualifiers
           source
           1..19
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1435
AR030976
LOCUS      AR030976      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5861501.
ACCESSION  AR030976
VERSION     AR030976.1 GI:5944190
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseiler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 8 19-JAN-1999;
FEATURES   Location/Qualifiers
           source
           1..19
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1436
AR030977
LOCUS      AR030977      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5861501.
ACCESSION  AR030977
VERSION     AR030977.1 GI:5944191
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseiler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 9 19-JAN-1999;
FEATURES   Location/Qualifiers
           source
           1..19
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1437
AR030978
LOCUS      AR030978      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5861501.
ACCESSION  AR030978
VERSION     AR030978.1 GI:5944192
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseiler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 10 19-JAN-1999;
FEATURES   Location/Qualifiers
           source
           1..19
           /organism="unknown"
           /mol_type="unassigned DNA"

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17
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Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
||||| ||||||| ||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1438
AR030981 LOCUS AR030981 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 13 from patent US 5861501.
ACCESSION AR030981
VERSION AR030981.1 GI:5944195
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 5861501-A 13 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
||||| ||||||| ||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1439
AR030982 LOCUS AR030982 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5861501.
ACCESSION AR030982
VERSION AR030982.1 GI:5944196
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 5861501-A 14 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
||||| ||||||| ||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1440
AR030983 LOCUS AR030983 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5861501.
ACCESSION AR030983
VERSION AR030983.1 GI:5944197
KEYWORDS

SOURCE Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 5861501-A 15 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
||||| ||||||| ||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1441
AR030984 LOCUS AR030984 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5861501.
ACCESSION AR030984
VERSION AR030984.1 GI:5944198
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 5861501-A 16 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
||||| ||||||| ||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1442
AR066286 LOCUS AR066286 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5849901.
ACCESSION AR066286
VERSION AR066286.1 GI:5996502
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Mablrat,C. and Pechere,J.-C.
TITLE DNA fragments of mycobacteria, amplification primers hybridization
probes, reagents and method for the detection of mycobacteria
JOURNAL Patent: US 5849901-A 9 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      242 CCGAGCGGATGGACAAG 258
Db      19 CCGAGCGGATGGACAAG 3

RESULT 1443
LOCUS   AR066287
DEFINITION Sequence 10 from patent US 5849901.
ACCESSION AR066287
VERSION   AR066287.1 GI:5996503
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS  Mabilat,C. and Pechere,J.-C.
TITLE    DNA fragments of mycobacteria, amplification primers hybridization
JOURNAL  probes, reagents and method for the detection of mycobacteria
PATENT:  US 5849901-A 10 15-DEC-1998;
FEATURES
source
Location/Qualifiers
1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      242 CCGAGCGGATGGACAAG 258
Db      1 CCGAGCGGATGGACAAG 17

RESULT 1444
LOCUS   AR066714/c
DEFINITION Sequence 62 from patent US 5851760.
ACCESSION AR066714
VERSION   AR066714.1 GI:5997936
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS  Evans,G.A. and Smith,M.W.
TITLE    Method for generation of sequence sampled maps of complex genomes
JOURNAL  Patent: US 5851760-A 62 22-DEC-1998;
FEATURES
source
Location/Qualifiers
1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      872 CTGACGAGGGGGGCGAGT 888
Db      17 CTGACGAGGGGGGCGAGT 1

RESULT 1445
LOCUS   AR083027
DEFINITION Sequence 53 from patent US 5976798.
ACCESSION AR083027
VERSION   AR083027.1 GI:10009817
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 19)

Parker,W.Davis., Herrnstadt,C., Ghosh,S. and Fahy,E.D.
Methods for detecting mitochondrial mutations diagnostic for
Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid
Patent: US 5976798-A 53 02-NOV-1999;
FEATURES
source
Location/Qualifiers
1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1932 CACACACGACCTGTACA 1948
Db      3 CACACACGACCTGTCCA 19

RESULT 1446
LOCUS   AR108814
DEFINITION Sequence 1 from patent US 6111095.
ACCESSION AR108814
VERSION   AR108814.1 GI:12824301
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS  Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE    Capped synthetic RNA, analogs, and aptamers
JOURNAL  Patent: US 6111095-A 1 29-AUG-2000;
FEATURES
source
Location/Qualifiers
1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTAATTTTAAATT 17

RESULT 1447
LOCUS   AR108817
DEFINITION Sequence 4 from patent US 6111095.
ACCESSION AR108817
VERSION   AR108817.1 GI:12824304
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS  Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE    Capped synthetic RNA, analogs, and aptamers
JOURNAL  Patent: US 6111095-A 4 29-AUG-2000;
FEATURES
source
Location/Qualifiers
1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTAATTTTAAATT 17

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RESULT 1466
AR205768
LOCUS AR205768 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6369208.
ACCESSION AR205768
VERSION AR205768.1 GI:21503434
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole, J.L., Kuo, L.C., Olsen, D.B. and Benseler, F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 6 09-APR-2002;
FEATURES
    Location/Qualifiers
        source
            1..19
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Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATT 17

RESULT 1467
AR205769
LOCUS AR205769 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 7 from patent US 6369208.
ACCESSION AR205769
VERSION AR205769.1 GI:21503435
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole, J.L., Kuo, L.C., Olsen, D.B. and Benseler, F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 7 09-APR-2002;
FEATURES
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        source
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                /mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATT 17

RESULT 1468
AR205770
LOCUS AR205770 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 8 from patent US 6369208.
ACCESSION AR205770
VERSION AR205770.1 GI:21503437
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole, J.L., Kuo, L.C., Olsen, D.B. and Benseler, F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 8 09-APR-2002;
FEATURES
    Location/Qualifiers
        source
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Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATT 17

RESULT 1469
AR205771
LOCUS AR205771 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 9 from patent US 6369208.
ACCESSION AR205771
VERSION AR205771.1 GI:21503438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole, J.L., Kuo, L.C., Olsen, D.B. and Benseler, F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 9 09-APR-2002;
FEATURES
    Location/Qualifiers
        source
            1..19
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATT 17

RESULT 1470
AR205772
LOCUS AR205772 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 10 from patent US 6369208.
ACCESSION AR205772
VERSION AR205772.1 GI:21503439
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole, J.L., Kuo, L.C., Olsen, D.B. and Benseler, F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 10 09-APR-2002;
FEATURES
    Location/Qualifiers
        source
            1..19
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATT 17

RESULT 1471
AR205775
LOCUS AR205775 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 13 from patent US 6369208.
ACCESSION AR205775
VERSION AR205775.1 GI:21503443
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TITLE Diagnostic method based on quantification of extramitochondrial DNA
JOURNAL Patent: US 6441149-A 50 27-AUG-2002;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1932 CACACAGCAGCTGTACA 1948
Db 3 CACACACACCTGTCCA 19

RESULT 1477
AR241182/c 19 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION Sequence 9 from patent US 6468983.
ACCESSION AR241182
VERSION AR241182.1 GI:27286412
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Silverman,R.H., Kondo,S., Cowell,J.K., Li,G. and Torrence,P.F.
TITLE RNase L activators and antisense oligonucleotides effective to
treat telomerase-expressing malignancies
JOURNAL Patent: US 6468983-A 9 22-OCT-2002;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2558 TGCCTTGCACACCGG 2574
Db 18 TGCATTGCACCCCGG 2

RESULT 1478
AR241929 19 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION Sequence 217 from patent US 6472154.
ACCESSION AR241929
VERSION AR241929.1 GI:27287741
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 217 29-OCT-2002;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2832 ATATATATATATACAT 2848
Db 1 ATATATATATATATAT 17

RESULT 1479
AR279766 19 bp RNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 12 from patent US 6518017.
ACCESSION AR279766
VERSION AR279766.1 GI:29714911
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Riley,T.A., Brown,B.D. and Arnold,L.J.
TITLE Combinatorial antisense library
JOURNAL Patent: US 6518017-A 12 11-FEB-2003;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1434 GCTGGTGGAGTACGCGG 1450
Db 1 GCTGGTTGAGTACTCGG 17

RESULT 1480
AR279780 19 bp RNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 26 from patent US 6518017.
ACCESSION AR279780
VERSION AR279780.1 GI:29714925
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Riley,T.A., Brown,B.D. and Arnold,L.J.
TITLE Combinatorial antisense library
JOURNAL Patent: US 6518017-A 26 11-FEB-2003;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1434 GCTGGTGGAGTACGCGG 1450
Db 1 GCTGGTTGAGTACTCGG 17

RESULT 1481
AR292645/c 19 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 4380 from patent US 6537751.
ACCESSION AR292645
VERSION AR292645.1 GI:31679929
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4380 25-MAR-2003;
FEATURES Location/Qualifiers
source
1. .19

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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2751 CTTTACCTTTTATGCAA 2767
Db 17 CTATACCTTTTGTGCAA 1

RESULT 1482
AR293082/c
LOCUS AR293082 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4817 from patent US 6537751.
ACCESSION AR293082
VERSION AR293082.1 GI:31680366
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 4817 25-MAR-2003;
Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 887 GTGTGTATGCAGGCATC 903
Db 19 GTGTGTATGTAGTCATC 3

RESULT 1483
AR293964/c
LOCUS AR293964 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5699 from patent US 6537751.
ACCESSION AR293964
VERSION AR293964.1 GI:31681248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 5699 25-MAR-2003;
Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1347 TCAGATGGAGATGATCA 1363
Db 17 TGAGATGAAGATGAAGA 1

RESULT 1484
AR294605/c
LOCUS AR294605 19 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 6340 from patent US 6537751.
ACCESSION AR294605.1 GI:31681889
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 6340 25-MAR-2003;
Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3449 AGATGTTACAGTTTAT 3465
Db 18 AGATGTTACAGTTTAT 2

RESULT 1485
AR451358
LOCUS AR451358 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6673917.
ACCESSION AR451358
VERSION AR451358.1 GI:42682383
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Korneluk,R.G., LaCasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense IAP nucleic acids and uses thereof
JOURNAL Patent: US 6673917-A 3 06-JAN-2004;
FEATURES Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2831 CATATATATATATAACA 2847
Db 1 CAGATATATATGTAACA 17

RESULT 1486
AX039732
LOCUS AX039732 19 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 121 from Patent WO0063441.
ACCESSION AX039732
VERSION AX039732.1 GI:11229761
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS artificial sequences.
TITLE
JOURNAL
FEATURES Patent: WO 0063441-A 121 26-OCT-2000;
MITOKOR (US)
Location/Qualifiers
source 1..19
/mol_type="synthetic construct"

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Query Match          0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1932 CACACGACCTGTACA 1948
Db 2 CACACACCACTGTCCA 18
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

RESULT 1487
LOCUS AX039733 19 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 122 from Patent WO0063441.
ACCESSION AX039733
VERSION AX039733.1 GI:11229762
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Herrnstadt,C. and Davis,R.E.
TITLE Single nucleotide polymorphisms in mitochondrial genes that segregate with Alzheimer's disease
JOURNAL Patent: WO 0063441-A 122 26-OCT-2000; MITOKOR (US)
FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

Query Match          0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 3 CACACACCACTGTCCA 19
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/note="PCR primer"

RESULT 1488
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DEFINITION Sequence 104 from Patent WO0129257.
ACCESSION AX114435
VERSION AX114435.1 GI:14031399
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Schork,N. and Skierczynski,B.
TITLE Methods of genetic cluster analysis and use thereof
JOURNAL Patent: WO 0129257-A 104 26-APR-2001; GENSET (FR)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="upstream amplification primer 99-1480 for SEQ 41"

primer_bind

Query Match          0.4%; Score 13.8; DB 1; Length 19;
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QY 1932 CACACGACCTGTACA 1948
Db 3 CACACACCACTGTCCA 19
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/note="Cdk3 ribozyme binding site"

RESULT 1489
LOCUS AX129117 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 335 from Patent WO0130362.
ACCESSION AX129117
VERSION AX129117.1 GI:14135422
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 335 03-MAY-2001; IMMUSOL, INC. (US)
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/db_xref="taxon:9606"
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Query Match          0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1880 AGCTTCTCAAGCTGCTG 1896
Db 3 ACCTTTCAGCTGCTG 19
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/mol_type="unassigned DNA"
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/note="Cdk3 ribozyme binding site"

RESULT 1490
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LOCUS AX129130 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 348 from Patent WO0130362.
ACCESSION AX129130
VERSION AX129130.1 GI:14135435
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 348 03-MAY-2001; IMMUSOL, INC. (US)
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/note="Cdk3 ribozyme binding site"

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LOCUS AX130618 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1836 from Patent WO0130362.
ACCESSION AX130618
VERSION AX130618.1 GI:14136923
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 1836 03-MAY-2001;
IMMUSOL, INC. (US)
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Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1830 GGAGATCTTCACGCTGG 1846
|||||
Db 2 GGAGGTCTTCCCGCTGG 18
RESULT 1492
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LOCUS AX130619 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1837 from Patent WO0130362.
ACCESSION AX130619
VERSION AX130619.1 GI:14136924
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 1837 03-MAY-2001;
IMMUSOL, INC. (US)
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/mol_type="unassigned DNA"
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Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1830 GGAGATCTTCACGCTGG 1846
|||||
Db 1 GGAGGTCTTCCCGCTGG 17
RESULT 1493
AX130906/c
LOCUS AX130906 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 2124 from Patent WO0130362.
ACCESSION AX130906
VERSION AX130906.1 GI:14137211
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 2124 03-MAY-2001;
IMMUSOL, INC. (US)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3490 GAGTTTTTACAAGATGT 3506
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Db 17 GAGTTTTTACAACATT 1
RESULT 1494
AX131095/c
LOCUS AX131095 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 2313 from Patent WO0130362.
ACCESSION AX131095
VERSION AX131095.1 GI:14137400
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 2313 03-MAY-2001;
IMMUSOL, INC. (US)
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QY 2869 GGTACACGGAGGCGCTG 2885
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LOCUS AX411903 19 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 3 from Patent WO0226968.
ACCESSION AX411903
VERSION AX411903.1 GI:21444368
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 3 04-APR-2002;
University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
FEATURES
Location/Qualifiers

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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="based on Homo sapiens"

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2831 CATATATATATAACA 2847
Db 1 CAGATATATGTAA 17

RESULT 1496
AX472591
LOCUS AX472591 19 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 5 from Patent WO0207757.
ACCESSION AX472591
VERSION AX472591.1 GI:22207494
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Lue,T.F., Lin,C.S. and Kan,Y.W.
TITLE Prevention and treatment of sexual arousal disorders
JOURNAL Patent: WO 0207757-A 5 31-JAN-2002;
Lue, Tom (US)
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/note="VEGFR-1B Primer"

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Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
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Db 1 ATGCTGGATTGTGGCA 17

RESULT 1497
AX643396/C
LOCUS AX643396 19 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 262 from Patent WO02099099.
ACCESSION AX643396
VERSION AX643396.1 GI:28551047
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Penger,A., Sprenger,R. and Brinkmann,U.
TITLE Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 02099099-A 262 12-DEC-2002;
Epidaurus Biotechnologie AG (DE)
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Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2827 TATACATATATATAT 2843
Db 1 TATACATATATATAT 18

RESULT 1498
AX643399
LOCUS AX643399 19 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 265 from Patent WO02099099.
ACCESSION AX643399
VERSION AX643399.1 GI:28551051
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Penger,A., Sprenger,R. and Brinkmann,U.
TITLE Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 02099099-A 265 12-DEC-2002;
Epidaurus Biotechnologie AG (DE)
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QY 2827 TATACATATATATAT 2843
Db 2 TATACATATATATAT 18

RESULT 1499
AX659444/C
LOCUS AX659444 19 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 46 from Patent WO02102824.
ACCESSION AX659444
VERSION AX659444.1 GI:29161674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Beimfohr,C. and Snaidr,J.
TITLE Method for specific fast detection of relevant bacteria in drinking
water
JOURNAL Patent: WO 02102824-A 46 27-DEC-2002;
Vermicon AG (DE)
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Db 18 TTCGGCTAGGGGTCAT 2

RESULT 1500
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LOCUS AX763838 19 bp RNA linear PAT 25-JUN-2003
DEFINITION Sequence 11 from Patent WO03040294.
ACCESSION AX763838
VERSION AX763838.1 GI:32258200
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KEYWORDS      .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1
AUTHORS        de Backer,M.D. and Harris,A.N.
TITLE          Method for the in vitro synthesis of short double stranded RNAs
JOURNAL        Patent: WO 03040294-A 11 15-MAY-2003;
               JANSSEN PHARMACEUTICA N.V. (BE)
FEATURES      source
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Db 2 CACCGCAAGCTGCCCG 18

RESULT 1501
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LOCUS          AX776236                19 bp    DNA        linear    PAT 14-JUL-2003
DEFINITION    Sequence 6 from Patent WO03048362.
ACCESSION     AX776236
VERSION       AX776236.1 GI:32693892
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1
AUTHORS        Farrar,G.J., Humphries,P., Millington-Ward,S. and Kenna,P.F.
TITLE          Suppression of polymeric alleles
JOURNAL        Patent: WO 03048362-A 6 12-JUN-2003;
               College of the Holy and Undivided Trinity of Queen Elizabeth (IE)
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Db 3 GAGATGATCAAGATGAT 19

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LOCUS          AX804504                19 bp    DNA        linear    PAT 25-NOV-2003
DEFINITION    Sequence 672 from Patent WO03060160.
ACCESSION     AX804504
VERSION       AX804504.1 GI:38521645
KEYWORDS      Oreochromis niloticus
SOURCE        Oreochromis niloticus
ORGANISM      Oreochromis niloticus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
               Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
               Labroidae; Cichlidae; Oreochromis.
REFERENCE      1
AUTHORS        Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
TITLE          Verification of food origin based on nucleic acid pattern

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recognition
Patent: WO 03060160-A 672 24-JUL-2003;
Genomar ASA (NO)
FEATURES      source
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Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3399 AGACGGTTTCCAGGAG 3415
Db 1 AGCCGGTTTCCAGTCAG 17

RESULT 1503
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LOCUS          BD070496                19 bp    DNA        linear    PAT 27-AUG-2002
DEFINITION    Methods for detecting mitochondrial mutations diagnostic for
               Alzheimer's disease and methods for determining heteroplasmy of
               mitochondrial nucleic acid.
ACCESSION     BD070496
VERSION       BD070496.1 GI:22616099
KEYWORDS      JP 2001514500-A/53.
SOURCE        unidentified
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Parker,W.D., Herrnstadt,C., Ghosh,S. and Fahy,E.D.
TITLE          Methods for detecting mitochondrial mutations diagnostic for
               Alzheimer's disease and methods for determining heteroplasmy of
               mitochondrial nucleic acid
JOURNAL        Patent: JP 2001514500-A 53 11-SEP-2001;
               MITOKOR
COMMENT        OS Unidentified
               PN JP 2001514500-A/53
               PD 11-SEP-2001
               PF 27-FEB-1998 JP 1998537738
               PR 28-FEB-1997 US 08/810599
               PI WILLIAM DAVIS PARKER,CORINNA HERRNSTADT,SOUMITRA GHOSH,BOIN D
               FI FAHY
               PC C12Q1/68,C07H21/04
               CC Strandedness: Double;
               CC Topology: Linear;
               CC Methods for detecting mitochondrial mutations diagnostic for
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               CC disease and methods for determining heteroplasmy of CC
               mitochondrial nucleic
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QY 1932 CACACACGACCTGTACA 1948
Db 3 CACACACGACCTGTCCA 19

RESULT 1504
BD084645/C
LOCUS          BD084645                19 bp    DNA        linear    PAT 27-AUG-2002

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DEFINITION RNase L activators and antisense oligonucleotides effective to
treat telomerase-expressing malignancies.
ACCESSION BD084645
VERSION BD084645.1 GI:22630255
KEYWORDS JP 2001524100-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Silverman,R.H., Kondo,S., Cowell,J.K., Li,G. and Torrence,P.F.
TITLE RNase L activators and antisense oligonucleotides effective to
treat telomerase-expressing malignancies
JOURNAL Patent: JP 2001524100-A 9 27-NOV-2001;
THE CLEVELAND CLINIC FOUNDATION,NATIONAL INSTITUTES OF HEALTH
COMMENT OS Artificial Sequence
PN JP 2001524100-A/9
PD 27-NOV-2001
PF 13-APR-1998 JP 1998546125
PR 21-APR-1997 US 60/044507,03-FEB-1998 US 09/018125 PI
ROBERT H SILVERMAN,SEIJI KONDO,JOHN K COWELL,GUYIYING LI,PAUL F
PI TORRENCE
PC C07H21/00,C07H21/02,C12Q1/68,A61K48/00
CC Description of Artificial Sequence: oligonucleotide FH Key
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FT Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Job time : 111 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 12:35:44 ; Search time 118 Seconds

(without alignments)

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Maximum Match 100%

Listing first 447 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	35.6	0.9	46	1	AZ773878
7	35.6	0.9	50	1	AZ471416
8	35.4	0.9	47	1	AZ471416
9	35.4	0.9	47	1	AZ441623
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67	33.8	0.9	43	1	AZ367342
68	33.8	0.9	43	1	AZ367342
69	33.8	0.9	44	1	AZ433034
70	33.8	0.9	44	1	AZ586159
71	33.8	0.9	45	1	AZ586159
72	33.8	0.9	45	1	AZ367342
73	33.8	0.9	45	1	AZ367342
74	33.8	0.9	46	1	AZ433034
75	33.8	0.9	46	1	AZ586159
76	33.8	0.9	46	1	AZ586159
77	33.6	0.9	47	1	AZ433034
78	33.6	0.9	48	1	AZ586159
79	33.4	0.9	36	1	AZ373001
80	33	0.9	47	1	AL040422
81	33	0.9	47	1	AL040422
82	33	0.9	47	1	DR23D13T
83	32.8	0.9	36	1	AZ514497
84	32.8	0.9	36	1	AZ766984
85	32.8	0.9	36	1	AZ939576
86	32.8	0.9	36	1	DR12B17S
87	32.8	0.9	37	1	AZ308741
88	32.8	0.9	37	1	AZ346800
89	32.8	0.9	37	1	AZ426831
90	32.8	0.9	37	1	AZ456482
91	32.8	0.9	37	1	AZ826021
92	32.8	0.9	37	1	AZ95480
93	32.8	0.9	38	1	AZ504337
94	32.6	0.9	40	1	AZ837355
95	32.6	0.9	43	1	AZ848637
96	32.4	0.9	35	1	AZ343541
97	32.4	0.9	35	1	AZ612777
98	32.4	0.9	35	1	AZ623738
99	32.4	0.9	35	1	AZ643234
100	32.4	0.9	35	1	AZ819087
101	32.4	0.9	36	1	AZ411170
102	32.4	0.9	36	1	AZ422282
103	32.4	0.9	36	1	AZ579564
104	32.4	0.9	36	1	AZ848143
105	32.4	0.9	40	1	AZ603138
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ACCESSION:AZ514610
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ACCESSION:AZ945104
ACCESSION:AZ320258
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ACCESSION:AZ471416
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ACCESSION:AZ653918
ACCESSION:AZ326400
ACCESSION:AZ367342
ACCESSION:AZ433034
ACCESSION:AZ586159
ACCESSION:AZ816720
ACCESSION:AZ968714
ACCESSION:AZ345520
ACCESSION:AZ418950
ACCESSION:AZ470417
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ACCESSION:AZ587825
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ACCESSION:AZ497644
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ACCESSION:AZ795539
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ACCESSION:AZ665896
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ACCESSION:AZ819582
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ACCESSION:AZ613732
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ACCESSION:AZ939576
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ACCESSION:AZ343541
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ACCESSION:AZ411170
ACCESSION:AZ422282
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ACCESSION:AZ848143
ACCESSION:AZ603138
ACCESSION:AZ838755

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0532 row: H column: 16
Seq primer: CGTTGTAACAGCAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0532H16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnates/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gil4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.0%; Score 38.2; DB 1; Length 47;
Best Local Similarity 93.0%; Pred. No. 3.9;
Matches 40; Conservative 0; Mismatches 3; Indels 0; Gaps 0

Qy 2309 GCCTTGCTGTGTGTGTGTGTGTGCCTGTGTGTGTGTGTGTG 2351
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Db 5 GCCTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 47

RESULT 2
AZ760053/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

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1M053M22F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM053M22 F, genomic survey sequence.

AZ760053
AZ760053.1 GI:12867475
GSS.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 48)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

C 399	17.8	0.5	23	1	TA300F12P	ACCESSION:AL490817
C 400	17.8	0.5	25	1	AZ644875	ACCESSION:AZ644875
C 401	17.8	0.5	25	1	AZ775159	ACCESSION:AZ775159
C 402	17.8	0.5	38	1	BG920906	ACCESSION:BG920906
C 403	17.6	0.5	24	1	AZ811237	ACCESSION:AZ811237
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C 417	17.4	0.5	22	1	AZ514387	ACCESSION:AZ514387
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C 424	17	0.4	32	1	AW250841	ACCESSION:AW250841
C 425	17	0.4	42	1	AZ483421	ACCESSION:AZ483421
C 426	16.8	0.4	20	1	AZ654458	ACCESSION:AZ654458
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C 432	16.6	0.4	23	1	AZ411764	ACCESSION:AZ411764
C 433	16.6	0.4	23	1	AZ618720	ACCESSION:AZ618720
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C 437	16.4	0.4	21	1	AZ626965	ACCESSION:AZ626965
C 438	16.4	0.4	21	1	BX054011	ACCESSION:BX054011
C 439	16.4	0.4	37	1	BX64796	ACCESSION:BX64796
C 440	16.4	0.4	40	1	CN546803	ACCESSION:CN546803
C 441	16.4	0.4	43	1	AZ476580	ACCESSION:AZ476580
C 442	16.2	0.4	21	1	AJ016967	ACCESSION:AJ016967
C 443	16.2	0.4	22	1	PCH303886	ACCESSION:PCH303886
C 444	16.2	0.4	22	1	PCH303886	ACCESSION:PCH303886
C 445	16.2	0.4	22	1	AZ300F12P	ACCESSION:AZ300F12P
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ALIGNMENTS

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AZ837595.1 GI:13007503
GSS.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0132 row: N column: 21
Seq primer: CACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGClM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.9%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred.No. 7.7; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 3;
QY 2313 TGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGC 2352
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clone UUGClM0091J18 F, genomic survey sequence.
ACCESSION
AZ352709
VERSION
AZ352709.1 GI:10431946

AZ837595.1 GI:13007503
GSS.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0132 row: N column: 21
Seq primer: CACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC2M0132N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGClM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.9%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred.No. 7.7; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 3;
QY 2313 TGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGC 2352
||| ||||||||||||||||||||||||||||||||||
1 TCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTC 40

DB

RESULT 13
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LOCUS
DEFINITION
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clone UUGC2M0133P13 F, genomic survey sequence.
ACCESSION
AZ837815
VERSION
AZ837815.1 GI:13007723
KEYWORDS
GSS.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: J column: 18
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Class: plasmid ends
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/clone_lib="Mouse 10kb plasmid UUGClM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.9%; Score 35.2; DB 1; Length 46;
Best Local Similarity 92.5%; Pred.No. 8.7; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 3;
QY 2312 TTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTC 2351
||| ||||||||||||||||||||||||||||||||||
1 TTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTC 40

DB

RESULT 13
AZ837815
LOCUS
DEFINITION
2M0133P13F Mouse 10kb plasmid UUGClM library Mus musculus genomic
clone UUGC2M0133P13 F, genomic survey sequence.
ACCESSION
AZ837815
VERSION
AZ837815.1 GI:13007723
KEYWORDS
GSS.

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adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* X10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Best Local Similarity 86.4%; Pred. No. 12;
Matches 38: Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGCATCC 2358

pB
44 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAGTAC 1

RESULT	26
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	IMW15D06F Mouse 10kb plasmid UGCGM library Mus musculus genomic
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ACCESSION	AZ389462				
VERSION	AZ389462.1	GI:10503170			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 39)				
AUTHORS	Islan, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.				

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0150 row: D column: 06
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 39.

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                /clone_lib="Mouse 10kb plasmid UUGICM1 library"
                /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to
    
```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (G1/47321419b/AP129072.1), a copy-number regulated inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 34.2; DB 1; Length 39;
Best Local Similarity 92.3%; Pred. No. 9.6;
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

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DEFINITION	
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clone INTGC1W0562C19 R genomic survey sequence.	Mus musculus genomic

ACCESSION	AZ765740
VERSION	AZ765740.1
KEYWORDS	GSS

ACKNOWLEDGMENTS	Mus musculus (house mouse)
SOURCE	Mus musculus
ORGANISM	Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE	1 (bases 1 to 39)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingy, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE	Mouse whole genome scaffolding with paired end reads from long plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

BALL, USA# 5606
Tel.: 801 585 5706
Fax: 801 585 7177
Email: daun@gznetics.utah.edu
E-mail: daun@gznetics.utah.edu
Phone: 0563 10000 Std Error: 0.00
Date: 0563 row: C column: 19
Size primer: CACACAGGAACACATGACC
Type: plasmid ends
High quality sequence stop: 39.

FEATURES	Location/Qualifiers
source	1. .39

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/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD4nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

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Best Local Similarity 83.0%; Pred. No. 12;

Query Match 0.9%; Score 34; DB 1; Length 47;
Best Local Similarity 88.1%; Pred. No. 12;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

[illegible]

[illegible]

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REFERENCE      Mammalia; Eutheraia; Rodentia; Sciurognathi; Muridae; Musineae; Mus  
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T.T., Duval,B., Hamil,C.,  
              Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
              Reilly,W., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
              Niederhasenr,A. and Wright D.,Weiss,R.  
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL        Plasmid inserts  
COMMENT        Unpublished (2000)  
               Contact: Robert B. Weiss  
               University of Utah Genome Center  
               University of Utah  
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
               84112, USA  
               Tel.: 801 585 5606  
               Fax: 801 585 7177  
               Email: ddunn@genetics.utah.edu  
               Insert Length: 10000 Std Error: 0.00  
               Plate: 0347 row: F column: 09  
Seq primer: CACGAGGAACAAGCTATGCACC  
Class: plasmid ends  
High quality sequence stopc: 41.  
  
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     /strain="C57BL/6j"  
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     /clone="UUGCLM0347F09"  
     /sex="Male"  
     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
     /clone_lib="Mouse 10kb plasmid UUGCLM library"  
     /note="Vector: PWD42nv; Purified genomic DNA from M.  
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           Laboratory Mouse DNA Resource  
           (http://www.jax.org/resources/documents/dnares/). The DNA  
           was hydrodynamically sheared by repeated passage through a  
           0.005 inch orifice at constant velocity. The sheared DNA  
           was blunt end-repaired with T4 DNA polymerase and T4  
           polynucleotide kinase. Adaptor oligonucleotides were  
           ligated to the blunt ends in high molar excess. The  
           10.5 kb range using preparative agarose gel  
           electrophoresis. Vector DNA was prepared from a derivative  
           of pMD42 (gi|4732114|gb|AFI29072.1), a copy-number  
           inducible derivative of plasmid RI. The vector was ligated  
           with adaptors complementary to the insert adaptors and  
           purified. The sheared, adaptor mouse DNA was annealed to  
           adaptor vector DNA, and transformed into  
           chemically-competent E.coli XL10-Gold (Stratagene) cells  
           and selected for ampicillin resistance."
```

REFERENCE 1 (bases 1 to 41)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
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 Seq primer: CACACAGAAACAGCTATGACC
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 High quality sequence stop: 41.
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 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 33.8; DB 1; Length 41;
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 Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
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 5 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 41

Db 5 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 41

RESULT 59
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 LOCUS 2M0210M16R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 DEFINITION clone UUGC2M0210M16 R, genomic survey sequence.
 ACCESSION AZ947931
 VERSION AZ947931.1 GI:13819158
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 41)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0210 row: M column: 16
 Seq primer: CACACAGAAACAGCTATGACC
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 High quality sequence stop: 41.
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 1..41
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 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 33.8; DB 1; Length 41;
 Best Local Similarity 94.6%; Pred. No. 11;
 Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
 |||||
 5 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 41

Db 5 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 41

RESULT 60
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 LOCUS 1M0059101R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0059101 R, genomic survey sequence.
 ACCESSION AZ331554
 VERSION AZ331554.1 GI:10394361
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 42)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE	JOURNAL	COMMENT
Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Petersen, T., Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niedenausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddumegenetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0059 row: I column: 01 Seq primer: CACACAGGAGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 42. Location/Qualifiers		

Location/Qualifiers
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/clone_1ib="Mouse 10kb plasmid UUC1M library"
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Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [g14732114[9b]/AF12072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adapored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

[illegible]

REFERENCE AUTHORS	KEYWORDS	VERSION	ACCESSION	LOCUS	DEFINITION	RESULT 61
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,	mus musculus (house mouse)	GS5.	AZ593813.1 GI:11716003	AZ593813	42 bp DNA linear	GS5 13-DEC-2000
	Mus musculus		clone U05K02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.		clone U05K02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic			
	1 (bases 1 to 42)		AZ593813			
			AZ593813.1 GI:11716003			

TITLE	Relly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0405 row: K column: 02 Seq primer: CACACAGCAAAACACTATGACC Class: plasmid ends High quality sequence stop: 42. location/Qualifiers 1..42..
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/clone_id="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD4N9, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnars/). The DNA
was hydrolytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repeated with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (gll4732114[gb|AI129072.1], a copy-number
inducible derivative of plasmid R1). The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match          0.9% Score 33.8; DB 1; Length 42;
Best Local Similarity 94.6%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT	62
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LOCUS	AZ851228
DEFINITION	42 bp DNA linear GSS 21-FEB-2001
ACCESSION	U00153E22F Mouse 10kb plasmid UUGCM library Mus musculus genomic clone UUGCM0153E22 F, genomic survey sequence.
VERSION	AZ851228
KEYWORDS	AZ851228.1 GI:13037016
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
	Mus musculus
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 42)
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Retilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
AUTHORS	


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/clone_idb="Mouse 10kb plasmid UNGCM library"
/nodec="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match	0.9%;	Score 33.8;	DB 1;	Length 45;
Best Local Similarity	94.6%;	Pred. No. 12;		
Matches 35; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

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REFERENCE
1 (bases 1 to 45)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

TITLE Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kbp

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0547 row: P column: 02
Seq primer: CACACAGAAACGCTATGACC
Class: Plasmid ends
High quality sequence stop: 45.

FEATURES

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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[illegible]

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			BX548613	BX548613			
			BX548613.1	GI:33298846			
			EST.				

REFERENCE

Title Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N

Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5
end of the cDNA all p1c reads are from
the 3' end.

FEATURES	Location/Qualifiers
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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
(Pages 1 to 37)				
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tilgney, A., von Niederhuser, A. and Wright, D.		Mouse whole genome scaffolding with paired end reads from 10kb	Paenid Insects	Unpublished (2000)
			Contact: Robert B. Weiss	
			University of Utah	
			Genome Center	
			University of Utah	

/clone="UUGC2M0189A20"
 /sex="Male"
 /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Query Match
 Best Local Similarity 91.9%; Pred. No. 16;
 Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 DB 37 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 37

RESULT 109
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 accession clone UUGC2M0071A18 R, genomic survey sequence.
 AZ808181
 VERSION AZ808181.1 GI:12973460
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 40)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0071 row: A column: 18
 Seq primer: CACACGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 40.
 Location/Qualifiers
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 /clone="UUGC2M0071A18"

/sex="Male"
 /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
 Best Local Similarity 91.9%; Pred. No. 17;
 Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
 DB 1 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 37

RESULT 110
 LOCUS AZ387857 41 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0147122R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 accession clone UUGC1M0147122 R, genomic survey sequence.
 AZ387857
 VERSION AZ387857.1 GI:10501565
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 41)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0147 row: L column: 22
 Seq primer: CACACGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 41.
 Location/Qualifiers
 1..41
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0147122"
 /sex="Male"

/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 32.2; DB 1; Length 42;
Best Local Similarity 91.9%; Pred. No. 18;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
DB 42 GTATGATGTCGTGTCGTGTCGTGTCGTGTCGTG 6

RESULT 113
AZ355175 42 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0094D20R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM10094D20 R, genomic survey sequence.
ACCESSION AZ355175
VERSION AZ355175.1 GI:10467323
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 42)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 20
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 42.

FEATURES
source location/Qualifiers
1..42
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM10094D20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 32.2; DB 1; Length 42;
Best Local Similarity 91.9%; Pred. No. 18;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
DB 2 GTGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 38

RESULT 114
AZ371099 44 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0122G02F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM10122G02 F, genomic survey sequence.
ACCESSION AZ371099
VERSION AZ371099.1 GI:10484799
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 44)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0122 row: G column: 02
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 44.

FEATURES
source location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM10122G02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

0.005 inch orifice at constant velocity. The sheared

11085200 0117

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R⁺). The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

RESULT	135
LOCUS	AZ370273
DEFINITION	AZ370273 35 bp DNA linear GSS 02-OCT-2000
ACCESSION	I0612B13F Mouse 10kb plasmid UUCIM library Mus musculus genomic
VERSION	clone UUCIM012B13 F, genomic survey sequence.
KEYWORDS	AZ370273
SOURCE	AZ370273.1 GI:10483973
ORGANISM	GSS.
REFERENCE	Mus musculus (house mouse)
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 35) Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellay,M., Rose,R., Rose,R., Stokes,R., Tinley,A., von Niederhausern,A. and Wright,D.,Weise,R;
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0121 row: B column: 13 Seq primer: CGTGTGTAAGACGACGCCAAG Class: plasmid ends High quality sequence stop: 35.

FEATURES

Source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0121B13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PBD42ny. Purified genomic DNA from M.
 musculus C57BL/6J (male). was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repeated with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PBD42 (G114732114[g]/AF129372.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match	0.8%	Score	31.4	DB	1	Length	35
Best Local Similarity	97.0%	Pred. No.	18				
Matches	32	Conservative	0	Mismatches	1	Indels	0
						Gaps	0

Dy 2319 GTGTGTTGGTCTGACCGATGTGTTGTTGGT 2353
|||||
Db 3 GTGTGTTGGTCTGACCGATGTGTTGTTGGT 35

RESULT 136

AC430974	LOCUS	AC430974	37 bp	DNA	linear	GSS 03-OCT-2000
	DEFINITION	IM0215L08R Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M0215L08 R, genomic survey sequence.				
	ACCESSION	AC430974				
	VERSION	AC430974.1	GI:10554987	GSS.		
	KEYWORDS					
	SOURCE	Mus musculus (house mouse)				
	ORGANISM	Mus musculus				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	REFERENCE	1 (bases 1 to 37)				
	AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weis, R.				
	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
	JOURNAL	Unpublished (2000)				
	COMMENT	Contact: Robert B. Weis				

FEATURES

Source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U083C1M0215108"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_library="Mouse 10kb plasmid UUGIC library"
 /note="Vector: pMDA2nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrolytically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMDA2 (gll|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match	0.8%	Score 31.4	DB 1	Length 37
Best Local Similarity	97.0%	Pred. No. 19		
Matches 32, Conservative	0	Mismatches	1	Indels 0
				Gaps 0

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Dy      2319 GTGTGTTGTGTGTCCGTGTGTGTGTGTGTG 2351
          |||||
Dd      5   GTGTGTGTGTGTGTGTGTGTGTGTGTGTG 37
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AZ397262

LOCUS	AZ397262	40 bp	DNA	linear	GSS 03-OCT-2000
DEFINITION	IWO16211E.F Mouse 10kb plasmid UOCCIM library Mus musculus genomic clone UOCCIM0162112.F, genomic survey sequence.				
ACCESSION	AZ397262				
VERSION	AZ397262.1	GI:10512334			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murine; Mus.				
AUTHORS	1 (bases 1 to 40) Dunn,D., Aoyagi,A., Barber,M., Baccorn,T., Duval,B., Hamill,C., Iellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Nedderhassern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 plate: 0162 row: I column: 12 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 40.				

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FEATURES
SOURCE
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U061M0162112"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb Plasmid genomic library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptorized DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (y14732114[yb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptorized mouse DNA was annealed to
adaptorized vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
0.8%; Score 31; DB 1; Length 40;
Best Local Similarity 87.2%; Pred. No. 24;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCA 2353
DB 2 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA 40
RESULT 138
AZ819018 40 bp DNA linear GSS 20-FEB-2001
LOCUS

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DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
280089119F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0089119 F. genomic survey sequence.	AZ819018								
	AZ819018.1	GI:12988926	GSS.	Mus musculus (house mouse)					
				Mus musculus					
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus-					
				1 (bases 1 to 40)					
				Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Petersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.					
				Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts					
				Unpublished (2000)					
				Contact: Robert B. Weiss					
				University of Utah Genome Center					
				Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA					
				Tel.: 801 585 5606					
				Fax: 801 585 7177					
				Email: dunn@genetics.utah.edu					
				Insert Length: 10000					
				Std Error: 0.00					
				Plate: 0089					
				row: 1					
				Seq primer: CGTGTAAAACGACGGCCAGT					
				Class: plasmid					
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/strain="C57BL/6J"
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/cclone_idb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number indelible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

[illegible][illegible]

[illegible][illegible]

SOURCE
 ORGANISM
 Mus musculus
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 38)
 Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamli,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
 Relly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 UNPUBLISHED (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY OF UTAH
 GENOME CENTER
 308 Rm.
 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: dunn@genetics.utah.edu
 INSERT LENGTH: 10000
 STD ERROR: 0.00
 PLATE: 0311
 ROW: B
 COLUMN: 02
 SEQ PRIMER: CACACAGGAACAGCTATGACC
 CLASS: plasmid ends
 HIGH QUALITY SEQUENCE STOP: 38.
 LOCATION/QUALIFIERS
 1..38

ORGANISM	Mus musculus
REFERENCE	Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia, Eutheria: Rodentia, Scturognathii, Muridae, Murinae; Mus. 1 (bases 1 to 39)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished. (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0081 row: N column: 12 Seq primer: CACACAGGAACAGCATATGACC Class: plasmid ends High quality sequence stop: 39. Location/Qualifiers 1. .39
FEATURES	
SOURCE	

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	Best Local Similarity	89.2%;	Pred. No. 25;		
	Matches	33;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	2319	GTGTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGCACA	2355		
Db	2	GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATATAA	38		
RESULT 144	AZ346424				
LOCUS	AZ346424				
DEFINITION	1M0081N12 Mouse 10kb plasmid UUCGCM library Mus musculus genomic	39 bp	DNA	linear	GSS 29-SEP-2000
ACCESSION	AZ346424				
VERSION	AZ346424.1				
KEYWORDS	GI:10425661				
SOURCE	GSS.				
	Mus musculus (house mouse)				

	Query Match	0.8*	Score 30.67	DB 1	Length 39;
	Best Local Similarity	89.2%	Pred. No. 26;		
Matches	33;	Conservative	0;	Mismatches	4; Indels 0; Gaps 0;
OY	2315	GTCGTGCTGTGTGTGTGCCTGTGTGTGTGTGTC	2351		
Dd	1	GTGTGTTTCTGTGTGTGTGTGTGTGTGTGTGTG	37		
RESULT 145	AZ480184				
LOCUS	AZ480184				
DEFINITION	AZ480184	39 bp	DNA	linear	GSS 04-OCT-2000
	IM0301E04 Mouse 10kb plasmid UUCGM library Mus musculus genomic				
ACCESSION	AZ480184				
VERSION	AZ480184.1	GI:10641249			
KEYWORDS	GSS.				
SOURCE	Mus musculus	(house mouse)			
ORGANISM	Mus musculus				

REFERENCE
AUTHORS
1 (bases 1 to 39)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0301 row: E column: 04
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 39.
Location/Qualifiers
1. 39
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M031B04"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 30.6; DB 1; Length 39;
Best Local Similarity 89.2%; Pred. No. 26;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
|||
Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 37

RESULT 146
AZ3074885
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
1 (bases 1 to 39)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0249 row: P column: 09
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 39.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone_1lb="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 30.6; DB 1; Length 39;
Best Local Similarity 89.2%; Pred. No. 26;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
|||
Db 2 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 38

RESULT 147
AZ307970
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	1 (bases 1 to 32)
1	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhassern, A., and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0010 row: A column: 03 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 32. Location/Qualifiers
FEATURES	1..32
SOURCE	/organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUC1M0010A03" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match	0.8%; Score 30.4; DB 1; Length 32;
Best Local Similarity	96.9%; Pred. No. 22;
Matches	31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	2318 TGTGTGTGTGTGTGTGCGGTGTGTGTGTGTG 2349
Db	1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 32
RESULT 148	
AZ311840	
LOCUS	32 bp DNA linear GSS 29-SEP-2000
DEFINITION	IM0027M21F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0027M21 F, genomic survey sequence.
ACCESSION	AZ311840
VERSION	AZ311840.1 GI:10355201
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 32)

AUTHORS	TITLE	JOURNAL	COMMENT
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Niederhansen, A., and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	
Contact: Robert B. Weiss			
University of Utah			
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA			
Tel: 801 585 5606			
Fax: 801 585 7177			
Email: ddunn@genetics.utah.edu			
Insert Length: 10000	Std Error: 0.00		
Plate: 0027	row: M	column: 21	
Seq primer: CGTTGTAACGACGCGCAGT			
Class: plasmid ends			
High quality sequence stop: 32.			
FEATURES	source	Location/Qualifiers	
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	/db_xref="taxon:10090"		
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	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"		
	/clone_lid="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse Resource		
	(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[GB AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	Best Local Similarity	0.8%; Score 30.4; DB 1; Length 32;	
Matches	31; Conservative	0; Mismatches	1; Indels
0y	2318	TGTTGTGTGTGTGTGTGCGTGTGTGTGTGTG	2349
Db	1	TGTTGTGTGTGTGTGTGTGTGTGTGTGTG	32
RESULT 149	AZ495235		
LOCUS	AZ495235		
DEFINITION	1M0331E05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0331E05 F, genomic survey sequence.		
ACCESSION	AZ495235		
VERSION	AZ495235.1	GI:10670567	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 32)		
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,		

TITLE
JOURNAL
COMMENT

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0331 row: E column: 05
Seq primer: CTTGTAAACGACGCCGCGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers

FEATURES
source

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/organism="Mus musculus"
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/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|9b|AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapored mouse DNA was annealed to
adapored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 96.9%; Pred. No. 22;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGGTGTGTGTGTG 2349
|||||
1 TGTGTGTGTGTGTGTGTGTGTGTGTGTG 32
|||||

RESULT 150
BX559884 33 bp mRNA linear EST 10-OCT-2003
BX559884 Glosina morsitans morsitans adult infected gut Glosina
morsitans morsitans cDNA clone Tse46c02_plc, mRNA sequence.
ACCESSION BX559884
VERSION BX559884.1 GI:33367775
KEYWORDS EST.
SOURCE Glosina morsitans morsitans
ORGANISM Glosina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glosina.
REFERENCE 1 (bases 1 to 33)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly *Glossina*
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix plc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
Location/Qualifiers

FEATURES
source

1..33
/organism="Glosina morsitans morsitans"
/mol_type="mRNA"
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/db_xref="taxon:37546"
/clone="Tse46c02_plc"
/tissue_type="adult infected gut"
/clone_lib="Glosina morsitans morsitans adult infected
gut"
/note="Country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match
Best Local Similarity 93.9%; Pred. No. 27;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGCGGTGTGTGTGTGTG 2351
|||||
1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTG 33
|||||

RESULT 151
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LOCUS IM0498820R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0498820 R, genomic survey sequence.
ACCESSION AZ638769
VERSION AZ638769.1 GI:11760959
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 33)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 row: B column: 20
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends


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/clone="UUGC1M0493004"
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/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

RESULT 187
AZ440652
LOCUS AZ440652 31 bp DNA linear GSS 03-OCT-2000
DEFINITION clone231N14R Mouse 10kb plasmid UUCGM1 library Mus musculus genomic
ACCESSION clone UUCGM0231N14 R, genomic survey sequence.
VERSION AZ440652
KEYWORDS AZ440652.1 GI:10564665
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
REFERENCE Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Ridley,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niedelhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid insets
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std. Error: 0.00
Plate: 0231 row: N column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
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Source location/Qualifiers
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/strain="C57BL/6J"
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RESULT	188
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ACCESSION	U0066F11R Mouse 10kb plasmid UGCGM library Mus musculus genomic
VERSION	clone UUGCGM0064F17 R, genomic survey sequence.
KEYWORDS	AZ335085.1 GI:10403046
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus. 1 (bases 1 to 32) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islami,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0064 row: F column: 17 Seq primer: CACACAGGAACACACTATGACC Class: plasmid ends High quality sequence stop: 32. Location/Qualifiers 1..32 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCGM0064F17" /sex="Male"
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SOURCE	

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

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/db_xref="taxon:10090"
/clone="UCSC1M0333B07"
/sex="Male"
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AZ659684

LOCUS

DEFINITION 31 bp DNA linear GSS 14-DEC-2000
1M0537C17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0537C17 F, genomic survey sequence.

ACCESSION AZ659684
VERSION AZ659684
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0537 row: C column: 17
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 31.

FEATURES

source

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
ligated DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

Best Local Similarity 93.3%; Pred. No. 56;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2345
DB 2 TATGTGTGTGTGTGTGTGTGTGTGTGTGT 31

RESULT 196

AZ626646

LOCUS

DEFINITION 33 bp DNA linear GSS 13-DEC-2000
1M0467E06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0467E06 F, genomic survey sequence.

ACCESSION AZ626646
VERSION AZ626646
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0467 row: E column: 06
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 33.

FEATURES

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
ligated DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

Best Local Similarity 93.3%; Pred. No. 60;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2348
DB 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 30

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RESULT 197
LOCUS      AZ642584
DEFINITION 33 bp DNA linear GSS 14-DEC-2000
            1M0505K12R Mouse 10kb plasmid U06C1M library Mus musculus genomic
            clone U06C1M0505K12 R, genomic survey sequence.
ACCESSION  AZ642584
VERSION     AZ642584.1
KEYWORDS    GI:11769336
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Mus.
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,S., Pedersen,T.,
            Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contract: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: dunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0505 row: K column: 12
            Seq primer: CACACAGGAAACAGTAGACC
            Class: plasmid ends
            High quality sequence stop: 33.
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                 /strain="C57BL/6J"
                 /db_xref="taxon:10090"
                 /clone="U06C1M0505K12"
                 /sex="Male"
                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                 /clone.lib="Mouse 10kb plasmid U06C1M library"
                 /note="Vector: PMD42nv, Purified genomic DNA from M.
                 musculus C57BL/6J (male) was obtained from the Jackson
                 Laboratory Mouse DNA Resource
                 (http://www.jax.org/resources/documents/dnares/). The DNA
                 was hydrodynamically sheared by repeated passage through a
                 0.005 inch orifice at constant velocity. The sheared DNA
                 was blunt end-repaired with T4 DNA polymerase and T4
                 polynucleotide kinase. Adaptor oligonucleotides were
                 ligated to the blunt ends in high molar excess. The
                 adapted DNA was purified and size-selected for a 9.5 to
                 10.5 kb range using preparative agarose gel
                 electrophoresis. Vector DNA was prepared from a derivative
                 of pMDA2 (gi|4732114|gb|AF129072.1), a copy-number
                 inducible derivative of plasmid R1. The vector was ligated
                 with adaptors complementary to the insert adaptors and
                 purified. The sheared, adapted mouse DNA was annealed to
                 adapted vector DNA, and transformed into
                 chemically-competent E. coli XL10-Gold (Stratagene) cells
                 and selected for ampicillin resistance."
Query Match      0.7%; Score 26.6; DB 1; Length 33;
Best Local Similarity 87.9%; Pred. No. 63;
Matches 29; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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[illegible]

	AZ983391	38 bp	DNA	linear	GSS 27-APR-2001
LOCUS	AZ983391				
DEFINITION	clone d64105R Mouse 10kb plasmid tUGC2M library Mus musculus genomic				
ACCESSION	clone tUGC2M0264105 R, genomic survey sequence.				
VERSION	AZ983391				
KEYWORDS	AZ983391.1 GI:13854618				
SOURCE	GSS.				
ORGANISM	Mus musculus (house mouse)				
TAXID	Mus musculus				
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 38)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Malmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nedehausen,A., and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0..00 Plate: 0264 row: I column: 05 Seq primer: CACACAGCAAACTACTATGACC Clasas: plasmid ends High quality sequence stop: 38.				
JOURNAL					
COMMENT					

1. 38
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UMGC2M0264105"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UMGCG library"
/note="Vector: PMD429; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repeated with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD2 (gii473211|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```
Query Match      0.7%; Score 26.6; DB 1; Length 38;
Best Local Similarity 87.9%;
Matches 29; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Dy 2311 TTTCGTCTGTCATCTGTCAGTCCGTATCAG 2343
 |||||
Db 6 TGTGATGGTGATCTGTCATCTGTCATCAG 38

RESULT 200
BX553058

LOCUS	28 bp	RNA	linear	EST 10-OCT-2003
DEFINITION	BX553058 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse127a09_plc, mRNA sequence.			
ACCESSION	BX553058			
VERSION	BX553058.1			
KEYWORDS	GI:33377257			
SOURCE	EST.			
ORGANISM	Glossina morsitans morsitans			
REFERENCE	Glossina morsitans morsitans			
AUTHORS	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.			
TITLE	1 (bases 1 to 28)			
JOURNAL	Lehane, M.J., Aksoy, S., Gibson, M., Kethnou, A., Beriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.			
MEDLINE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes			
PUBMED	Genome Biol. 4 (10), R63 (2003)			
COMMENT	28881942 14519198			
	Contact: Hall N			
	Pathogen Sequencing Unit			
	The Sanger Institute The Wellcome Trust Genome Campus			
	Hinxton, Cambridge, CB10 1SA, UK			
	Request for clones, please contact: Mike Lehane			
	Prof. M.J.Lehane			
	School of Biological Sciences,			
	University of Wales,			
	Bangor LL57 2UW			
	All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.			

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1. 28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="Country: Zimbabwe, EST from adult gut infected with
.brucei"

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Query Match	0.7%	Score 26.4	DB 1	Length 28
Best Local Similarity	96.4%	Pred. No. 56		
Matches 27, Conservative	0	Mismatches	1	Indels 0
				Gaps 0

Oy		2319 GTGTGTTGTGTGTCCCTGTCGGTGT	2346
Dd	1	GTTGTGTGTGTGTGTGTGTGTGT	28

RESULT 201

LOCUS BX559897 28 bp mRNA linear EST 10-OCT-2003
DEFINITION BX559897 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans CDNA clone Tse46d02_p1c, mRNA sequence.

ACCESSION	BX559897
VERSION	BX559897.1
KEYWORDS	GI:33367800 EST.

SOURCE ORGANISM	<i>Glossina morsitans morsitans</i>	<i>Glossina morsitans morsitans</i>
1		
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100		

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Nematocera; Clasičníd; Cloninae

REFERENCE
1 (bases 1 to 28)
Tahara M, T. Akao S, Gibson W, Keshornou A, Berriman M.
hipoboscoidae; grossinidae; grossina.

TITLE	ADJUNCTS
Adult midgut expressed sequence tags from the tsetse fly <i>Glossina</i>	Lehane, M. C., Gibson, M., McEldowney, J., Deane, M. C., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.

morsitans mors
response genes

	Query March	0.7%	Score 26.4;	DB 1;	length 28;
	Best Local Similarity	96.4%;	Pred. No. 56;		
	Matches 27; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
OY	2317 CTGTCGTCTGTCGTCTGCCTGTCGTCT				
Dd	1 CTGTCGTCTGTCGTCTGCCTGTCGTCT				

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

TITLE	DESCRIPTION
Mouse whole genome scaffolding with paired end reads from 10Kbp plasmid inserts	

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert length: 10000 Srd Error: 0.00
Plate: 0278 row: C column: 15
Seq primer: CGTGTAAACGACGCCACT
Class: plasmid ends
high quality sequence stop: 28.

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FEATURES
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	Query Match	0.7%;	Score 26.4;	DB 1;	Length 28;
	Best Local Similarity	96.4%;	Pred. No. 56;		
	Matches 27;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	2318 TGTGTTGTGTGTGTGCCTGTGTGTGTCG	2345			
Db	1 TGTGTGTGTGTGTGTGTGTGTGTGTGTG	28			

RESULT 205	28 bp	DNA	linear	GS5 05-OCT-2000
AZ514363				
LOCUS				
DEFINITION				
	AZ514363			
	1M0361G05F Mouse 10kb plasmid U06C1M library Mus musculus genomic			
	clone U06C1M0361G05 F, genomic survey sequence.			

SOURCE ORGANISM	Mus musculus (house mouse)
Mus musculus	
Mus musculus	

REFERENCE	1 (pages 1 to 28)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Hartung, W., Hertzog, P., Kohnen, E.

TITLE	Author	Year	Journal	Volume	Issue	Page(s)	DOI	PMID	PubMed URL
Mouse whole genome scaffolding with paired end reads from 10Kbp plasmid inserts	Wang J, et al.	2009	Nature Methods	6	7	583-588	10.1038/nmeth.1371	19401221	https://pubmed.ncbi.nlm.nih.gov/19401221/

UNPUBLISHED (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA
Tel.: 801 585 75606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: G column: 05
Seq primer: CGTTCGTAACAGACGGCCAT
Class: plasmid ends
High quality sequence stop: 28.

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FEATURES
SOURCE
1..28
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"

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/clone="UUGCIM0361G05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42mv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

/sex="Male"
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/c1one_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to the adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

RESULT	206
AZ644345	
LOCUS	28 bp DNA linear GSS 14-DEC-2000
DEFINITION	M0508B1ef Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUCG1M0508E16 F, genomic survey sequence.
ACCESSION	AZ644345
VERSION	AZ644345.1 GI:11772782
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weise,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weise University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0508 row: E column: 16 Seq primer: CGTTGTAAACGACGGCCAGT Class: plasmid ends High quality sequence atbp: 28. Location/Qualifiers 1..28 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUCG1M0508E16"
FEATURES	
source	

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RESULT 207
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DEFINITION AZ648665 28 bp DNA linear GSS 14-DEC-2000
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ACCESSION  AZ648665
VERSION     AZ648665.1
KEYWORDS    GI:11781356
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Kelly,R., Rose,M., Rose,R., Stokes,R., Tinney,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL     Contact: Robert B. Weiss
COMMENT     University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: dunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0517 row: J column: 18
            Seq primer: CACACAGCAAAACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 28.
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            /clone="UUCG1M0517J18"
            /sex="Male"

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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 [g14732114|3D|A123072.1], a copy-number inducible derivative of Plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.7%	Score 26.4;	DB 1;	length 30;
Best Local Similarity	96.4%;	Pred. No. 60;		
Matches 27; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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QY      2317 CTGTGTGTGTGTGTGCGTGTGTGT 2344
          |||||
Db      3 CTGTGTGTGTGTGTGTGTGTGT 30

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RESULT 211					
AZ961995					
LOCUS	AZ961995	30 bp	DNA	linear	GS5 27-APR-2001
DEFINITION	2M0230G12R Mouse 10kb plasmid UGC2M library Mus musculus genomic				
ACCESSION	clone UGC2M0230G12 R, genomic survey sequence.				
	AZ961995				

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE
AUTHORS

1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kbp plasmid inserts

JOURNAL COMMENT
Unpublished (2000) Weiss
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606

Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.007
Plate: 0230 row: G column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

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FEATURES      Location/Qualifiers
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/mol_type="genomic DNA"
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/clone_id="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWDm229. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson

```

(<http://www.jax.org/resources/documents/natres/>). The DNA was hydrodynamically sheared by repeated passages through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1472314[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match      0.7%; Score 26.4; DB 1; Length 32;
Best Local Similarity 96.4%; Pred. No. 65;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
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LOCUS	DEFINITION	LOCUS	DEFINITION
AZ623245	36 bp DNA linear	AZ623245	36 bp DNA linear
LOCUS	1M0460C1R Mouse 10kb plasmid UUC1M library Mus musculus genomic	LOCUS	1M0460C1R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION	clone UUC1M0460C1s R, genomic survey sequence.	DEFINITION	clone UUC1M0460C1s R, genomic survey sequence.
ACCESSION	AZ623245	ACCESSION	AZ623245
VERSION	AZ623245.1	VERSION	AZ623245.1
KEYWORDS	GSS.	KEYWORDS	GSS.

ORGANISM	TITLE	JOURNAL	COMMENT
Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.			
REFERENCE			
1 (bases 1 to 36)			
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isalam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tinley, A., von Niedernhausen, A. and Wright, D., Weiss, R.			
Authors			
	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
	Unpublished (2000)		
	Contact: Robert B. Weiss		
	University of Utah Genome Center		

COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dduan@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0460 row: C column: 15 Seq primer: CACACAGCAACAGCTATGACC Class: plasmid ends High quality sequence stop: 36. Location/Qualifiers 1. .36 /organism="Mus musculus" (seq) type="genomic dna"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="HUGClM0460C15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGClM library"
/notes="vector: PMD429; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

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RESULT 220
 AZ425112 30 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0205101F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION Clone UUGC1M0205101 F, genomic survey sequence.
 ACCESSION AZ425112
 VERSION AZ425112.1 GI:10549125
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 30)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0205 row: 1 column: 01
 Seq primer: CATTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.

FEATURES

source

1..30
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 /clone="UUGC1M0205101"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 25.8; DB 1; Length 30;
 Best Local Similarity 93.1%; Pred. No. 71;
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2319 GTGCTGTGCTGTGCGCTGTGCTGTG 2347
 DB 2 GCGTGTGTGTGTGTGTGTGTGTGTG 30

RESULT 221
 AZ304813 32 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0005118F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION Clone UUGC1M0005118 F, genomic survey sequence.
 ACCESSION AZ304813
 VERSION AZ304813.1 GI:10341207
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 32)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0005 row: 1 column: 18
 Seq primer: CATTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 32.

FEATURES

source

1..32
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0005118"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 25.8; DB 1; Length 32;
 Best Local Similarity 93.1%; Pred. No. 76;
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2319 GTGCTGTGCTGTGCGCTGTGCTGTG 2347
 DB 4 GCGTGTGTGTGTGTGTGTGTGTGTG 32

RESULT 222

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FEATURES
source
34 bp DNA linear GSS 20-FEB-2001
LOCUS
A2807557
DEFINITION
2M0070B06R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0070B06 R, genomic survey sequence.
ACCESSION
A2807557
VERSION
A2807557.1 GI:12972024
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Bascorn,T., Duval,L.C.,
Jellam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0070 row: B column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers
1..34

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Query March	0.74	Score 25.81	DB 1	Length 34
Best Local Similarity	93.1%	Pred. No. 81		
Matches 27	Conservative	0	Mismatches 2	Indels 0
2325	GTGTGTGTGCGTGTGTGTGTGTGTGCA	2353		
1	GTGTGTGTGTGTGTGTGTGTGTGTGTGAA	29		

RESULT 223
AZ491991

LOCUS	AA4931991	35 bp	DNA	linear	GENS 05-OCT-2000
DEFINITION	IM0325C2R Mouse 10kb plasmid UNGCM library Mus musculus genomic				
ACCESSION	clone UNGCM0325C2R, genomic survey sequence.				
VERSION	AA491991				
KEYWORDS					
SOURCE	AA491991.1	GI:10664237			
ORGANISM	GSS.				
	Mus musculus (house mouse)				
	Mus musculus				
	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 35)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,				
	Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,				
	Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von				
	Niederhausern,A. and Wright D. Weis,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb				
	plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weis				
	University of Utah Genome Center				
	University of Utah				
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT				
	84112, USA				
	Tel.: 801 585 5606				
	Fax: 801 585 7177				
	Email: ddunn@genetics.utah.edu				
	Insert Length: 10000				
	Std Error: 0.00				
	Plate: 0325				
	row: C				
	column: 24				
	Seq primer: CACACAGAAACAGCTATGACC				
	Class: plasmid ends				
	High quality sequence stop: 35.				
FEATURES	Location/Qualifiers				
source	1..35				

Query Match	0.7%;	Score 25.8;	DB 1;	Length 35;
Best Local Similarity	93.1%;	Pred. No. 83;		
Matches 27;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;			

QY	2319	GTGTGCTGTGTGTGCTGTGTGTGTGTG	2347
	7	GCCTGTGTGTGTGTGTGTGTGTGTGTG	35

RESULT 224		
AZ661921		
LOCUS		
AZ661921	32 bp	DNA linear
		GSS 14-DEC-2000

DEFINITION	U0540B17R Mouse 10kb plasmid U05C1M library Mus musculus genomic clone U05C1M0540B17 R, genomic survey sequence.
ACCESSION	A2661921
VERSION	A2661921.1
KEYWORDS	GI:11799067
SOURCE	GSF.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 32)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Baccom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmond, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausem, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid insets
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0540 row: B column: 17 Seq primer: CACACAGGAACACGTATGACC Class: plasmid ends High quality sequence stop: 32.

FEATURES
source

1. 32
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGGCM library"
/note="Vector: PMD429; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative of
pMD2 (gil1473111[gb|AF123072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	0.7%	Score 25.6	DB 1	Length 32
Best Local Similarity	87.5%	Pred. No. 80		
Matches 28	Conservative	0	Mismatches 4	Indels 0
				Gaps 0

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Qy      2318 TGTGCTGTCGTGTCGCATGTCGTGTCGTG 2349
          ||| ||||| ||||| ||||| |||||
Ddb     1 TGTTCCTGTCGTGTCGTGTCGTGTCGTG 32
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RESULT	225				
AZ814562					
LOCUS	AZ814562	34 bp	DNA	linear	GSS 20-FEB-2001
DEFINITION	2M00824222f Mouse 10kb plasmid U00C1M library Mus musculus genomic				

ACCESSION clone U06C2M0082A22 F, genomic survey sequence.
 VERSION AZ814562
 KEYWORDS
 SOURCE
 ORGANISM Mus musculus (house mouse)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 34)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Petersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0082 row: A column: 22
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 34.

FEATURES

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"organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U082M0082A22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid U082M library"
/note="Vector: pMD29, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD29 (g31473211430/A129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match	0.7%	Score 25.6	DB 1	Length 34
Best Local Similarity	87.5%	Pred. No. 85		
Matches 28; Conservative	0	Mismatches 4	Indels 0	Gaps 0

Oy		2319	GTCGTCTGATGAGTGCCTGTGATGTCGTGCT	2350
Dd		3	GGGTGTCTGACGTACTGTGTCTGACTGCT	34

RESULT 226	
AZ342492	
LOCUS	AZ342492
DEFINITION	1M0075004R Mouse 10kb plasmid U08C1M library Mus musculus genomic clone U08C1M0075004 R, genomic survey sequence.
	27 bp DNA linear GSS 29-SEP-2000

ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)
REFERENCE	Dunn,D., Acyagil,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,P.,Weise,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu
COMMENT	Insert Length: 10000 Std Error: 0.00 Plate: 0550 row: G column: 18 Seq primer: CGTTGTAAAGACGCGCCACT Class: plasmid ends High quality sequence stop: 27.
FEATURES	Location/Qualifiers 1..27 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /cclone="UUGCIM0550G18" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /cclone_idb="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrotamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 [gil4732114(gblAFI29072.1)] a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
SOURCE	Source 1..27
DB	Query Match 0.7%; Score 25.4; DB 1; Length 27; Best Local Similarity 96.3%; Pred. No. 71; Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	2319 GTGGTGTGTGTGTGTGCCTGTGTGTGTG 2345 Dbb 1 GTGGTGTGTGTGTGTGTGTGTGTGTG 27
RESULT 231	AZ981811 27 bp DNA linear GSS 27-Apr-2001
LOCUS	AZ981811/c
DEFINITION	ZMO262D23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
ACCESSION	ZMO262D23F
VERSION	AZ981811
KEYWORDS	AZ981811.1 GI:13853038
GSS	Mus musculus (house mouse)
ORIGIN	Mus musculus

REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumkariota; Euteheria; Rodentia; Sciurognatha; Muridae; Mus.
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright D.Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0262 row: D column: 23 Seq primer: CGTGTAAAACGACGGCAGT Class: plasmid ends High quality sequence stop: 27. Location/Qualifiers
FEATURES	1..27 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /cclone="UMGC2M0262D23" /gsex="Female" /lab_host="E. coli strain XL10-Gold, Ti-resistant, F-" /cclone_lbb="Mouse 10kb plasmid UMGCM library" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gil473114[gb AF129072.1]), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
SOURCE	
Query Match	0.7%; Score 25.4; DB 1; length 27;
Beech Local Similarity	96.3%; Pred. 0.71;
Match 26; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	2318 TGTTGTTGTTGTTGTTGCGTGTTGTTGT 2344
Db	27 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1
RESULT 232	
AZ405219	28 bp DNA linear GSS 03-OCT-2000
LOCUS	IM0173N2.R Mouse 10kb plasmid UMGC1M library Mus musculus genomic
DEFINITION	Clone UMGC1M0173N2.R, genomic survey sequence.
ACCESSION	AZ405219
VERSION	AZ405219.1 GI:10529232
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Thu Oct 28 12:48:27 2004

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 28)	Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Malmoud,M., Meenen,B., Pedersen,T., Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0173 row: N column: 21 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 28.
FEATURES	location/Qualifiers			
source	1..28			

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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM013N21"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PMD42ny. Purified genomic DNA from *M. musculus* C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD2 (g1473111[9B]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

	Query Match	0.7%	Score 25.4	DB 1,	Length 28;
	Best Local Similarity	96.3%	Pred. No. 74;		
	Matches 26; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
OY	2318 TGTGTTGTGTGTGTGCCTGTGTGTGT	2344			
Dd	1 TGTGTGTGTGTGTGTGTGTGTGTGTGT	27			

RESULT	233		
LOCUS	AZ443611		
DEFINITION	AZ443611	28 bp	DNA linear GSS 04-OCT-2000
ACCESSION	U00238N03R	Mouse 10kb plasmid	UUC1M library Mus musculus genomic
VERSION	AZ443611		
KEYWORDS	AZ443611.1	GI:10591759	
SOURCE	GSS.		
ORGANISM	Mus musculus (house mouse)		
	Mus musculus		
	Eumaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		

REFERENCE	1 (bases 1 to 28)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rielly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0238 row: N column: 03 Seq primer: CACACAGAAACAGCATGTACCC Class: plasmid ends High quality sequence stop: 28. Location/Qualifiers 1..28
FEATURES	
source	

`/organism="Mus musculus"`
`/mol_type="genomic DNA"`
`/strain="C57BL/6J"`
`/db_xref="taxon:10090"`
`/clone="UGGCM0238ND3"`
`/sex="Male"`
`/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"`
`/clone.lib="Mouses 10kb plasmid UGGCM library"`
`/note="Vector: pMD24ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/shares/). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD24 (gii147331114\[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."`

	Query Match	0.7%	Score 25.4;	DB 1;	Length 28;
	Best Local Similarity	96.3%;	Pred. No. 74;		
	Matches	26; Conservative	0; Mismatches	1; Indels	0; Gaps
Oy	TGTTGTGGTGTGTGCCTGTTCCTC	2344			
Dn	TGTGTGTGTGTGTGTGTGTGTGTGT	28			

RESULT	234
AZ782113	
LOCUS	AZ782113 28 bp DNA linear GSS 16-FEB-2001
DEFINITION	M20022N03F Mouse 10kb plasmid UNGCJM library Mus musculus genomic clone UNGC2M0022N03 F, genomic survey sequence.
ACCESSION	AZ782113
VERSION	AZ782113.1 GI:12915480
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0236 row: B column: 17
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 27.
FEATURES
 source
 1. .27
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0236B17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[14732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 25; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2327 GTGTGTGCGTGTGTGTGTGTGTG 2351
 |||||
DB 27 GTGTGTGCGTGTGTGTGTGTGTG 3

RESULT 239
LOCUS A2766046 33 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0563N18F Mouse 10kb plasmid UGGCM library Mus musculus genomic
ACCESSION A2766046
VERSION A2766046.1 GI:12882702
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 33)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0563 row: N column: 18
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 33.
FEATURES
 source
 1. .33
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0563N18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[14732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 25; DB 1; Length 33;
Best Local Similarity 84.8%; Pred. No. 97;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2312 TTGCTGTGTGTGTGTGTGTGTGTGTGTGT 2344
 |||||
DB 1 TTGCCCATGTGTGTGTGTGTGTGTGTGT 33

RESULT 240
LOCUS A2875700 34 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0190D19F Mouse 10kb plasmid UGGCM library Mus musculus genomic
ACCESSION A2875700
VERSION A2875700.1 GI:13085970
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 34)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMW42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 96.2%; Pred. No. 93;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344
DB 2 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 255
AZ801217 27 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0059P03R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGM0059P03 R, genomic survey sequence.

ACCESSION AZ801217 GI:129353540
VERSION AZ801217.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0059 Row: P Column: 03
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends

High quality sequence stop: 27.
Location/Qualifiers

FEATURES

Source

1.27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0059P03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMW42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 96.2%; Pred. No. 93;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344
DB 2 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 256
AZ807584 29 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0070H04R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGM0070H04 R, genomic survey sequence.

ACCESSION AZ807584 GI:12972078
VERSION AZ807584.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0070 Row: H Column: 04
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends

High quality sequence stop: 29.
Location/Qualifiers

FEATURES

Source

1.29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0070H04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: H column: 01
Seq primer: CACACAGAAACGCTATACAC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2342
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 266
LOCUS AZ404057 25 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0172D10F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0172D10 F, genomic survey sequence.
ACCESSION AZ404057
VERSION AZ404057.1 GI:10528070
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: D column: 10
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
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/db_xref="taxon:10090"
/clone="UUCG1M0172D10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2343
DB 25 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 267
LOCUS AZ769673 25 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0570D12R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0570D12 R, genomic survey sequence.
ACCESSION AZ769673
VERSION AZ769673.1 GI:12890050
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 25)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0570 Row: D Column: 12
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1..25
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 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
 /clone="UUGC1M0570D12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1b="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.1e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2319 GGTGTGTGTGTGTGTGTGTGTG 2343
 Db 1 GGTGTGTGTGTGTGTGTGTGTG 25

RESULT 268
 LOCUS AZ771881 25 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0574F23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 ACCESSION AZ771881
 VERSION AZ771881
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 25)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0574 Row: F Column: 23
 Seq primer: CGTTGTAAACGACGCGCGT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0574F23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1b="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.1e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2319 GGTGTGTGTGTGTGTGTGTGTG 2343
 Db 1 GGTGTGTGTGTGTGTGTGTGTG 25

RESULT 269
 LOCUS AZ646850 26 bp DNA linear GSS 14-DEC-2000
 DEFINITION 1M0513J06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 ACCESSION AZ646850
 VERSION AZ646850
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE Niederhauser, A. and Wright, D., Weiss, R.
JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid inserts
 Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plates: 0122 row: J column: 05
 Seq primer: CGTTGTAAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence step: 30.

FEATURES
 source
 Location/Qualifiers
 1..30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M012305"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42ny, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 23.4; DB 1; Length 30;
 Best Local Similarity 96.0%; Pred. No. 1.4e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2319 GTGTGTGTGTGTGTGTGTGTGTG 2343
 |||||
 6 GTGTGTGTGTGTGTGTGTGTGTG 30

RESULT 272 TA245A09Q 33 bp DNA linear GSS 13-DEC-2000
 TA245A09Q/c
LOCUS T. brucei sheared genomic DNA clone 245A09, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL482142
KEYWORDS AL482142.1 GI:11848147
SOURCE GSS.
ORGANISM Trypanosoma brucei
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 33)
REFERENCE Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. W. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source
 Location/Qualifiers
 1..33
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="245A09"

Query Match 0.6%; Score 23.4; DB 1; Length 33;
 Best Local Similarity 96.0%; Pred. No. 1.5e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2317 CTGTGTGTGTGTGTGTGTGTGTG 2341
 |||||
 25 CTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 273 AZ419877 26 bp DNA linear GSS 03-OCT-2000
 AZ419877/c
LOCUS IM0196N03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0196N03 R, genomic survey sequence.
ACCESSION AZ419877
KEYWORDS AZ419877.1 GI:10543890
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhauser, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plates: 0196 row: N column: 03
 Seq primer: CACACAGAAACGCTATACAC
 Class: plasmid ends
 High quality sequence step: 26.

FEATURES
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 Location/Qualifiers
 1..26
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0196N03"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2318 TGTGTCGTGTCGTGTCGTGTCGTG 2343
DB 26 TGTGTCGTGTCGTGTCGTGTCGTGAG 1

RESULT 274
LOCUS AZ494629 26 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0330F01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ494629
VERSION AZ494629.1 GI:10669392
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0330 row: F column: 01
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0330F01"
/sex="Male"

FEATURES

source

1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0330F01"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2312 TTGGTCTGTGTCGTGTCGTGTCGTG 2337
DB 1 TTGGTCTGTGTCGTGTCGTGTCGTG 26

RESULT 275
LOCUS AZ766495 26 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0564D08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ766495
VERSION AZ766495.1 GI:12883629
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: D column: 08
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564D08"
/sex="Male"

FEATURES

source

1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564D08"
/sex="Male"

/clone_1lb="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PWD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 22.8; DB 1; Length 26;
 Best Local Similarity 92.3%; Pred. No. 1.4e+02;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2319 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344
 Db 1 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 276
 AZ781130 26 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0019A07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 DEFINITION clone UUGCM0019A07 F, genomic survey sequence.
 ACCESSION AZ781130
 VERSION AZ781130.1 GI:12913513
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islan, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0019 row: A column: 07
 Seq primer: CATTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCM0019A07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGCIM library"

/note="Vector: PWD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 22.8; DB 1; Length 26;
 Best Local Similarity 92.3%; Pred. No. 1.4e+02;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2343
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 277
 AZ404479 27 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0172F18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 DEFINITION clone UUGCIM0172F18 R, genomic survey sequence.
 ACCESSION AZ404479
 VERSION AZ404479.1 GI:10528408
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islan, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0172 row: F column: 18
 Seq primer: CACACAGAAACAGCATATGACC
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0172F18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PWD42nv, Purified genomic DNA from M.


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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C2M0160P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb Plasmid U06C1M library"
/notes="Vector: PMW429; Purified genomic DNA from M.
labaculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

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/organism="Glossina morsitans morsitans"
/mol_type="rRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse47a03_plc"
/clouse_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

```

Query Match: 0.6%; Score 22.4; DB 1; Length 24;

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0556 row: K column: 17
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.

FEATURES

source

1. .25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0556K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2319 GTCGTGTCGTGTCGTGTCGT 2342
DB 1 GTCGTGTCGTGTCGTGTCGT 24

RESULT 291
AZ467063 26 bp DNA linear GSS 04-OCT-2000
LOCUS IM0278007F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0278007 F, genomic survey sequence.
ACCESSION AZ467063
VERSION AZ467063.1 GI:10625188
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0278 row: O column: 07
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source

1. .26
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0278007"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 22.4; DB 1; Length 26;
Best Local Similarity 95.8%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2317 CTTGTGTCGTGTCGTGTCGT 2340
DB 3 CTTGTGTCGTGTCGTGTCGT 26

RESULT 292
AZ625192 28 bp DNA linear GSS 13-DEC-2000
LOCUS IM0464322F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0464322 F, genomic survey sequence.
ACCESSION AZ625192
VERSION AZ625192.1 GI:11747382
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0464 row: J column: 22
Seq primer: CATTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES Location/Qualifiers

source

1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0464J22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 22.2; DB 1; Length 28;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 293
AZ386218 30 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0145W04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0145W04 F, genomic survey sequence.
ACCESSION AZ386218
VERSION AZ386218.1 GI:10499918
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: M column: 04
Seq primer: CATTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 30.

FEATURES Location/Qualifiers

source

1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145W04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 22.2; DB 1; Length 30;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2312 TTGGTCTGTGTGTGTGTGTGTGTGTGTGTGT 2338
DB 4 TTGGTCTGTGTGTGTGTGTGTGTGTGTGTGT 30

RESULT 294
AZ640238 30 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0502H1OF Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0502H10 F, genomic survey sequence.
ACCESSION AZ640238
VERSION AZ640238.1 GI:11763638
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606

0.6%; Score 21.6; DB 1; Length 29;
 10.5; kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (gll473111[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 amplified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

/db_xref="taxon:10090"
 /clone="TUCGCM0367E06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_1b="Mouse 10kb plasmid TUCGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114[gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

	Query Match	0.6%	Score 21.6; DB 1;	Length 29;
	Best Local Similarity	85.7%	Pred. No. 2.le+02;	
	Matches 24; Conservative	0;	Mismatches 4;	Indels 0;
OY	2322 TGTGTCGTGCAGTGTGTGTGTGTG	2349		
Db	2 TATATATGTCGTGTGTGTGTGTGTG	29		

	Query Match	0.6%;	Score 21.6;	DB 1;	Length 30;
	Best Local Similarity	85.7%;	Pred. No. 2.2e+02;		
	Matches 24;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Oy	TTTGTCTGTCGTGTCGTGTCGTGT	2338			
Dd	TGtGTGTGTGTGTGTGTGTGTGTGT	3			

RESULT 301	
LOCUS	AZ579506/c
DEFINITION	AZ579506 30 bp DNA linear GSS 13-DEC-2000
ACCESSION	U00367E06F Mouse 10kb plasmid U00C1M library Mus musculus genomic
VERSION	clone U00C1M0367E06 F, genomic survey sequence.
KEYWORDS	AZ579506
SOURCE	AZ579506.1 GI:11693935
ORGANISM	GSS.
REFERENCE	Mus musculus (house mouse)
AUTHORS	Mus musculus
	Euarystota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus. 1 (bases 1 to 30) Dunn, D., Aoyagi, A., Barber, M., Baecom, T., Duval, B., Hamil, C., Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellay, M., Rose, M., Rose, R., Stokes, R., Tinger, A., von Niederhausen, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0367 row: E column: 06 Seq primer: CGTGTAAACGACGGCCAGT Class: plasmid end High quality sequence stop: 30. Location/Qualifiers 1..30 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6u"
JOURNAL	
COMMENT	
TITLE	
FEATURES	
source	

RESULT 302	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AL943661	30 bp	DNA	linear	GSS	31-MAR-2004		
AL943661	Arabidopsis thaliana T-DNA flanking sequence GK-276A12-015154,						
AL943661	genomic survey sequence.						
AL943661	GI:24400267						
GSS.							
Arabidopsis thaliana (thale cress)							
Arabidopsis thaliana							
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;							
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;							
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
MEDLINE							
PUBMED							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
MEDLINE							
PUBMED							
REFERENCE							
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AUTHORS							
TITLE							
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MEDLINE							
PUBMED							
REFERENCE							
AUTHORS							

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 307 23 bp DNA linear GSS 13-DEC-2000
AZ637290/c 23 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0496005R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0496005 R, genomic survey sequence.
ACCESSION AZ637290
VERSION AZ637290.1 GI:11759480
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0496 row: 0 column: 05

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0496005"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
DB 23 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 308 23 bp DNA linear GSS 16-FEB-2001
AZ789907/c 23 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0038613F Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0038613 F, genomic survey sequence.
ACCESSION AZ789907
VERSION AZ789907.1 GI:12931412
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0038 row: 0 column: 13

Seq primer: CGGTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0038613"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

REFERENCE 1 (bases 1 to 30)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0367 row: D column: 03
 Seq primer: CATTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers
 1..30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC2M0017J19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 21.2; DB 1; Length 30;
 Best Local Similarity 88.5%; Pred. No. 2.4e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3461 TTTATATATATATATATATATTT 3486
 Db 29 TTTATATATATATATATATATAT 4

RESULT 320
 LOCUS AZ780500/c 25 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0017J19R Mouse 10kb plasmid UUC2M library Mus musculus genomic clone UUC2M0017J19 R, genomic survey sequence.
 ACCESSION AZ780500
 VERSION AZ780500.1 GI:12912224
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0017 row: J column: 19
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC2M0017J19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.8; DB 1; Length 25;
 Best Local Similarity 91.7%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTGTGTGTGTG 2339
 Db 24 TTTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 321
 LOCUS AZ589684 27 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0398017R Mouse 10kb plasmid UUC2M library Mus musculus genomic clone UUC2M0398017 R, genomic survey sequence.
 ACCESSION AZ589684
 VERSION AZ589684.1 GI:11711874
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0398 row: 0 column: 17
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

1. 27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0398017"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.5%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 2.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2821 GGTATATATACATATATATATA 2844
Db 1 GATATATATATATATATATATA 24

RESULT 322
AZ823694
LOCUS 27 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M038017R Mouse 10kb plasmid UGGCM library Mus musculus genomic
clone UGGCM038017 R, genomic survey sequence.
ACCESSION AZ823694
VERSION AZ823694.1 GI:11711874
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0398 row: 0 column: 17
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

1. 27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0398017"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.5%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 2.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2823 TATATATACATATATATATATAC 2846
Db 24 TATATATATATATATATATATATC 1

RESULT 323
AZ823699
LOCUS 27 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0097G23R Mouse 10kb plasmid UGGCM library Mus musculus genomic
clone UGGCM0097G23 R, genomic survey sequence.
ACCESSION AZ823699
VERSION AZ823699.1 GI:12993607
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

JOURNAL COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0045 row: H column: 20
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES

source

1..22
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0045H20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 95.5%; Score 20.4; DB 1; Length 22;
 Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2323 GTGTGTGTGTGTGTGTGTGT 2344
 DB 1 GTGTGTGTGTGTGTGTGTGT 22

RESULT 328
 AZ985497 22 bp DNA linear GSS 27-APR-2001
 LOCUS 2M0267D23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 DEFINITION clone UUGC2M0267D23 F, genomic survey sequence.
 ACCESSION AZ985497
 VERSION AZ985497.1 GI:13856724
 KEYWORDS GSS.
 SOURCE Mus musculus
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0267 row: D column: 23
 Seq primer: CTTCTTAAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES

source

1..22
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0267D23"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 95.5%; Score 20.4; DB 1; Length 22;
 Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2319 GTGTGTGTGTGTGTGTGTGT 2340
 DB 1 GTGTGTGTGTGTGTGTGTGT 22

RESULT 329
 TA324H01P 22 bp DNA linear GSS 13-DEC-2000
 LOCUS T. Brucei sheared genomic DNA clone 324h01, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL493407
 VERSION AL493407.1 GI:11867772
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Omond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 JOURNAL

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

location/Qualifiers

1. 22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="324h01"

FEATURES

source

1. 22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="324h01"

Query Match 0.5%; Score 20.4; DB 1; Length 22; Best Local Similarity 95.5%; Pred. No. 2.2e+02; Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 TATATATATATATATATATA 22

QY 2823 TATATATACATATATATATA 2844

LOCUS TA324H01P 22 bp DNA linear GSS 13-DEC-2000

DEFINITION T. brucei sheared genomic DNA clone 324h01, forward sequence,

ACCESSION AL493407 GI:11867772

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 22)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

location/Qualifiers

1. 22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="324h01"

QY 2823 TATATATACATATATATATA 2844

Db 22 TATATATATATATATATATA 1

RESULT 331

LOCUS AZ371475

DEFINITION 23 bp DNA linear GSS 02-OCT-2000

ACCESSION AZ371475

VERSION AZ371475.1 GI:10485175

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0122 row: K column: 19

Seq primer: CACACAGAAACAGCATGACCC

Class: Plasmid ends

High quality sequence stop: 23.

location/Qualifiers

1. 23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCM0122K19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PMD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 23; Best Local Similarity 95.5%; Pred. No. 2.3e+02; Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2317 CTTGTGTTGTTGTTGTTGTTGTT 2338
 Db 2 CTTGTGTTGTTGTTGTTGTTGTT 23

RESULT 332
 AZ584665 24 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0389A23F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0389A23 F, genomic survey sequence.

ACCESSION AZ584665
 VERSION AZ584665.1 GI:11705779
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Authors: Dunham, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

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 JOURNAL Unpublished (2000)
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 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunham@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0389 row: A column: 23
 Seq primer: CGTGTCTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
 Location/Qualifiers

1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
 /clone="UGCGIM0389A23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 2.4e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844

Db 1 TATATATATATATATATATATA 22

RESULT 333
 AZ584665 24 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0389A23F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0389A23 F, genomic survey sequence.

ACCESSION AZ584665
 VERSION AZ584665.1 GI:11705779
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Authors: Dunham, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunham@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0389 row: A column: 23
 Seq primer: CGTGTCTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
 Location/Qualifiers

1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
 /clone="UGCGIM0389A23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 2.4e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844

Db 24 TATATATATATATATATATA 3

RESULT 334
TA280H02Q 24 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 280h02, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL485433 GI:11851540
VERSION AL485433.1 GI:11851540
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submision
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 CUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="280h02"

FEATURES
source

Query Match 0.5%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 2 TATATATATATATATATATATA 23

RESULT 335
TA280H02Q/C 24 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 280h02, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL485433
VERSION AL485433.1 GI:11851540
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submision
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and

COMMENT nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 CUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="280h02"

FEATURES
source

Query Match 0.5%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 23 TATATATATATATATATATATA 2

RESULT 336
AZ585116 25 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0389124R Mouse 10kb plasmid UGCCIM library Mus musculus genomic
DEFINITION clone UGCCIM0389124 R, genomic survey sequence.
ACCESSION AZ585116
VERSION AZ585116.1 GI:11706514
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0389 row: L column: 24
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCCIM0389124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 2.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
DB 1 TATATATATATATATATATATA 22

RESULT 337 25 bp DNA linear GSS 13-DEC-2000
AZ585116
LOCUS IM0369L24R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0369L24 R, genomic survey sequence.
ACCESSION AZ585116
VERSION AZ585116.1 GI:11706514
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weis, R.
Museum whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0389 row: L column: 24
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

FEATURES

source 1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0369L24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 2.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
DB 24 TATATATATATATATATATATA 3

RESULT 338 27 bp DNA linear GSS 13-DEC-2000
TA319C02P
LOCUS T. brucei sheared genomic DNA clone 319c02, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL482452 GI:11867396
VERSION AL482452.1 GI:11867396
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 27)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submision

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

FEATURES

source 1..27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="319c02"

Query Match 0.5%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 2.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
 Db 1 TATATATATATATATATATA 22

RESULT 339
 TAJ19C02P/C 27 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 319C02, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL492452
 VERSION AL492452.1 GI:11867396
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
 AUTHORS 1 (bases 1 to 27)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Acklin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajadream, M.A. and Barrell, B.G.
 Direct Submision
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venier, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source
 1..27
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="319C02"

Query Match 0.5%; Score 20.4; DB 1; Length 27;
 Best Local Similarity 95.5%; Pred. No. 2.7e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
 Db 26 TATATATATATATATATATA 5

RESULT 340
 AZ287831 28 bp DNA linear GSS 02-OCT-2000
 LOCUS AZ287831
 DEFINITION IM0147F22R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0147F22 R, genomic survey sequence.
 ACCESSION AZ287831
 VERSION AZ287831.1 GI:10501539
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL
 COMMENT
 Plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0147 row: F column: 22
 Seq primer: CACACAGAAACGCTATGACC
 Class: Plasmid ends
 High quality sequence stop: 28.

FEATURES
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 1..28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0147F22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid RI-. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 28;
 Best Local Similarity 95.5%; Pred. No. 2.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
 Db 27 TATATATATATATATATATA 6

RESULT 341
 AZ648796 28 bp DNA linear GSS 14-DEC-2000
 LOCUS AZ648796
 DEFINITION IM0518A05F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0518A05 F, genomic survey sequence.
 ACCESSION AZ648796
 VERSION AZ648796.1 GI:11781618
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0518 row: A column: 05
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers

FEATURES
source

1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0518A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 28;
Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2823 TATATACATATATATATA 2844
1 TATATATATATATATATATA 22

RESULT 342
AZ459694 25 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0264P10R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0264P10 R, genomic survey sequence.
ACCESSION AZ459694
VERSION AZ459694.1 GI:10617819
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: P column: 10
Seq primer: CACACAGGAAAAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

FEATURES
source

1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0264P10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2319 GTGTGTGTGTGTGTGTGTGTG 2343
1 GTGTGTGTGTGTGTGTGTGTG 25

RESULT 343
AZ766498 25 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0564E08F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0564E08 F, genomic survey sequence.
ACCESSION AZ766498
VERSION AZ766498.1 GI:12883635
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0564 row: B column: 08
 Seq primer: CGTTGTAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

source

1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0564E08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_11b="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|g2|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 88.0%; Score 20.2; DB 1; Length 25;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGT 2342

Db 1 TGTGTGTGTGTGTGTGTGTGTGTGAGT 25

RESULT 344
 TAL94F01Q 26 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 194f01, reverse sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL477302
 VERSION AL477302.1 GI:11841328
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 26)

REFERENCE

AUTHORS

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh1@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v+ i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. .26
 /organism="Trypanosoma brucei"
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 /db_xref="taxon:5691"
 /clone="194f01"

Query Match

Best Local Similarity 88.0%; Score 20.2; DB 1; Length 26;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGT 2342

Db 1 TGTGTGTGTGTGTGTGTGTGTGTG 25

RESULT 345

LOCUS

AZ579497 30 bp DNA linear GSS 13-DEC-2000
 AZ579497 1M0367D03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0367D03 F, genomic survey sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,

Niederhuesern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0367 row: D column: 03

Seq primer: CGTTGTAACGACGCCACT

Class: plasmid ends

High quality sequence stop: 30.

FEATURES

source

1. .30

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0367D03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_11b="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorized mouse DNA was annealed to adaptorized vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 3.2e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3455 TACAAGTTATATATCTATATATA 3480
DB 1 TATATTTTATATATTTTATATATA 26

RESULT 350
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LOCUS AZ781477
DEFINITION 2M0019H24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0019H24 R, genomic survey sequence.

ACCESSION AZ781477
VERSION AZ781477.1 GI:12914209
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

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JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0019 row: H column: 24
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
source Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0019H24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorized mouse DNA was annealed to adaptorized vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.6; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2313 TGGTCTGTGTGTGTGTGTGTGTGTGT 2338
DB 3 TGGTGGGTTGTGTGTGTGTGTGTGT 28

RESULT 351
AZ310642 21 bp DNA linear GSS 29-SEP-2000
LOCUS AZ310642
DEFINITION 1M0025N09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0025N09 R, genomic survey sequence.

ACCESSION AZ310642
VERSION AZ310642.1 GI:10352832
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
COMMENT Unpublished (2000)
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Tel: 801 585 5606
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: N column: 09
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0025N09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGT 2338
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 352
AZ333309 21 bp DNA linear GSS 29-SEP-2000
LOCUS IM0062P13F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0062P13 F, genomic survey sequence.

ACCESSION AZ333309
VERSION AZ333309.1 GI:10397798
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

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COMMENT Contact: Robert B. Weiss
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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: P column: 13
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
Location/Qualifiers
1..21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0062P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD22nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGT 2338
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 353
AZ513902 21 bp DNA linear GSS 05-OCT-2000
LOCUS IM0360A13F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0360A13 F, genomic survey sequence.

ACCESSION AZ513902
VERSION AZ513902.1 GI:10695218
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: A column: 13
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
Location/Qualifiers
1..21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0360A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD22nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTGTGT 2338
Db 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 360
A2854856 21 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0158109R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCG2M0158109 R, genomic survey sequence.

ACCESSION A2854856
VERSION A2854856
KEYWORDS GI:13044389
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0158 row: 1 column: 09
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1. 21
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0158109"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD29v. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTGTGT 2338
Db 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 361
A2780002 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0016J20R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCG2M0016J20 R, genomic survey sequence.

ACCESSION A2780002
VERSION A2780002
KEYWORDS GI:12911227
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: J column: 20
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

source

1. 22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0016J20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD29v. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2824 ATATATACATATATATATA 2844
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 DB 22 ATATATATATATATATATA 2

RESULT 366
 AZ822069 24 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0095D03F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGCM0095D03 F, genomic survey sequence.
 ACCESSION AZ822069
 VERSION AZ822069.1 GI:12991977
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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 Unpublished (2000)
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 JOURNAL University of Utah Genome Center
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 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0095 row: D column: 03
 Seg primer: CCGTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /clone="UGCGM0095D03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 24;
 Best Local Similarity 95.2%; Pred. No. 3.1e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2326 TGTGTGTGTGTGTGTGTGTGT 2346
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 DB 4 TGTGTGTGTGTGTGTGTGT 24

RESULT 367
 TA170G05P 27 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 170G05, forward sequence.
 DEFINITION genomic survey sequence.
 ACCESSION AL473335
 VERSION AL473335.1 GI:11838934
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 1 (bases 1 to 27)
 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
 Direct Submision
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..27
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TRU927"
 /db_xref="taxon:5691"
 /clone="170G05"

Query Match 0.5%; Score 19.4; DB 1; Length 27;
 Best Local Similarity 95.2%; Pred. No. 3.5e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3462 TTATATATCTATATATATA 3482
 |||||
 DB 7 TTATATATATATATATATA 27

RESULT 368
 AZ650121 27 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0520C09F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0520C09 F, genomic survey sequence.
 ACCESSION AZ650121
 VERSION AZ650121.1 GI:11784286
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

REFERENCE
 AUTHORS

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: C column: 09
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source
1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCIM0520C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 27;
Best Local Similarity 95.2%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATAT 2843
DB 7 TATATATATATATATATATAT 27

RESULT 369
AZ650121/c 27 bp DNA linear GSS 14-DEC-2000
LOCUS IM0520C09F Mouse 10kb plasmid UGCIM library Mus musculus genomic
DEFINITION clone UGCIM0520C09 F, genomic survey sequence.
ACCESSION AZ650121
VERSION AZ650121.1 GI:11784286
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: C column: 09
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source
1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCIM0520C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 27;
Best Local Similarity 95.2%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATATA 2844
DB 27 ATATATATATATATATATATA 7

RESULT 370
AA995094/c 19 bp mRNA linear EST 27-AUG-1998
LOCUS cu89909.s1 NCI_CGAP Kid3 Homo sapiens cDNA clone IMAGE:1635040 3
DEFINITION similar to TR_069566 Q69566; contains TARI.12 MER35 repetitive
element ;, mRNA sequence.
ACCESSION AA995094
VERSION AA995094.1 GI:3181583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaabbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmerit-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1087 Std Error: 0.00
 Seg primer: -40m3 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1635040"
 /lab_host="DH10B"
 /clone_lib="NCI-CCAP_Kid3"
 /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.5%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred.No. 2.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2333 GCCTGTGTGTGTGTGTG 2351
 Db 19 GCCTGTGTGTGTGTGTG 1

RESULT 371 22 bp DNA linear GSS 13-DEC-2000
 AZ579516 1M0367G01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 LOCUS clone UUGC1M0367G01 F, genomic survey sequence.
 DEFINITION
 ACCESSION AZ579516 GI:11693945
 VERSION AZ579516
 KEYWORDS GSS.

SOURCE
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0367 row: G column: 01
 Seg primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends

FEATURES

source

High quality sequence stop: 22.

Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0367G01"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/shares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred.No. 3.2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2336 TGTGTGTGTGTGTGTGCAC 2354
 Db 22 TGTGTGTGTGTGTGTGCAC 4

RESULT 372 22 bp DNA linear GSS 29-SEP-2000
 AZ314354 1M0031B07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 LOCUS clone UUGC1M0031B07 F, genomic survey sequence.
 DEFINITION
 ACCESSION AZ314354 GI:10360159
 VERSION AZ314354
 KEYWORDS GSS.

SOURCE
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0031 row: B column: 07
 Seg primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends

High quality sequence stop: 22.

FEATURES

source

Location/Qualifiers

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0031B07"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

0.5%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.4e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2324 TGTGTGTGTGCGTGTGTGTG 2345

Db 22 TGGGTGTGTGCTGTGTGTGTG 1

RESULT 373

AZ64442

LOCUS 22 bp DNA linear GSS 04-OCT-2000

DEFINITION 1M0273N14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic

clone UUGCIM0273N14 R, genomic survey sequence.

ACCESSION AZ64442

VERSION AZ64442.1 GI:10622367

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhusern,A. and Wright,D. Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0273 row: N column: 14

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0273N14"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

0.5%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.4e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2322 TGTGTGTGTGCGTGTGTGTG 2343

Db 1 TGTGTGTGTGAGTGTATGTG 22

RESULT 374

AZ784203

LOCUS 22 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0026G16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic

clone UUGCIM0026G16 R, genomic survey sequence.

ACCESSION AZ784203

VERSION AZ784203.1 GI:12919695

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhusern,A. and Wright,D. Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0026 row: G column: 16

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

source

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0259H17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 90.9%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2312 TTGGTCTGTGTGTGTGTGTG 2333
1 TAGGTGTGTGTGTGTGTGTG 22

RESULT 377
AZ456517 23 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0259H17P Mouse 10kb plasmid UGGCM library Mus musculus genomic
DEFINITION clone UGGCM0259H17 F, genomic survey sequence.
ACCESSION AZ456517
VERSION AZ456517.1 GI:10614558
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0259 row: H column: 17
Seq primer: CGTTGTAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

/db_xref="taxon:10090"
/clone="UGGCM0259H17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 90.9%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
1 TACATATACATATATATATATA 22

RESULT 378
AZ792245 26 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0043N01R Mouse 10kb plasmid UGGCM library Mus musculus genomic
DEFINITION clone UGGCM0043N01 R, genomic survey sequence.
ACCESSION AZ792245
VERSION AZ792245.1 GI:12935977
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0043 row: N column: 01
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

/clone="UUGC2M0043N01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.8; DB 1; Length 26;
 Best Local Similarity 90.9%; Pred. No. 4e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATTACATATATATATA 2844
 |||||
 26 TATATTAAATATATATATA 5

RESULT 379
 AZ498814 25 bp DNA linear GSS 05-OCT-2000
 LOCUS
 DEFINITION
 clone UUGC1M0336H14 F, genomic survey sequence.

ACCESSION
 AZ498814
 VERSION
 AZ498814.1 GI:10677018
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0336 row: H column: 14
 Seq primer: CATTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

source
 1.25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0336H14"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.6; DB 1; Length 25;
 Best Local Similarity 84.0%; Pred. No. 4e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2327 GGTGTGCGTGTGTGTGTGTGTG 2351
 |||||
 1 GTGCACACGTGTGTGTGTGTGTG 25

RESULT 380
 AZ760251 25 bp DNA linear GSS 16-FEB-2001
 LOCUS
 DEFINITION
 clone UUGC1M0553E20 R, genomic survey sequence.

ACCESSION
 AZ760251
 VERSION
 AZ760251.1 GI:12867877
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0553 row: E column: 20
 Seq primer: CACACAGAAACGATATGACC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

source
 1.25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0553E20"
 /sex="Male"

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 95.0%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTGTGT 2336
DB 2 CTGTGTGTGTGTGTGTGTGT 21

RESULT 389
AZ645446 21 bp DNA linear GSS 27-APR-2001
LOCUS 1M0510H22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0510H22 R, genomic survey sequence.

ACCESSION AZ645446
VERSION AZ645446.1 GI:11774942
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0275 row: K column: 17

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0510H22"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv. Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 95.0%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
DB 21 GTGTGTGTGTGTGTGTGTGT 2

RESULT 390
AZ645446 24 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0510H22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0510H22 R, genomic survey sequence.

ACCESSION AZ645446
VERSION AZ645446.1 GI:11774942
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0510 row: H column: 22

Seq primer: CACACAGGAACAGCATATGACC

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1. 24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0510H22"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv. Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi4732114|db|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.4; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2334 CCGTGTGTGTGTGTGTGCA 2353
Db 1 CTTGTGTGTGTGTGTGCA 20

RESULT 393
TA197D12P/c 25 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION T. Brucei sheared genomic DNA clone 197d12, forward sequence,
ACCESSION AL475774
VERSION AL475774.1 GI:11842542
KEYWORDS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 25)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Aktin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.B., Rajadream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
n1@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="197d12"

Query Match 0.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2330 TGTGCGTGTGTGTGTGTGTC 2352
Db 25 TATGTGTGTGTGTGTGTTC 3

RESULT 394
AG200915 26 bp DNA linear GSS 06-MAR-2004
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-083C08.TU, genomic survey

sequence.
ACCESSION AG200915
VERSION AG200915.1 GI:45233090
KEYWORDS
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE 1
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE BAC end sequences of Library RP-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 26)

AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@kribb.re.kr, URL: <http://pbs.grc.kribb.re.kr/>,
Tel: 82-42-866-7181, Fax: 82-42-860-4403)

Clones are derived from the chimpanzee BAC library RP-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TU

LIBRARY
Vector 1 : pBAC3.6
R.site 1 : EcoRI
R.site 2 : EcoRI.
Location/Qualifiers

1..26
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-083C08.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 0.5%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2845
Db 2 TACACATATATATATATATATA 24

RESULT 395
AG200915/c 26 bp DNA linear GSS 06-MAR-2004
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-083C08.TU, genomic survey
sequence.

ACCESSION AG200915
VERSION AG200915.1 GI:45233090
KEYWORDS
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE 1
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE BAC end sequences of Library RP-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 26)

AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);

52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,
Tel: 82-42-866-7181, Fax: 82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS

Sequencing: TV

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1. 26

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-083C08.TV"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 0.5%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATTA 2845

DB 23 TATATATATATATATATATGTTAA 1

RESULT 396

AZ415089

LOCUS AZ415089 21 bp DNA linear GSS 03-OCT-2000

DEFINITION IM0189G17R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

clone UGCGIM0189G17 R, genomic survey sequence.

AZ415089

VERSION AZ415089.1 GI:10539102

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0189 row: G column: 17

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCGIM0189G17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrolytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTG 2339

DB 1 GTGTGTGTGTGTGTGTGTGTG 21

RESULT 397

AZ665302

LOCUS AZ665302 21 bp DNA linear GSS 14-DEC-2000

DEFINITION IM0546J09R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

clone UGCGIM0546J09 R, genomic survey sequence.

AZ665302

VERSION AZ665302.1 GI:11802448

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0546 row: J column: 08

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCGIM0546J09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGIM library"

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0338A23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-
clone_11b="Mouse 10kb plasmid UUCGCM library"
/notes="Vector: PMD42uv; Purified genomic DNA from M.

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Query Match	0.5%	Score 17.8;	DB 1;	Length 23;
Best Local Similarity	90.5%;	Pred. No. 4.6e+02;		
Matches 19;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

QY 2830 ACATATATATATATACATAT 2850
 Db 22 AATATATATATATATATAT 2

RESULT 400
 AZ644875 25 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0510E03F Mouse 10kb plasmid UGCLM library Mus musculus genomic
 DEFINITION clone UGCLM0510E03 F, genomic survey sequence.

ACCESSION AZ644875
 VERSION AZ644875.1 GI:11773823
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 25)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE
 AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0510 row: E column: 03
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends

FEATURES
 source High quality sequence stop: 25.

Location/Qualifiers

1. 25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0510E03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (GI4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 4.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2327 GTGTGTGCGTGTGTGTGTGTG 2347

Db 5 GTGTGCGCATGTGTGTGTG 25

RESULT 401
 AZ775159 25 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0007F13F Mouse 10kb plasmid UGCLM library Mus musculus genomic
 DEFINITION clone UGCLM0007F13 F, genomic survey sequence.

ACCESSION AZ775159
 VERSION AZ775159.1 GI:12901359
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 25)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE
 AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0007 row: F column: 13
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends

FEATURES
 source High quality sequence stop: 25.

Location/Qualifiers

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
 /clone="UGCLM0007F13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (GI4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 4.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2311 TTTGTGTGTGTGTGTGTGTG 2331

Db	5	TTTACTGATGTCGTGTCGTG	25	
RESULT	402			
LOCUS	BG920906/c			
DEFINITION	602822814r1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4951803 5'			
ACCESSION	BG920906			
VERSION	BG920906.1	GI:14301382		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 38)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: InCyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LILAM10908 row: K column: 04 High quality sequence stop: 38.			
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	/clone="IMAGE:4951803"			
	/sex="female, virgin"			
	/tissue_type="infiltrating ductal carcinoma"			
	/dev_stage="5 months"			
	/lab_host="DH10B"			
	/clone_1fb="NCI CGAP Mam6"			
	/note="Organ: mammary; Vector: pCMV-SPORE6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"			
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Best Local Similarity	67.6%;	Pred. No. 7.1e-02;		
Matches	25;	Conservative 0;	Mismatches 12;	Indels 0;
			Gaps 0;	
Qy	3362	TAATTTATTTGCTTGTCTTTTCAGAGCAATTAGA	3238	
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RESULT	403			
LOCUS	AZ811237			
DEFINITION	2M0077K19P Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUCG2M0077K19 F, genomic survey sequence.			
ACCESSION	AZ811237			
VERSION	AZ811237.1	GI:12979487		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 24)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,K.			

[illegible]

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 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
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 adaptor vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 4.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATCATATATATATAT 2842
 DB 1 ATATATATATATATATATAT 19

RESULT 407
 AZ401252 19 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0167E20R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0167E20 R, genomic survey sequence.
 ACCESSION AZ401252
 VERSION AZ401252.1 GI:10516326
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
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 Unpublished (2000)
 Contact: Robert B. Weiss
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 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0167 row: E column: 20
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /clone="UGCGIM0167E20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1b="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
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 polynucleotide kinase. Adaptor oligonucleotides were
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adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
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 and selected for ampicillin resistance."

Query Match 0.5%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 4.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATCATATATATATAT 2841
 DB 19 TATATATATATATATATAT 1

RESULT 408
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 LOCUS 1M0216G18R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0216G18 R, genomic survey sequence.
 ACCESSION AZ431700
 VERSION AZ431700.1 GI:10555713
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
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 Unpublished (2000)
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 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0216 row: G column: 18
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /clone="UGCGIM0216G18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1b="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
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 was blunt end-repaired with T4 DNA polymerase and T4
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 adaptor DNA was purified and size-selected for a 9.5 to

adaptoed vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGTG 2333
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Db 1 GTCGTGTGTGTGTGTGTG 19

RESULT 415

AZ822936 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0096E08R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCG2M0096E08 R, genomic survey sequence.

ACCESSION AZ822936
VERSION AZ822936.1 GI:12992844
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: B column: 08
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UGCG2M0096E08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

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Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGTG 2333
|||
Db 1 GTCGTGTGTGTGTGTGTG 19

RESULT 416

AZ827177 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0103A05R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCG2M0103A05 R, genomic survey sequence.

ACCESSION AZ827177
VERSION AZ827177.1 GI:12997085
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: A column: 05
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0103A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

VERSION AZ482421.1 GI:10643486
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0307 row: P column: 01
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 High quality sequence stop: 20.
 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0307P01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0528 row: G column: 10
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
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 /strain="C57BL/6J"
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 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0307P01"
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Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTG 2337
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 Db 1 TGTGTGTGTGTGTGTGTG 20

RESULT 427
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 DEFINITION clone UUC1M0528G10 R, genomic survey sequence.
 ACCESSION AZ654458
 VERSION AZ654458.1 GI:11791604

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTG 2337
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 Db 1 TGTGTGTGTGTGTGTGTG 20

RESULT 428
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 LOCUS 2M0225I06R Mouse 10kb plasmid UUC2M library Mus musculus genomic
 DEFINITION clone UUC2M0225I06 R, genomic survey sequence.
 ACCESSION AZ958303
 VERSION AZ958303.1 GI:13829530
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
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 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0225 row: I column: 06
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0225106"
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 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3465 TATATCTATATATATAT 3484
 Db 20 TATATCTATATCTATAGT 1

RESULT 429
 AZ635078/c
 LOCUS 23 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M041C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M041C14 F, genomic survey sequence.
 ACCESSION AZ635078
 VERSION AZ635078.1 GI:11757268
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0491 row: C column: 14
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers
 1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0491C14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 23;
 Best Local Similarity 90.0%; Pred. No. 5.9e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTG 2337
 Db 22 TGTGTGTGTGTGTGTGCGTG 3

RESULT 430
 CF333289
 LOCUS 30 bp mRNA linear EST 18-AUG-2003
 DEFINITION JMT--02-C01.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--02-C01, mRNA sequence.
 ACCESSION CF333289
 VERSION CF333289.1 GI:33814856
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriaristidae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..30
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--02-C01"
/issue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="pJMT-overexpressing transgenic rice plasmid
CDNA library (JMT)"
/note="Vector: pCR4-TOPO, Site_1: EcoRI; oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis jasmonate Carbonyl
methyltransferase overexpression line."

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 30;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3264 TTTTATGCTTGTCTTTTCAGGAG 3291
Db 2 TTTTATGCTTGTCTTTTCAGGAG 29

RESULT 431
CP298071/c 34 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--01-E22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-E22, mRNA
sequence.
ACCESSION CP298071 GI:33669832
VERSION CP298071
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriaristidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 34)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 34;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3310 TTTTCTTAGAGATTATTTTGA 3337
Db 29 TTTTCTTAGATTTTCTTTTGA 2

RESULT 432
AJ658745 23 bp mRNA linear EST 28-JUN-2004
LOCUS AJ658745 KN277 Sus scrofa cDNA clone C0005213_102, mRNA sequence.
DEFINITION AJ658745
ACCESSION AJ658745 GI:49342814
VERSION EST.
KEYWORDS Sus scrofa (pig)
SOURCE Sus scrofa
ORGANISM Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 23)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
CONTACT: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -mnscore 20
and -mismatch 12 options. Vector:phuescriptII(SK+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pooled early embryos, from 8-cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.airygenomics.org.

FEATURES
source
1..23
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005213_102"
/issue_type="embryo"
/clone_lib="KN277"
/note="Vector: phuescriptII(SK+); Site_1: EcoRI; Site_2:
NotI; single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."

Query Match
Best Local Similarity 0.4%; Score 16.6; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2924 GGGGCGTGGGGGGCGTGAAGG 2946
Db 1 GGGGCGTGGGGGGGGGGGGG 23

RESULT 433
AZ411764 23 bp DNA linear GSS 03-OCT-2000
LOCUS AZ411764
DEFINITION IM0184022R Mouse 10kb plasmid UUC1M library Mus musculus genomic

accession AZ411764 GI:10535777
 version AZ411764.1
 keywords GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
 authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
 title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 journal Unpublished (2000)
 comment Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 insert length: 10000 Std Error: 0.00
 plate: 0184 row: 0 column: 22
 seq primer: CACACAGAAACAGCATATGACC
 class: plasmid ends
 high quality sequence stop: 23.
 location/qualifiers
 1. 23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0184O22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 6.2e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2920 GGGCGGGCGCTGGGGGGCGCTGC 2942
 DB 1 GGGGGGGGGCGGGGGGGGGGGGG 23

RESULT 434
 LOCUS AZ618720 23 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0450019F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0450019 F, genomic survey sequence.

accession AZ618720 GI:11740826
 version AZ618720.1
 keywords GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
 authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
 title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 journal Unpublished (2000)
 comment Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 insert length: 10000 Std Error: 0.00
 plate: 0450 row: 0 column: 19
 seq primer: CGTTGTAACGACGCGCAGT
 class: plasmid ends
 high quality sequence stop: 23.
 location/qualifiers
 1. 23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0450019"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 6.2e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2924 GGGCGCTGGGGGGGGGGGGGAGG 2946
 DB 23 GGGGGGGGGGGGGGGGGGGGGGG 1

RESULT 435
 LOCUS AZ764518 23 bp DNA linear GSS 16-FEB-2001
 DEFINITION IM056011R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M056011 R, genomic survey sequence.

VERSION A2764518.1 GI:12879563
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0560 row: L column: 11
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 FEATURES
 Location/Qualifiers
 1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="TUGC1M0560111"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid TUGC1M library"
 /note="Vector: PMD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 6.2e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2924 GGGGCGTGGGGGGCGTGAAGG 2946
 Db 23 GGGGGGGGGGGGGGGGGGGGG 1
 RESULT 436
 CDS77045/c 38 bp mRNA linear EST 15-JUN-2004
 LOCUS
 DEFINITION
 Igot1_c12_Q3_088 ESTs from wild-caught Anopheles funestus populations Anopheles funestus cDNA 5', mRNA sequence.
 CDS77045
 ACCESSION
 VERSION CDS77045.1 GI:48718060

KEYWORDS EST.
 SOURCE Anopheles funestus
 ORGANISM Anopheles funestus
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 REFERENCE 1 (bases 1 to 38)
 AUTHORS Beasnsky, N.J., Serazin, A.C. and Dana, A.
 TITLE Towards the transcriptome of Anopheles funestus: a molecular snapshot
 JOURNAL Unpublished (2003)
 COMMENT Contact: Andrew Serazin
 Collins/Beasnsky Lab
 Center for Tropical Disease Research and Training, University of Notre Dame
 317 Galvin Life Science, Notre Dame, IN 46556, USA
 Tel: 5746319321
 Email: nbeasnsk@nd.edu
 These sequences may be of either nuclear or mitochondrial origin.
 FEATURES
 Location/Qualifiers
 1..38
 /organism="Anopheles funestus"
 /mol_type="mRNA"
 /strain="West African"
 /db_xref="taxon:62324"
 /sex="male and female"
 /dev_stage="embryo, larvae, pupae, and adult"
 /clone_lib="ESTs from wild-caught Anopheles funestus populations"
 /note="Vector: LambdaTriplEx2"

Query Match 0.4%; Score 16.6; DB 1; Length 38;
 Best Local Similarity 71.0%; Pred. No. 9.4e+02;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 3310 TTTTCTTGAAGATTATTTTGGACTT 3340
 Db 34 TTTTCTTGTGAGATTATTTTGGAAAT 4
 RESULT 437
 A2786779 19 bp DNA linear GSS 16-FEB-2001
 LOCUS
 DEFINITION
 2M0032C01R Mouse 10kb plasmid TUGC1M library Mus musculus genomic clone UUGC2M0032C01 R, genomic survey sequence.
 A2786779
 ACCESSION A2786779.1 GI:12924882
 VERSION
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0032 row: C column: 01
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0032C01"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 94.4%; Score 16.4; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2313 TGGTGTGTGTGTGTGTGT 2330

Db 1 TGGTGTGTGTGTGTGTGT 18

RESULT 438

AZ626965

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0467E15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 21;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2320 TGTGTGTGTGTGTGTGTGT 2337

Db 4 TGTGTGTGTGTGTGTGTGT 21

RESULT 439

BU054011

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 37
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL048p20"
/tissue_type="whole embryo"

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 21;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2320 TGTGTGTGTGTGTGTGTGT 2337

Db 4 TGTGTGTGTGTGTGTGTGT 21

RESULT 439

BU054011

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 37

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="XL048p20"

/tissue_type="whole embryo"

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0295 row: G column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

source

1. 21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCIM0295G04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42uv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|g14732114|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 6.3e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2329 GTGTGCTGTGTGTGTGTGTG 2349

Db 1 GTGTGTGTGTGTGTGTGTGTGTG 21

RESULT 443
 A1016967 22 bp mRNA linear EST 27-AUG-1998
 LOCUS A1016967/c
 DEFINITION ou27h03.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
 IMAGE:1627541 3' similar to TR:069566 Q69566 ;, mRNA sequence.
 ACCESSION A1016967
 VERSION A1016967.1 GI:3231303
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 22)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 This clone is available royalty-free through INLNL; contact the
 IMAG Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 961 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham
 High quality sequence stop: 1;
 Location/Qualifiers

FEATURES

source

1. 22

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1627541"
 /lab_host="DH10B"
 /clone_lib="Soares NFL T GBC S1"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbH19W, testis NHT, and B-cell NCI CGAP GC81) were mixed and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

Query Match 0.4%; Score 16.2; DB 1; Length 22;

Best Local Similarity 85.7%; Pred. No. 6.6e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2319 GTGTGCTGTGTGTGTGTGTG 2339

Db 21 GTCTGTGTGTGTGTGTGTGTGTG 1

RESULT 444
 PCH303886 22 bp DNA linear GSS 03-APR-2001
 LOCUS PCH303886
 DEFINITION Plasmodium chabaudi genome survey sequence, clone PC4d10.p1t,
 genomic survey sequence.
 ACCESSION AJ303886
 VERSION AJ303886.1 GI:11141349
 KEYWORDS GSS; genome survey sequence.
 SOURCE Plasmodium chabaudi
 ORGANISM Plasmodium chabaudi
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 22)
 Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harris,D.,
 Bowman,S., Phillips,R.S. and Turner,C.M.
 Gene discovery in Plasmodium chabaudi by genome survey sequencing
 Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
 PUBMED 11295179
 REFERENCE 2 (bases 1 to 22)
 Janssen,C.S.
 Direct Submision
 Submitted (06-NOV-2000) Division of Infection & Immunity,
 University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
 bases 477 to 498 (Q1 to Q3).
 Location/Qualifiers
 1. 22
 /organism="Plasmodium chabaudi"
 /mol_type="genomic DNA"
 /db_xref="taxon:5825"
 /clone="PC4d10.p1t"

FEATURES

source

Query Match 0.4%; Score 16.2; DB 1; Length 22;

Best Local Similarity 85.7%; Pred. No. 6.6e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATAT 2843

Db 2 TATATATCATATGTGTATATAT 22

RESULT 445
 PCH303886 22 bp DNA linear GSS 03-APR-2001
 LOCUS PCH303886/c
 DEFINITION Plasmodium chabaudi genome survey sequence, clone PC4d10.p1t,
 genomic survey sequence.

ACCESSION AJ303886
 VERSION AJ303886.1 GI:11141349
 KEYWORDS GSS; genome survey sequence.
 SOURCE Plasmodium chabaudi
 ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE
 AUTHORS Janssen, C.S., Barrett, M.P., Lawson, D., Quail, M.A., Harris, D., Bowman, S., Phillips, R.S., and Turner, C.M.
 TITLE Gene discovery in Plasmodium chabaudi by genome survey sequencing
 JOURNAL Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
 MEDLINE 21192558
 PUBMED 11295179

REFERENCE
 AUTHORS Janssen, C.S.
 TITLE Direct Submision
 JOURNAL Submitted (06-NOV-2000) Division of Infection & Immunity, University of Glasgow, Joseph Black Building, Glasgow G12 80Q, UK
 COMMENT bases 477 to 498 (OL to OR).
 FEATURES
 source Location/Qualifiers
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 /organism="Plasmodium chabaudi"
 /mol_type="genomic DNA"
 /db_xref="taxon:5825"
 /clone="PC4d10.plt"

Query Match 0.4%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 6.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATATA 2844
 DB 22 ATATACATATATATATATATA 2

RESULT 446
 TA300F12P 23 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 300F12, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL490817
 VERSION AL490817.1 GI:11865290
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submision
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRU927/4 GOTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.
 Location/Qualifiers
 1..23
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TRU927"

/db_xref="taxon:5691"
 /clone="300F12"

Query Match 0.4%; Score 16.2; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 6.9e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2817 ATATGATATATATATATATAT 2837
 DB 2 ATATGATATATATATATATTT 22

RESULT 447
 AZ615581 23 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0445F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0445F09 F, genomic survey sequence.
 ACCESSION AZ615581
 VERSION AZ615581.1 GI:11737867
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std. Error: 0.00
 Plate: 0445 Row: F Column: 09
 Seq primer: CGTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers
 1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0445F09"
 /sex="Male"
 /lab_host="E. Coli strain X110-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi:4732114|gb|AF199072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into (Stratagene) cells chemically-competent E. coli X110-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.4%; Score 16.2; DB 1; Length 23;

Best Local Similarity 85.7%; Pred. No. 6.9e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2309 GCTTGGCTGCTGCTGCTGCTG 2329
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 Db 3 GCTATGCTGCTGCTGCTGCTG 23

Search completed: October 28, 2004, 12:38:04
 Job time : 122 secs

